Run on:

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(without alignments)
4526.442 Million cell updates/sec
                                                                             November 5, 2001, 23:47:01; Search time 6769.47 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                     1344157 seqs, 7733874588 residues
                                                 OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	U31462 Lactuca sat	U34817 Nicotiana t	AJ250433 Spinacia	U44133 Arabidopsis	AF288196 Orvza sat	AC003981 Genomic s	U39452 Arabidonsis	AC006932 Genomic s
	ID	LSU31462	NTU34817	SOL250433	ATU44133	AF288196	AC003981	ATU39452	AC006932
	DB	14	14	15	14	13	12	14	12
	Query re Match Length DB ID	1760	1589	1686	1555	1173	133843	2884	89479
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                                                                     A.025064 clone BAO
AC018664 Homo sapi
AX083744 Sequence
AX083745 Sequence
AC03757 Mus muscu
AC009612 Homo sapi
AC005822 Homo sapi
AC005822 Homo sapi
AC018647 Homo sapi
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AL358235 Homo sapi
AL162502 Homo sapi
AC068640 Homo sapi
AC068649 Plasmodiu
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Y13901 Homo sapien
AL589701 Mus muscu
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AC069113 Homo sapi
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AC023779 Mus muscu
AC023427 Mus muscu
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Direct Submission
Submitted (12-JUL-1995) Plant Molecular Physiology, University of Hawaii, 3190 Maile Way, Honolulu, HI 96822, USA
Local Molecular Local Maile May and the Mayaii. 1760 Maile May and Maile May
                                                                                                                                                                                                                                      AC027726 Homo sapi
AC010647 Homo sapi
AL390958 Homo sapi
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Leishmani
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                 AY008297
                                             AC009601 I
AC005804 I
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AF276759
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AC022779
AC023427
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87
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2.8 201978

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NDAWGGYGGSYLYTRSAVLPESITBELGTAAQKVGRDFPFFTTDAPCOGFFPFTFTDAPCOGFFTRSAVLDSTIPELGTAAQKVGRDFPFTFTTDAPCOGFFTRSAVLDSTIPELGTAAQKVGRDFPTFTTDAPCOGFFTRSAVLDSTIPELGTAAQKVGRDFPTFTTDAPCOGFFTFTDAPCOGFFTFTDAPCOGFFTFTTDAPCOGFFTTTTAPCOGFFTTTTAPCOGFFTTTTAPCOGFFTTTTAPCOGFFTTTTAPCOGFFTTTTAPCOGFFTTTTAPCOGFFTTTTAPCOGFFTTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGFFTTAPCOGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         la (bases 1 to 1589)
Bugos, R.C., Hieber, A.D. and Yamamoto, H.Y.
Xanthophyll cycle enzymes are members of the lipocalin family, the first identified from plants
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Submitted (25-AUG-1995) Robert C. Bugos, Plant Molecular
Physiology, University of Hawaii, 3190 Maile Way, Honolulu, HI
96822, USA
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                                                                           NTU34817 1589 bp mRNA PLN 15-JUN-1998 Nicotiana tabacum violaxanthin de-epoxidase precursor (TVDEI),
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/protein_id="AAC50031.1"
/db_xref="GI:1463123"
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98288256
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/organism="Nicotiana tabacum"
/strain="Xanthi"
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Bugos, R.C. and Yamamoto, H.Y.
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/gene="TVDE1"
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                                                       497 TGCGAAGTGCATTTCGAACCCTGCATGTGCCAGCTAATGTTGCTGCTCTCCAGACTTGCAA 556
                                                                                                          843 tgtgggtgaattcccggttccggatcgtaatgcagtggttcaaaaattttaacatgaaaga 902
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663 tgcaaaatgtatagcaaacccatcttgtgcggcaaacgttgcctgtctacagacttgcaa 722
                                                                                             723 caatcgtcctgacgagaccgaatgtcagataaaatgtggtgacttgttcgaaaacagtgt 782
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NMADFNGKWFISSGLNPTFDAFDCQLHEFHLEDGKLVGNLSWRIKTPDGGFFTRTAVQ
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FLYTRSATVPENIYPELINRAAQSVGKDFNKFIRTDNTCGPEPPLVERLEKTVEEGERT
IIKEVEQLEGEIEGDLEKVGKTEMTLFQRLLEGFQELQKDEEYFLKELNKEERELLED
LKMDAGEVEKLFGLALPIRKLR"
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RNIRFNDRKLSCTKFIGASEKLOHSKSPKSGLISCGWEVNSSKVVSNAVIPKKWNLLK
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                                                                                                         Spinacia oleracea mRNA for violaxanthin de-epoxidase (svdel gene). AJ250433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-OCT-1999) Emanuelsson A.K., Dept. of Plant Biochemistry, Lund University, Chemistry Center, POB 117, 221
                                                                                                 21-0CT-1999
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                                                                                                                                                                                                                                                                                                                               Emanuelsson, A.K., Eskling, M. and Akerlund, H.E. Cloning and sequencing of Spinacia olercea violaxanthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.3%; Score 621; DB 15; Length 1686; 72.5%; Pred. No. 1.7e-121;
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/db_xref="G1:6103243"
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                                                                                                                                                                                    svde1 gene; violaxanthin de-epoxidase.
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/country="Sweden"
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                                                                                              797 acgagtgtgcggtttcccgaaagaaatgtgtgccccggaaatcggatgtgggtgaattcc 856
                                                                                                                 cggttccggatcgtaatgcagtggttcaaaattttaacatgaaagactttagtgggaagt 916
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TSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPG
TLYNBUNGTALHYQDDWTILSSKIENRFEDYIFVYRGRNDAMGDYGANVYTRSSVLP
NSIIPELEKAALHYGENFSYFT FTDWTGGFPPALVERIEKTYFEGERIIVKEVEEIEE
EVEKEVEKYGRTEWTLFQRLABGFNELKQDEENFYRELSKEEMGFLDGIKMEASEVER
                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLA
CAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ
                                                                                                                          Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1555)
Bugos,R.C., Hieber,A.D. and Yamamoto,H.Y.
Xanthophyll cycle enzymes are members of the lipocalin family, the first identified from plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYI
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                                                                                                                                                                                                                                                                                                                                        Submitted (02-JAN-1996) Robert C. Bugos, Plant Molecular Physiology, University of Hawaii, 3190 Maile Way, Honolulu,
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72.5%; Pred. No. 1.5e-119;
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/db_xref="G1:1465735"
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Bugos, R.C. and Yamamoto, H.Y.
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PESIYVELLERAAKSYGRDFSTFIRTDNTCGPEPPLVERIEKTVEGGEKTIIREVQEIE
GEIEGEPKTELEEEVTLFKRLTDGLMEVKQDLMNFFQGLSKEEMELLDQMNMEATEVE
KVFSRALPIRKLR
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/db_xref="G1:10181228"
/translation="DEFNECAVSRKKCVPQKSDVGEFPVPDFSALVKNFNMADFNGKW
Molecular cloning and expression of rice violaxanthin de-epoxidase
                                                        Lin,R.-C., Xu,C.-C., Li,L.-B. and Kuang,T.-Y.
Direct Submission
Submitted (18-JUL-2000) Photosynthesis Research Center, Institute of Botany, Chinese Academy of Sciences, Xiangshan, Beijing 100093,
                                                                                                                                                                                                                         Submitted (18-SEP-2000) Photosynthesis Research Center, Institute of Botany, Chinese Academy of Sciences, Xiangshan, Beljing 100093,
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                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa subsp. indica"
/cultivar="Zhenhui-249"
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Lin,R.-C., Xu,C.-C., Li,L.-B. and Kuang,T.-Y.
Direct Submission
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Oryza sativa subsp. indica
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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                                850 gaatteeeggtteeggategtaatgeagtggtteaaaattttaacatgaaagaetttagt 909
                                                                         624 GAATTICCIGCCCCAGACCCTICTGTICTIGIACAGAACTICAACAICTCGGACTITAAC 683
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Schwartz, J., Southwi	Yu,G., Davis,R., Federsp TITLE Direct Submission JOURNAL Submitted (28-JUN-2000) Department of Biology.	REFERENCE 6 (bases 1 to 133843) AUTHORS ECKET,J.R. TITLE Direct Submission JOURNAL SUBMISSION DIRECT SUBMISSION		JOURNAL Submitted (29-JUL-2000) Department of Biology, U Hamilton Walk, Philadelp REFERENCE 8 (bases 1 to 133843)		Liul,S., Mukharsky,N., Ng Schwartz,J., Southwick,A Yu,G., Davis,R., Federsp TITLE Direct Submission JOURNAL Submitted (15-AUG-2000), Department of Biology, U	Hamilton Walk, Phila REFERENCE 9 (bases 1 to 13384 AUTHORS Shinn, P., Brooks, S.,		TITLE JOURNAL	Hamilton COMMENT On Jul 2 FEATURES SOURCE		CDS (2016)		SOO	3803. 3943,4030 // note="similar to EST dbj AN557
CCTGAATCAATAGTACCTGAGCTAGAAAGGGCGGCAAAAAGCGTAGGTCGCGACTTCTCC 540 aatttcataacaacgacaatagttgtgggcctgagcctccattggtggaaaggcttgag 1386	ACGITCATCAGGACGACAACAACACGGGTCCCGAGCCACCTCTGGTGGAGAATAGAG 600		gaagggtttaaggagttgcaacaagatgaagagattttgtgagggagttgagtaaagaa 1566 	gagaaggaaattctgaatgaacttcaaatggaagcgactgaagttgaaaagctttttggg 1626 	627 ogogogitacogaitaggaaacitagataaaiticgaigaitgaitcagacaaiaiai 1684 	AC003981 133843 bp DNA PLN 05-JAN-2001 Genomic sequence for Arabidopsis thaliana BAC F22013 from	AC003981	thale cress. Arabidopsis thaliana Enkaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta Magnoliophyta; eddicotyledons; core eudicots; Rosidae; eurosids II. Brassicales:	1 (bases 1 to 133843) Khan,S., Brooks,S., Buchler,E., Chao,Q., Johnson-Hopson,C., Kim,C. Shinn,P., AltefilH., Bei,Q., Chin,C., Chiou,J., Choi,E., Conn,L., Conway,A., Gonzales,A. Hange, N. Hown B. Woo, T. F., B.	Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thenseri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Phan, P., Sakano, H., Schwartz, J., Southwick, A., Thensel, M., Vaysberg, M., Yu, G., Federspiel, N.A., Phologie A., S., Sakano, M.,	incologies, and Eckel, J.R. Genomic sequence for Arabidopsis thaliana BAC F22013 from chromosome I	ished ses 1 J.R.	Direct Submission Submitted (08-JAN-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA	(bases 1 cker,J.R. irect Subm ubmitted (epartment amilton Wa	4 (bases 1 to 133843) Coker, Mr. Direct Submission Submitted (18-APR-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 5 (bases 1 to 133843)
Qy 1327	Db 541 Qy 1387	Db 601 Qy 1447 Db 661	Oy 1507 Db 721	Qy 1567 Db 781	Qy 1627 Db 841	RESULT 6 AC003981 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS		TITLE	AUTHORS	JOURNAL	KEFEKENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL REFERENCE

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uehler, E., Chao, Q., Johnson-Hopson, C.,
1, H., Bei, B., Chin, C., Chiou, J., Choi, E.,
nzalez, A., Hansen, N., Howing, B., Koo, T.,
Li, J., Liu, A., Liu, J., Liu, S.,
, Pallin, C., Pham, P., Sakano, H., Schwartz, J.,
A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R.,
is, A. and Ecker, J.
coks, S., Buehler, E., Chao, Q.,
In, S., Kim, C., Altafil, H., Bei, B., Chin, C.,
In, L., Conway, A., Gonzalez, A., Hansen, N.,
I.B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Nguyen, M., Palm, C., Pham, P., Sakano, H.,
I.A., Thaveri, A., Toriumi, M., Vaysberg, M.,
splel, N., Theologis, A. and Ecker, J.
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University of Pennsylvania, 38th Street and
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n.S., Kim,C., Altefi,H., Bei,B., Chin,C.,
n.L., Conway,A., Gonzalez,A., Hansen,N.,
B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J.,
Nguyen,M., Palm,C., Pham,P., Sakano,H.,
A., Thaveri,A., Toriumi,M., Vaysberg,M.,
spiel,N., Theologis,A. and Ecker,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKSOKPLRSYFYGKOIVFGDSQDESFRRSSAITAQTTLRIGTAQKWWEKGLKDNMREI
SSAQELVDSLTNAGDKLVVVDFFSPGCGGCKALHPKICQFAEMNPDVQFLQVNYEEHK
SWCYSLGVHVLPFFFFYRGSQGRVCSFSCTNAIIKKFRDALAKHGPDRCSLGPTKGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MAKYNEIAKKKREAKADRKRAIHGDPLTNKLKTRTPVPSVSGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRKLLRKWRREQKDMVEKGLVTMEDVEMASAQAASEDSKKSPRKFSVKKSLKLNKLNN
                                                                                                                                                      EBHELSAGIQDLIKLERLOTELTERSGROPTFAOMASAAGVDOKSLRORIHHGTLCKD
KMIKSNIRLVISIAKNYQGAGMNLQDLVQEGCRGLVRGAEKFDATKGFKFSTYAHWI
KQAVRKSLSDQSRMIRLPFHMVEATYRVKEARKQLYSETGKHPKNEEIAEATGLSMKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mayathcrtspchdrirffssddgighlgitrkringtflkil
ppigsadlrttggrssrplsafrsgfskgipdiyplpsknelkeltaplllklygyla
cafliypsadaydalktcacllkgcrielakcianpacaanyaclqtcnnrpdstecq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKCGDLFENSYVDEFNECAVSRKKCVPRKSDLGEFPADDFSVLVQNFNISDFNGKWYI
TSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPG
VLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSYVDLKKAAMKDMEAGPDFDLEMASTKADKMDENLSSFLEEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVÄREMGLISETLARIEQYHEESKGVHKAESVKSLRNKISNEIVSGLRKAKSIKSKLE
EMDKANKEIKRLSGTPVYRSRTAVTNGLRKKLKEVMMEPGGLRQKMMSEYKETVERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTEVISKTSLFLGACGNHHRVDDFSFSPVSFGGFGLKKSFSCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTVTGEHANDEMIEKIITDNAGGEEFLTRAIQEHGKGKVLETVVEIQDRYDAAKEIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLLELHQVFLDMAVMVESQANELKTAKSHQRNSRKWMCIGIIVLLLIILIVVIPIITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKELVALAANKELNFTYTPKPVPVEKEAATPDSNPSLPVPLPSMSSNDEKTLVSAGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(13219. .13280,13397. .13477,13866. .13932,
/translation="mSSCLLPQFKCPPDSFSIHFRTSFCAPKHNKGSVFFQPQCAVST
SPALLTSMLDVAKLRLPSFDTDSDSLISDRQWTYTRPDGPSTEAKYLEALASETLLTS
                                                                 DEAVVVAAAAEAVALARAAVKVAKDATLFKNSNNTNLLTSSTADKRSKWDQFTEKERA
GILGHLAVSDNGIVSDKITASASNKESIGDLESEKQEEVELLEEQPSVSLAVRSTRQT
                                                                                                                              ERKARRAKGLEKTASGIPSVKTGSSPKKKRLVAQEVDHNDPLRYLRMTTSSSKLLTVR
                                                                                                                                                                                                                                                             LMAVILLSPKPPRSLDQKIGMNQNLKPSEVIADPEAVTSEDILIKEFMRQDLDKVLDSL
                                                                                                                                                                                                                                                                                         GTREKQVIRWRFGMEDGRMKTLQEIGEMMGVSRERVRQIESSAFRKLKNKKRNNHLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to thioredoxin-like 1
gb|AAD35005.1|AF144387_1; similar to ESTs gb|T46281.1,
dbj|AV442467.1, and dbj|AV549179.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14113. .14274))
/note="unknown protein; similar to EST dbj|AV530752.1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to receptor protein kinase-like protein
                                                                                                                                                                                                                                                                                                                                                          join[5386. .5601,5679. .5845,6111. .6207,6312. .6706,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(7702. .7832,7895. .8606))
// note="similar to s-syntaxin-like protein
gplack0648.11Acc009540_25; similar to ESTs
dbjjav556140.1, dbjjav566414.1, and dbjjav55627.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similar to ESTs dbj AV522839.1,
                                                                                                                                                                                                                                                                                                                                                                                         6798. .7311)
/note="similar to viiolaxanthin de-epoxidase emb[cAB59211.1; similar to ESTs gb[AI994713.1, db] aV440942.1, and db] aV521985.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental/product="F22013.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="F22013.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental/product="F22013.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAF99754.1"
/db_xref="G1:9802552"
/transl-t:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAF99782.1"
/db_xref="G1:9802580"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF99783.1"
/db_xref="G1:9802581"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAF99753.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGKKKKNQKASGEKSADCMLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:9802551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="F22013.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFGKALPIRKVR"
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CDS

emb|CAB66905.1;

CDS

CDS

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ELSSLETIILGYNGFMGEIPEEFGKLITRLOYLDLAVGNLTGQIPSSLGQLKQLTTYYL
YQNRLTGKLPRELGGMTSLVFLDLSDNQITGEIPMEVGELKNLQLLNLMRNQLTGIIP
SKIAELPNLEVLELMQNSLMGSLPVHLGKNSPLKWLDVSSNKLSGDIPSGLCYSRNLT
                                                                                                                                                                           LOALDISNNAFESSIPKSLSNITSLKVIDVSVNSFFGTFPYGLGMATGLTHVNASSNN
FSGFLPEDLGNATTLEVLDFRGGYFEGSVPSSFKNLKNIKFLGLSGNNFGGKVPKVIG
                                                                                                                               /translation="MAIPRLFFLFYYIGFALFPFVSSETFQNSEQEILLAFKSDLFDP
                                                                                                                                                       SNNLQDWKRPENATTFSELVHCHWTGVHCDANGYVAKLLLSNMNLSGNVSDQIQSFPS
                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1041 tttctttactcgatctgctgtgcaaacatttgttcaagatccagatcttgtgggggact 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1142 -----ggtacatattatcttcccaaatcgaaacaaaccgatgattacatat 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1190 tcgtatactaccgaggtcgaaacgacgcatgggatggatacggtgggtccgtgatctaca 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6845 TIGTATACTACCGIGGCGAAACGAIGCTIGGGAIGGAIATGGIGGIGGIGCTAGTATACA 6904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1250 cccgaagcccgacactccccgaatcgatcatcccaaacctacaaaaagcagccaaatccg 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6905 CGAGAAGTICTGTATTACCCAATAGCATTATACCAGAAACTGGAAAAAGCAAAAAGCA 6964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1310 tgggtcgagactttaacaatttcataacaaccgacaatagttgtgggcctgagcctccat 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6965 TAGGCAGAGACTICAGCACATICATIAGAACGGATAACACATGTGGTCCTGAACCTGCGC 7024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7025 ICGIGGAGAAIIGAGAAGACAGIGGAAGAAGGIGAAAGGAIAAICGIAAAAGGGIIG 7084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    984 ggaaaatg---ataaacttgttgggaacttaacatggcgcataaaaactttggatggtgg 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6785 ATGATITITGCAGGIATATCCIGICAICAAGAIAGAGAATAAACCTGAAGACIATAIAT 6844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6425 AGACCCTTCTGTTCTTGTACAGAACTTCAACATCTCGGACTTTAACGGGAAGTGGTACAT 6484
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6305 ATATCAGATTAAATGTGGGGATCTGTTTGAGAACAGTGTTGTTGATGAGTTCAACGAGTG 6364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           864 ggatcgtaatgcagtggttcaaaattttaacatgaaagactttagtgggaagtggtatat 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  924 aacaagtggtttaaatcctacatttgatgcatttgattgtcaacttcatgagtttcata 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6485 TACAAGTGGCTTGAATCCAACCTTTGATGCCTTCGACTGCCAGCTGCATGAGTTCCACAC 6544
                                                                                                                                                                                                                                                                                                                                                                                                           744 atgtcagataaaatgtggtgacttgttcgaaaacagtgtggtggaccaattcaacgagtg 803
                                                                                                                                                                                                                                                                                                                                                               94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1370 tggtggaaaggcttgagaaaacagcggaagagggcgagaagttgttgataaaagaagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      804 tgcggtttcccgaaagaaatgtgtgccccggaaatcggatgtgggtgaattcccggttcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6365 IGCIGIGICGAGAAAAAGIGIGTICCTAGAAAAICIGAICICGGAGAAITICCIGCCC
                                                                                                                                                                                                                                                                                                                  Length 133843;
                                                                                                                                                                                                                                                                                                                  Score 406.4; DB 12; Length
Pred. No. 6.6e-76;
0; Mismatches 246; Indels
dbj|AV528375.1, and dbj|AV541093.1"
                                             /evidence=not_experimental
/product="F22013.7"
                                                                                    /protein_id="AAF99755.1"
/db_xref="GI:9802553"
                            /codon_start=1
                                                                                                                                                                                                                                                                                                                      20.5%;
                                                                                                                                                                                                                                                                                                                                                                       Matches 668; Conservative
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1142 -----
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                      Best Local
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Eukaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

( (Dases I to 2596)

Lukowitz, M., Mayer, U. and Jurgens, G.

Cytokinesis in the Arabidopsis embryo involves the syntaxin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKSIKSKLEEMDKANKEIKRLSGTPYYRSRTAVTNGIRKKLKEVMMEPGGLKOKMMSE
YENTVERRETTYGEHANDENIEKIITDNAGGEEFLTRAIOEHGKGKVLETVVEIQDR
YDAAKEIEKSLIELHQVFLDMAVWPESQGEQMDEIEHHVINASHYVADGANELKTAKS
HORNSKWMCIGIILLILLILLIVYIPVIPIITSFSSS"
569 c 582 g 900 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSSFLEEBAEYVKAEMGLISETLARIEQYHEESKGVHKAESVKSLRNKISNEIVSGLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MNDLMTKSFMSYVDLKKAAMKDWEAGPDFDLEMASTKADKMDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-OCT-1995) Wolfgang Lukowitz, Lehrstuhl fuer
Entwicklungsgenetik, Universitaet Tuebingen, Spemannstrasse 37-39,
D-72076 Tuebingen, Germany
1490 tgittcagaggitgcitgaagggittaaggagitgcaacaagaigaagagaattligiga 1549
                                                                                 1550 gggagttgagtaaagaagaagaaggaaattctgaatgaacttcaaatggaagcgactgaag 1609
                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana syntaxin related knolle mRNA, complete cds.
                      7205 GAGAGITAAGTAAAGAAGAAGATGGAGTTTTTGGATGAAATGAAATGGAAGTGAAG 7264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2789 TGCTCTCCAGCAAAAGTGTCTTAGAAAATCTGATCTCGGAGAATTTCCTGCCC 2730
                                                                                                                                                                                                                                                                                                                           09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744 atgicagataaaatgiggigactigitcgaaaacagigiggiggaccaaticaacgagig 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 804 tgcggtttcccgaaagaaatgtgtgcccggaaatcggatgtgggtgaattcccggttcc 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.4%; Score 404.8; DB 14; Length 2884; 66.2%; Pred. No. 1.1e-75;
                                                                                                                                                              1610 tigaaaagcititigggcgcgcgttaccgattaggaaacttagataaa 1657
                                                                                                                                                                                                        7265 TIGAAAATIGITIGGAAAGCTITGCCAATCAGGAAGGTCAGGTAGA 7312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                           N.I.d
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/db_xref="G1:1184167"
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DNA 11-UCT-2000
Arabidopsis thaliana BAC T27G7 from chromosome
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                       2729 AGACCCTTCTGTTGTACAGAACTTCAACATCTCGGACTTTAACGGGAAGTGGTACAT 2670
                                                                                                                 984 ggaaaatg---ataaacttgttgggaacttaacatggcgcataaaaactttggatggtgg 1040
                                                                                                                                                                                                                                                              1041 tttctttactcgatctgctgtgcaaacatttgttcaagatccagatcttcctggagcact 1100
                                                                                                                                                                                                                                                                                     2609 AGAAGGTGACAACAAGCTTGTTGGAAACATCTCTTGGAGAATAAAGACCCTAGACAGTGG 2550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1142 -----ggtacatattatcttcccaaatcgaaaacaaacccgatgattacatat 1189
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                                                                                   924 aacaagtggtttaaatcctacatttgatgcatttgattgtcaacttcatgagtttcatat 983
864 ggatcgtaatgcagtggttcaaaattttaacatgaaagactttagtgggaagtggtatat 923
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                1 (bases 1 to 89479)
Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C.,
Khan, S., Kinc., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E.,
Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T.,
Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S.,
Mukharsky, N., Nguyen, M., Palin, C., Pham, P., Sakano, H., Schwartz, J.,
Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G.,
Federspiel, N. A., Theologis, A. and Ecker, J.R.
Genomic sequence for Arabidopsis thaliana BAC T27G7 from chromosome
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Submitted (25-NOV-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
6 (bases 1 to 89479)
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//note="unknown protein gb|AAD21437.1; similar to EST</pre>
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Submitted (03-JAN-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
(bases 1 to 89479)
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/db_xref="taxon:3702"
/chromosome="1"
Brassicales; Brassicaceae; Arabidopsis.
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Ecker, J.R.
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HLPYSLIHGLNNNHPSSGFINQDGSSSFDFGELEEATVLOGVKYRNEEARPPPLGGGG
GATTLEMFPSWPIRTHQTLPTESSKSGGESSDSGSANFSGRAESQQPESPMSSKHLM
LOPHNNMANSSTSGLPSTSRTLAPPRPSEDKVLIIIIIIIIIIIFF"
join (11373. 11439, 11990. .12266, 12331. .12619, 12691. .12921, 13105. .13503)
                                                                                                                                                                                                                      .5796))
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FHPISQKIHPFSFLNSITVVVLLIGLISFLFMRHLKNELRSYSIGDEEERKEAGWKLV
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TSIVAGYTSTSFHSQFEGNKQKRSVRLAGILYPVPFFIILSVLNTVAITYGATAALPF
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GSTSSYGRYVLELARCFSTAEVEDNDRPAMDIGGPTNIRHVAHVTFDRFDGFLGLPSE
FEPDVPRKAPSARFHIIILEVFGSATVFGVSTESMQLSYDSRGNCVPVILLLLQSRLY
DOGGLQAEGYFRITGENSEEEFVREQINKGIIPDGIDVHCLAGLIKVLVVIAWFRELP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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NLALVFAPNMSQMADPLTALMYAVQVMKLLKSLTEKTVREREASSSVVDRRCSKEAED
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complement(join(14188. 14733,14829. 14985,15122. 15253,
15357. 15945,16043. 16083,16294. 16439))
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                                                                                                                                       LINYHEIPOGGHLIVHYDGICDTFILRALLKREBOOKLYKIN"

complement (join(1334, .2261,3126, .3268,4062, .4283,
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/note="similar to basic leucine zipper protein gil2865394;
similar to ESTS gb|H76000, gb|Aa651460"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAERCFIWMAGFRPSDLIKILVSOMDLLTEQOLMGIYSLQHSSQOAEEALSQGLEQLQ
QSLIDTLAASFYIDGMQQMAVALGKISNLEGFIRQADNLRQCTVHQLRRILTVRQAAR
CFLVIGEYYGRLRALSSLWLSRPRDSVSEQTRAAALAELRLISKQDPDSRLITADAGA
IPYLAETLYSSSHSSQENAAATLLNLSITSREPLMSSRGLLDALSHALRHHDTTTSPA
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LYPMRRSTMISLGAIPALFSLIVKDSRCGIVEDATAVMAQVAGCEDSEDGMRRVSGAN
VLADLLDPCTGSSLRIKENSVGALLNLARCGGAAARSEVAAAVASGADEGAMEGIVYV
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                                 IEELEVYLLFYDRSGYGASDSNTKRSLESEVEDIAELADQLELGPKLSGVAFVAPVVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKAVVOOLESSRIKLSQLEOELQRARSQGLFWGGGGPPGPNITSGAAIFDMEYGRWLE
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                                                                                                         ERNVFDTLRDDFMVCFGQWDFEPADLSISTKSYIHIWHGKEDKVVPFQLQRCILQKQP
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COMPLEMENT (191n) (5889 . 6646, 7024 . 7106, 7608 . .770

8179 . 8287, 8565 . 8654, 8797 . .8890, 9113 . .9184))

/note="hypothetical protein"
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/note="putative multispanning membrane protein
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/evidence=not_experimental
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/product="T27G7.4"
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1285 aacctacaaaaagcagccaaatccgtgggtcgagactttaacaatttcataacaaccgac 1344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 others
                                                                                                                                                                                                                                      1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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                Sequence 14 from patent US 5670367.
166494
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
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synthetic construct
artificial sequence.
1 (bases 1 to 1141)
Kunst, L. and Clemens, S.
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                                                                              I66494.1 GI:2724471
                                                                                                                                                                                                        Unclassified.
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                                                                                                                                                                              Unknown.
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                   DEFINITION
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                                                       SGEDHEWWWRYVELYCTARTESTOTTCED*

Join(17065...17069.17482...17701,17921...18116,18380...18528)

Anote="putative ribosomal procein LiO gi13860277; similar to ESTS gb1741143, gp1886781, gb1AA721952, emb[234253, combcantarior ribosomal procein LiO gi13860277; similar pb180489, gb1806781, gb1AA721952, emb[234253, combcantarior ribosomal procein LiO gi13860277; similar pb1806781, gb1806781, gb1AA721952, emb[234253, combcantarior ribosomal procein LiO gi13860277; similar procein L
                                                                                                                                                                                                                                                                                                                                                                                                    DKRESGSYKLPHIPPREMKICHLGDAGHVEBAEKMGLENMDYESLKKLNKKKLVKKL
AKKYHAFLASESVIKOIPRLLGPGLNKAGKFWLQLIFHFGNLSMEEKQIFONVOMSVN
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join (19189) 19347,19428 19605,19741 19885,20087 20143,
20295. 20409,26600. 21079,21145. 21201)
//note="similar to yeast dcpl q1|3169719; similar to ESTS
gb|H37036, emb|227040, gb|R90173, gb|A1999440.1"
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VFLGGFVPFSAVVLEWHQLYASLWGFKIYTSPGIMLFTFIVLIFLSSSVGIILTYIQL
                                                                                                                                                                                                                                                                                                                                                                             /translation="MSKLQSEAVREAITTITGKSEAKKRNFVETIELQIGLKNYDPQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RILSAYSKVNOKPKASSSKSEFEELEKKPTMAYMDGFLEPSSTARDAPDDPAFVNFFS
STMNLGNTASGSASGPYQSSAIPHQPHQPHQPTIAPPVAAAAPPQIQSPPPLQSSSPL
MTLEDNNPEYISSNSNIHTDLVTPSFFGPPRMAQPHLIPGVSMPTAPPLNPNNASHQ
QRSYGTPVLQPFPPPPPSLAPAPTGPVISRDKVKEALLSLLQEDEFIDKITFTLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSQNGKIIPNLDQNSTRLLNLTVLQRIDPYIEEILITAAHVTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFNIELSOWSRKDVEGSLFVVKRLLLSIFNYVYLIFNRLLKSDWILFFVSFRSTOPRF
QFIVMNRRNTDNLVENLLGDFEYEVQGPYLLYRNASQEVNGIWFYNKRECEEVATLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement(join(24182. .26122,26212. .26300,26373. .26501,
65645. .26839))
//notte="similar to inerleukin-1 beta convertase homolog A precursor spl955865"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLPMEHPLPLSFVLPNPATLPGLALGFIDGNFVDLODLLLRAST
LTSNLNHDGSDLNDRLLHLRTDLTKHAVSWISTSLSAKVSLEDLRLNLESLLCLHIEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89281 TGCTGTGTGGAGAAAAAGTGTGTTCCTAGAAATCTGATCTCGGAGAATTTCCTGCCCC 89340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             744 atgtcagataaaatgtggtgacttgttcgaaaacagtgtggtggaccaattcaacgagtg 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 tgcggtttcccgaaagaaatgtgtgccccggaaatcggatgtgggtgaattcccggttcc 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        864 ggatcgtaatgcagtggttcaaaattttaacatgaaagactttagtgggaagtggtatat 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  924 aacaagtggtttaaatcctacatttgatgcatttgattgtcaacttcatgagtttcatat 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 143.2; DB 12; Length 89479;
Pred. No. 3.5e-20;
0; Mismatches 68; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/product="T27G7.7"
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                                                                                                                                                                                                                                                                                                                  /protein_id="AAF22886.1"
/db_xref="G1:6664304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAF22887.1"
/db_xref="GI:6664305"
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/db_xref="G1:6664321"
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                                                                                                                                                                                                                                                                                                                             1090 WINHAKRGAIMCWYWYWIGINRRWCMRIYAMRIWYIRSNANWSCAIKBMWWIMKWYAIKY 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 ggtgacttgttcgaaaacagtgtggtggaccaattcaacgagtgtgcggtttcccgaaag 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 MWAAGASUBUTYNWCWRMTYMGKTMTNNNNNKAWYYRTKTVAWCNNRYYYDTAVWTBKR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 gttcaaaattttaacatgaaagactttagtgggaagtggtatataaacaagtggtttaaat 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      940 cctacatttgatgcatttgattgtcaacttcatgagtttcatatggaaaatgataaactt 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               645 agaatgcaggattgagcttgcaaaatgtatagcaaacccatcttgtgcggcaaacgttgc 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            705 ctgtctacagacttgcaaca----atcgtcctgacgagaccgaatgtcagataaaatgt 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 NNNNNRACVWHKHKMWRWTWKYMWKAACNNNNBKAMYMRVAWMMYSRDTTNTDWMMWTSD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 WBWHWYTVDYTMMRAWNNNNNNWRBCKTTSWMWWMDHMNTHCTYGNNTWGSAYBMAAMS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 NYKYCYAYBWYYBMYMGKHHWBWWRRABHRSWNMWWVKCRNKYMVSWHYHAMRYBKWABA 191

    1141
/note="consensus sequence of A.t., L.a., and B.n. FAE1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 gattcttgaaaagcaatggagacaattcatacaattggctatcgtattggtttgcacatt 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585 tgttatcgttcccagagttgatgccgttgatgctcttaaaacttgtgcttgtttactcaa 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         490 CNAKSMWRGNNWRAMKMWWAANNDAGAMDHWTYWMGNNTMWMRRAWKMMNMAWCRRAYCC 431
                                                                                                                                                                                                                                                                                                                                                                             110 atactgtacgccacttcgaacgctacaatgtttgaaaaaagacgcagattttacaaagac 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 ggagaagataataagetteaagtaeteegategteaggtggeetttggaageeaacaac 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 tggctatggctctttctcttcacactgtatttctctgcaaagaggaagccctcaatttat 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 atgcaagatcaccatgtaatgaaaggtttcacaggagtggacaacctcctaccaacataa 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               850 AWWIRINNNNNNNNNACRNIRIWWABWKHSWCNNNNNNNNNNNNNNNTWCHYITANABBC 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 ataagacaagttettteteagattetagecattgeaaggataaatete----agatatg 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            730 NMTNNNNNMWACTNNNNNMWKAYYAHATNNWGCWWNNTDARRTNNTTVMRRWMTNTK 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670 TRWYSTTRRHHYTGATNNNNNNNNNNNNNNSCCTCTRMMTMRWTMKGDGMTVRKKVKW 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 RDTICIYVDVWADSWVWWYANWMRCRDVTYTRNNTYCKSYAHSYWYWSNNAMWYRRYSAR 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 NWSSMARWITRNNWWMSGBVRMRWAGTMWWRHWNNNTDTRYYWWKRWARBITTVYDSM 491
                                                                                                                                                                                                                                                                                50 ataaggagtetaattteeettgtacaatttteeaatttetteeteegeeacatatat 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     970 AAAGNKWGCMAAMATWGBWWADTAGKMCNNNNNWTTDVRRMAMKAKNNNNNAYWTACY 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1030 RTAWYAMWCAWRINNNMWCATNGYAKSCATINNAMWYATTRWAAYAAAKWARWAGNIMRMYG 971
                                                                                                                                                                                  Query Match 3.0%; Score 60.4; DB 10; Length 1141; Best Local Similarity 11.5%; Pred. No. 0.0087; Matches 114; Conservative 360; Mismatches 509; Indels 10; Gaps
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/db_xref="taxon:32630"
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ECTORABLEARS IRENVELIRIKKLILOERNTSTAATEAQLTRVQEAYEDLLQKNQGIL
DTAHNAFLSQVNELKAELSESKKAVSLRTQLGDVSTLQITIKEFOYRVEDLEKERKL
LISDSYDRLLENNLDSSHQPLDSSHQPHWSTELTGKQLPPQVCPLLDOMGTALEETKVF
RQATNKAAQDGKLKFODTDILYQHEGBESLQSTATVASSPEELCELAAQPTLLEPQTD
QRESSEPRAQDENDLSQVLSELQVSHAETTLELEKTRDMLLLQRKINNCYQEELEATL
TKADRENRDHEEKLERLNHLLDFKNSRIKQLEGILREHGEFSEQLKOAYGTLEPPSL
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FETHCTPLSTGPQPLYDFTSQYVVQADYLLLHYLQGTSVRLDLHQAMASEYHYLATGW
FETHCTPLSTGPQPLYDFTSQYVVQADYLLLHYLQGTSVRLDLHQAMASEYHYLATGW
FETHCTPLSTGPERVHGLATLAGAGGEDLGVLEYWRLCLLPLFRPSLQACANKRKRQAYLS
VSVLGARRVQSNESRSETWAPQNELRYTTRPCGLRSRRLGRQPSPYWYRRFTFPDH
DTIILPASSNPYFRODALFPYLLYTSDLOQYLRREALSVYVFDDEDPEPGSYLGRAQVP
LLPLAONKSIKGDFNLTDSGERSNGSIKVQLDWKSHYLAPEGFQMSERERFERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases I to 4788)
Hong, D.H., Yue, G., Adamian, M. and Li, T.
Retinitis Pigmentosa GTPase Regulator (RPGR)-interacting Protein Is Stably Associated with the Photoreceptor Ciliary Axoneme and Anchors RPGR to the Connecting Cilium (2001)
J. Biol. Chem. 276 (15), 12091-12099 (2001)
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EEKKECQDIGYAYLELWQIFQSGKDILEQELEIVSPRNQAIQIGRLKVSLQAAAALHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MQHLLEYMPEDLPVRDTDSSPLLKGTSGKNVRAQPHLGRMNQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNCRRLHLHEEPTLVKEPSPKQRDKNRRRRTNVQRSTTTQPDLRTLAVLQEPERRRRP
WVSASPSPSAPPRAPVPGRKAHVQRLCPSTAVGSAQERVHAGERLPHTAGPNDRRSHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-SEP-2000) Berman-Gund Laboratory, Harvard Medical School, Massachusetts Eye & Ear Infirmary, 243 Charles Street,
190 VGCNNNWKDRMAHHHWCAINNNMMWWYAYMHHMKKGKAAWINNKTABRDDHBAHVKIY 131
                                                                                                                                                                                                                                                                                      10-APR-2001
                                                                                                                                                                                                                                                                                         Mus musculus RPGR-interacting protein mRNA, complete cds. AY008297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 4788)
Hong, D., Yue, G., Scimeca, M.S. and Li, T.
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                                                                                      1000 gttgggaacttaacatggcgcataaaaactttg 1032
                                                                                                                                               130 WYWRYDYWCAMCWMNAKAKVRTAMKHMWYYTDR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAG22857.1"
/db_xref="GI:11496167"
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Submitted (30-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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Homo sapiens chromosome 2 clone RP11-4117, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 156610)
Waterston, R.H.
The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1416 gataaaagaagctgtagagatagaagaagagttgaaaaagggtggagaaggttagaga 1475
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On Aug 26, 2000 this sequence version replaced gi:9755476
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      7: gap of unknown length
4: contig of 8867 bp in length
5: contig of 40357 bp in length
6: contig of 40357 bp in length
7: gap of unknown length
7: gap of unknown length
8: gap of unknown length
8: gap of unknown length
8: gap of unknown length
9: contig of 4114 bp in length
9: contig of 8570 bp in length
                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI mouse BAC library 23"
55239 a 43169 c 44386 g 58583 t 601 others
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Web site:http://genome.wustl.edu/gsc/index.shtml
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Local Similarity 51.0%; Pred. No. 0.099;
nes 133; Conservative 0; Mismatches 128;
                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-348M1"
                                                                                                                                                                                                                  Location/Qualifiers
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Waterston, R.H.
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152065:
152165:
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201978:
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Consensus quality: 200626 bases at least Q30
Consensus quality: 200212 bases at least Q30
Consensus quality: 201212 bases at least Q30
Estimated insert size: 2012080; agarose-fp estimation
Betimated insert size: 201728; sum-of-contigs estimation
Quality coverage: 10.36 in Q20 bases; agarose-fp estimation
Quality coverage: 10.53 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 14335: contig of 14235 bp in length
* 14336 40527: contig of uknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus clone RP23-348M1, WORKING DRAFT SEQUENCE, 7 ordered
                                       1356 gcctgagcctccattggtggaaaggcttgagaaaacagcggaagaggggggagaagttgtt 1415
                                                                                1416 gataaaagaagctgtagagatagaagaagagattgaaaaagaggtggagagaggttagaga 1475
                                                                                                                                               1476 tactgagatgactttgtttcagaggttgcttgaagggtttaaggagttgcaacaagatga 1535
                                                                                                                                                                                                                                              0; Gaps
  0; Mismatches 128; Indels
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HTG; HTGS_PHASE2; HTGS_DRAFT
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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Matches 133; Conservative
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AC079533/c
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consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11882: contig of 11882 bp in length 11982: gap of unknown length 27033: gap of unknown length 27033: gap of unknown length 46701: contig of 19568 bp in length 46801: gap of unknown length 69429: contig of 22628 bp in length 69429: contig of 22628 bp in length 95671: gap of unknown length 134805: contig of 26442 bp in length 134805: contig of 38734 bp in length 134905: gap of unknown length 136775: gap of unknown length 136775: gap of unknown length 14136: contig of 1210 bp in length 14136: contig of 5161 bp in length 14136: contig of 6307 bp in length 147843: contig of 6867 bp in length 156610: contig of 8667 bp in length
                                                                                                                                                                                                                                                                                                                        Quality coverage: 5.90 in Q20 bases; agarose-fp Quality coverage: 6.00 in Q20 bases; sum-of-contigs
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------ Project Information -------
                                                                                                           Sequential vector; prairies, or reads Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 15355 bases at least Q40 Consensus quality: 153849 bases at least Q30 Consensus quality: 153849 bases at least Q20 Insert size: 150000; agarose-fp Insert size: 155710; sum-of-contigs
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134906...136175
/note="assembly_name:Contig4"
136276...141436
/note="assembly_name:Contig7"
141537...147843
/note="assembly_name:Contig8"
147944...156610
/note="assembly_name:Contig9"
/note="assembly_name:Contig9"
/note="assembly_name:Contig9"
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/note="assembly_name:Contig11"
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/note="assembly_name:Contig12"
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                                           Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
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                     Center project name: H_NH0004117
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Submitted (28-AUG-1999) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA 2 (Dases I to 39987) Seattle, Mayler, P.J., Sisk, E., Cawthra, J., Handley, F., Vogt, C., Robertson, L., McDonagh, P., Ivens, A., Nguyen, D., Munden, H., Sunkin, S.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC009601 39987 bp DNA INV 20-JUN-2000
Leishmania major chromosome 35 clone L165 strain Friedlin, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I (bases I to 39987)
Myler,P.J., Sisk,E., Hixson,G., Kiser,P., Rickel,E., Hassebrock,M., Cawthra,J., Marsolini,F., Sunkin,S. and Stuart,K.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="611.6; ORFdelta; predicted using Glimmer, Testcode and CodonUsage, Glimmer predicts second ATG as start
                                                                                                                                 97312 AAGAGGAGGAGGAGGAGGAGGAAGAAGAATATGAACAGGATGAGAGAGCAGAAAG 97253
                                                                                                                                                                           1448 ttgaaaaagaggtggagaaggttagagatactgagatgactttgtttcagaggttgcttg 1507
                                                                                         1388 aaacagcggaagaggggggagagattgttgataaaagaagctgtagagatagaagaagagg 1447
                                                                                                                                                                                                                                                                     1508 aagggtttaaggagttgcaacaagatgaagagaattttgtgaggagttgagtaaagaag 1567
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/note="has similarity to nrk kinase, contains kinase
                                            Gaps
2.8%; Score 55.4; DB 75; Length 156610; 52.9%; Pred. No. 0.14;
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/prodouct="lesshmania NIMA-related Kinase 1"
/protein_id="AAF77207.1"
/db_xref="G1:8573034"
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                   1568 agaaggaaattctgaatgaacttcaaatggaagcgactgaagttg 1612
                                            106;
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                                               0; Mismatches
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4345. 5115
/gene="611.8"
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/chromosome="35"
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                                               Matches 119; Conservative
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/note="predicted using Glimmer, Testcode and CodonUsage

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/translation="MHLFALPLLSLVAGLMLAVPGRGASKCFVTDATPTVPFGLELCY
MHSHNACCLPGNDKDILTAYSALVPKGGGCVAGSQRIYTSLYALRQYLCLPCDPKEPL
YRFESVKGDIVDGGLVPPSTNSIAGEQTWRICRSFLYGKEGTRKGLMSDDGSRYAECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF77213.1"
/db_xref="G1:8573040"
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/translation="MIMCECTFASLCGNPCLPDPRWLGALYCLRLWGYACVRDPARPS
VEVARRVPRRADDQQPARKACFLSFCGWGSARGLSSATTELDSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMATPPPPSFRTSLÄHLSSIPRYFVSSHQHRRGTHAGAVYMTTGCRVIRNLTFTVLVL
AALALLCHCRKRAYARNTVGFLHAAAGAGGGGERVLWVALDGLQHADAARGVKRQYVL
FTNEYKPADRLSAESSDQHLLSLVERQFSIRLLRPVRFIYLRPALTRNLSGDAYPRLT
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AMTQRVRSGEVSHTNSPTVAWNPMLRCAKVYYYGVFSLLYRCMGFFPNVYLTNSSWTQ
NHVQSIFWPRACIRLYPPCDVAGFAAGSQPPALRNNRIVSVGQFRPEKNHMLQLVAFH
                                                                                                                                                                                                                                                                    VIVSSCMSTPVFNITAASFQSPSPSCVASNELIIPSVTFRGSPNPALEMLSMVTQSIP
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GKCVIGLHTWRDEHFGIVLLEYLAAGCIPLGHRSGGVELDILNSPDLGFLAVTAEEYA
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DYIKRVLGGASSADYEALQQENARLRAEVELLKKQLSGQAQ"
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LLRLAWNQFDPYFIATFGIDSPDAVVIDMRYPTVPASQLSQLHQLPINNLTWSPQNAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prosite profile Prokar_Lipoprotein and Prosite pattern
Prokaryotic membrane protein, contains Pfam Glycos Transf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains COG0438 Glycosyltransferases I, contains Prosite profile Prokar_Lipoprotein and Prosite pattern
                                                                                                                                                                                                                                                                                                                                                                               /note="predicted using Glimmer, Testcode, CodonUsage" 20647. .>22497 /gene="L165.1"
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/gene="L165.3"
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23148. .>23402
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/note="contains ALDEHYDE_DEHYDR_CYS Aldehyde dehydrogenases cysteine active site (from Prosite)"
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                                                                                                                                                                                                                                                                                             DFQIVIVNDSDPNYDYDKTPCFGRDATATVASAALSRWVSAVALALLLWL"
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                                                                                                             /protein_id="AAF77212.1"
/db_xref="G1:8573039"
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/db_xref="GI:8573041"
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/db_xref="G1:8573043"
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/gene="L165.1"
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/gene="L165.2"
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/gene="L165.2"
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/gene="L165.3"
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/gene="L165.4"
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                                                                     /note="contains Zinc finger domain, contains similarity to deoR family (bacterial regulatory proteins)"
                                                                                                                                                                                                                                                                          HVANGETRPVPWSVCTFFTQGKCLRDGCSFFHGTQAQLEELHASGAPVYRPODYMKIA
VPPAEYLNADGSIATHLSIAAVPWTPALHVVHGPTVSHENAVNSFQPVLVMQPNSQAI
APTWFASQGRTAHSTPSHFAEYANAIITSQMPTHSAATVLQPTLHTVQPTTFYQAANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="contains ATP/GTP binding domains, has similarity to
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NLGKITLDVLPRRLLRSSQSSIPLLESGSSTAATDGAQAAAGDDDGYAWTHHVETSDV
VERYPDHMRDVLQSLKGPLHHDGVPRRHQAPSVKNLDSPSDCTVISRKKGPISRVTAF
                                                                                                                                                                                                                                                 /translation="MSQQQWTPDQRRQQIAEMLRNKGVICRDFLFTGRCSRSPTCPYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAF77209.1"
/db_xref="GI:8573036"
/translation="MRATLRQCNVFDPAFMRKVKRTLSAYKGSMETSAKKSMSREAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIDEKGAAMYLGHMQSAANMLADKVKDADFILEIRDARLPFTTENPNIRKLTAGKPRL
IIFNKAELSNEDSNRAIQEYYERNGAFALFTSARRCWRDVVEAVQRFTTHILPPLPYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLCRGRGGDREDSVPLLATPRAFSGSRAADVPLISHDSAAEACAHVMORLLEHEARLL.
DALARATARIEATHVAATAENGELEALRARMNELTRVVTSGSSWWLKPPPEASAAQPP
EGVSSATARFAEARALAYEKTVQALNNELALLHENNAALSRARTREVDMLKRHMAEDQ
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IRRRIISPGLVQEYAYWLRHGGLVYTVSDVAELEEWMVQCLDDSPLFRRLAEAELCTP
EHKQVLEIVTGASEDAQRTARKGLQKHFAVHMRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVAHVGLVVGMPNVGKSTLINSLRLAHEYQFHREDFRRSRSPETVSITPGTTRGMKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLSKDPPVVLYDTPGLTLPGCFTKESGLKLAACGIIPTNDVSLPQGMVARYIYDILVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MANASAAASDELRRTQQYLVEVIDECVFVERQRELAERRLSSQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MVNPVVEFVDVGCAFGGMLFSLAAVFPATCMMGLEIRPKVVSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETQKTLVNDLFVVLHDVCRYTSTIEDAILPALLRTLPASSPARQQLLQSRNMVRDALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="predicted using Glimmer, Testcode and CodonUsage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted using Glimmer, Testcode and CodonUsage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="predicted using Glimmer, Testcode and CodonUsage,
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Testcode weak in 5' end"
17686. .>18486.
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methyltransferase domain, has Blastp similarity to
hypothetical protein W02B12.10 from Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glimmer predicts second ATG as start codon"
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                                                                                                                                                                                                                                                                                                                                                                     LLAQPQQHFAPVPQLNTPQQHQLTQQALGSRVYFHIQPH"
                                                                                                                                                                                     /protein_id="AAF77208.1"
/db_xref="GI:8573035"
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/db_xref="GI:8573037"
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/db_xref="GI:8573038"
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                                                                                                                                                                /product="611.8"
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13052. .>14005
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/gene="611.11"
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/gene="611.11"
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/gene="611.12"
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/gene="611.12"
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            4345. .>5115
/gene="611.8"
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Myler,P.J., Sisk,E., Hixson,G., Kiser,P., Rickel,E., Hassebrock,M.,
Cawthra,J., Marsolini,F., McDonagh,P., Stuart,K.D., Cunningham,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-0cT-1998) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA (pases 1 to 42160) Myler, P.J., Sisk, E., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M., Cawthra, J., Marsolini, F., McDonagh, P., Stuart, K.D., Cunningham, M.
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                     VMSA ICCSAGSPFEMDHRLEPVDFKLVFKSQADQDARTAFNLKHTDKVPQTIFLDGLM
EAPKASALVSFHNILTPAHVNNLAGTEQFLREWCRAPADGDRHRQLKLCFSSLLEKQT
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ISPAQQLVMKQYSGRIPPMHPLGQPLMVDSWSELVELHKPDNEYQLLPRRARNNNAYA
                                                                                                                                                                                                                                                                              1371 ggtggaaaggcttgagaaaacagcggaagagggcgagaagttgttgataaaagaagctgt 1430
                                                                                                                                                                                                                                                                                                                           gtttcagaggttgcttgaagggtttaaggagttgcaacaagatgaagagaattttgtgag 1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1551 ggagttgagtaaagaagaagaaggaaattctgaatgaacttcaaatggaagcgactgaagt 1610
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                                                                                                                                                                                                                                                                                                                                                                             AC005804 42160 bp DNA INV 31-MAY-2000 Leishmania major chromosome 35 clone 6.1.1 strain Friedlin,
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                                                                                                                                                                         DB 4; Length 39987;
                                                                                                                                                                              2.8%; Score 55; DB 4; Length 399
51.4%; Pred. No. 0.16;
/ative 0; Mismatches 120; Indels
                                                                  HLFLGTNAAPGRELLNYAKGKNIFVYAKKGMAFQYVP" 27619. .27753
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                                                                                                                         /gene="L165.5"
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1 (bases 1 to 42160)
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VIRSHHEKAVIALCTORREFEKCLANGIARLSIQPMLIGRYGLIGAMYQRLSTLYTLGW
ALNAFITVMADTFALEGYTKRWYCWSAVGGSVFALLYGLLPAKESSAKPAALHWIT
ALEMBNIDVERVALSEQITKRRPAAGPALVSWWWGTALIGIMISSVILGPLSDNGLAH
FGVYITAAILLLSGLI-FYFNLFEBERNKAARLEDAMIEFLOKTKSASSESTAGSPPSP
HKLOGHLTIDNRVEEEDDNVDEQEAAAMDAQGFVRPRMDTYLCGAVEMNRDVILRNWR
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IEPNSTMELLKSQRMAYKQWHKRYNDALLKKIYYCKABAYMDAKSRTQLFDVSVAAVR
DGFERMEVLLNGRIWSSQPQKWMSFTPTEWEDQIRQAF"
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RAAEGSTDVIPVARVKAKSSLTRPVHATPTSIPSTRSLWVEGSSVLNODVGHASAALT
HISDCVAQERELKVEMPRARIAKIRALRALARANVKYNEMOSFIDSTRSSRARSTSSVGGKVMSDT
LAVARCSVITNTLVGTVQNFRARTRSRLCAARGPVSGLQLFPNIAGGESDRETLSLY
SSAPGGAESSVNARSTYVSPNHSVSDYLEEEFSVSRIKQLYFDYFDCEAVSISSAVASGSD
MSIFAYSAASSISRPSSPVSRGDHSSFSHCASTTM"
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SSSPSMPFSSNAAMYSRDPALRLRKVLQSSVDVVFDKGTADALLSSFAGEYNPNMEAY
MGEALKVLRPGGLLFLISINSEDVLSPYALSADDGLKSFHLAYTDVIELGAHDLRHLR
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FNAILYLSLPGVLNTFYVAKPSCLPDGPHFSYTFYNAMNGFLGNIAGIGGTIVFTHLF
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MPMMMLMCRIAPRGSESMVFALLASIYHLGTSTSSAIGYLLMETIWPVVTQGQCDYSN
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QAGGSLSVAPRADSALTAPTANRLIRNEAALGGVDQIYQRLGENFNRTDILRKDVRKL
LEEKLVRAVQAQFDGAYRDEETGRGPLTSRSSLLPVLKHYQHGHHPLLRVSKSARELY
TDACACLORYYLTPLEDDYAVADIPSELATVVFELVYRRAIKVIQLDTSFFADPTKLF
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FIYR.REELLDGYVDAKGALERESLKEYARSMRRTEWFPSVDCTVHESTTNVLYFHKTL
LTSFYGSLRIVLYGSVIGANADYESCQEVEDY ITRGVMGAVDDLQVLAEAAAELQOEA
LAKRHHTKSNSLNLLTSDVRLSVDIFMINNLCFLEDNYRREACFTTRLAATEPPPKS
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DVKFWDVAQENITLTIEEMAKAARCYHPPFILPAVLTGKESSWEAIARCMDYLVYADD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPGRYRVPSAPESPPPQGAKYVHPVSAHVLRAAPFLGYIPVFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains similarity to T.brucei ESAG10, contains transporter motifs and multiple transmembrane domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains SAM-dependent methyltransferase domain"
                                                                                                                                                            /note="contains a Proline-rich region (PRO_RICH), contains recA family and SURF1 domains (Pfam)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Biopterin Transporter 1"
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7085. .>8977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:8122320"
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3675. >^^70
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gene

CDS

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VLRDISASIDDSLPLFAVPETSSPDSTPSMLRGAEVSAVVAAEVDKAVREGRAIIVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENLSFAGFHRFLEPSFQLSTGAVILGLVMEICGGEAETDASHAYVQALPNLHPVYSTE
RLTVLAADIGDLAKGVRGIPTVXVARYTTVADNVCLSVFLHDIVVKRIIAELKRRGRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSSRGGSFAFAPQVQEKYNTWNILVLGAPQVGKSLFINSYRAAITNTFRWPAAPVGIS
GFYGTTTVAPFPNHARQPTWLCIDTPGSLYTEKHAVLLEKLTEGMPWKTKLKGPNALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRQIKDISPIAANKAHQCIIVVPATDLIEDDGLINTLLWRNRYRPAGGVADIIFYLKG
LISSLRTLMDDASPFVVVTKMDKVGGARNSSACAALVSILGQCVPVNHVYFTAAVENR
ALLATGRTWVLESSTKQNLVRLHEDICLAVQWRNQVDAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSAEHDSPSLAHVRSGDVLFMNRKCLAMKDPLGMLLCGLSKTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFDHVGMFLKISEBELRKYPBARKRLAVLSPSGTYVLETNMRGITLYAABGRVSRTTA
NEVASRSVNVGDTEKQQEAQEAFLEQMETMYSTPYENEVFHLIPSICSPPDKMDRVRA
AHKFNTLRLEVAALTEMANTHPSQAEVYRAVAHKYQHAQSFLLSTYFPHLASTSPTDA
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VYKTCVDLPEGEESPESNPREHMYVLTTLVGRNPTTAAFVATRGSDPSEKVVAKFVML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAVNWITGHYWIDGVNNADKMYCSELICNLWHRVGLTVGYVPASSIRPFDFLENERFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSGRPPVGSLRAAAASSEPLPSRWVVQSNTRSDVIPNLWFRVFSSGVLFAVCAVPCA
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GSHTCSNLVDTRHPYYCTVVLYGLSALVAHLATTPLRNANISYHFGPVLPGPISMRRL
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LIGAFVATLVTDALFYPIATWATRRFWSDLYKPQRPPSFGRSLYAGYRYRLLSNLVIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORFgamma; predicted using Glimmer, Testcode and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains similarity to GTP binding proteins"
                                                                                                                                /note="ORFI; predicted using Glimmer, Testcode and
                                                                                                                                                                                                                       /gene="611.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Leishmania NIMA-related Kinase 1"
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                                                                                          /gene="611.1"
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/qene="611.3"
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EIMQQVLYGKYDPCPCPVSSSMQALLDPLLSKNPTERPTTQQLLQTEFLKYVANLFQD
LVRHSETISPNDRAEILKQLQBSGERAPLPSSIRYGYMTSQYTHGGYLKYGSDCRWK
KRYFYIGDGQLLISLSENPENDGVAPKSVNLETVGDVFPVPEVYSQKHPNQLVLMFNN
GQKIIAYANTWEDDRWISKFHRACGM"
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                                   SDSVSLDVASSFCGTPYYLAPELWERKRYSKKADMWSLGVILYELLTLHRPFKGPSQR
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NDDRQATYARSELHCLAACKHFGIVKHFDDFKSDDK1.LLIMEYGSGGDLNKQIKQRLK
                  EHLPFQEYEVGLLFYQIVLALDEVHSRRMMHRDLKSANIFLMPTGIIKLGDFGFSKQY
                                                                                                                                                                                                                                      /gene="611.8"
/note="contains Zinc finger domain, contains similarity
                                                                                                                                                                             /note="predicted using Glimmer, Testcode and CodonUsage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1431 agagatagaagaagaggttgaaaaagaggtggagaaggttagagatactgagatgacttt 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1551 ggagttgagtaaagaagaaggaaattctgaatgaacttcaaatggaagcgactgaagt 1610
                                                                                                                                                                                                                                                                                                                                                                                                  1371 ggtggaaaggcttgagaaaacagcggaagagggcgagaagttgttgataaaagaagctgt 1430
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Pred. No.
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/gene="611.8"
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Conservative
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Job time: 11236 sec
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November 5, 2001, 23:49:01; Search time 313.48 Seconds (without alignments) 3967.950 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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N_Geneseq_0601:*

| SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Oliaphicleotide D2	Oligonucleotide D2		Oligonucleotide D1		Oligonucleotide D1	Partial mouse WRN	Human secreted pro		Arabidopsis thalia	ß			Arabidopsis thalia	Arabidopsis thalia	O	p160	ecept	P. falciparum eq5	Borrelia burgdorfe	LEMMI 10 cDNA. LV	Genomic clone G11F	Plasmodium falcipa	P. falciparum tran	Arabidopsis thalia	Methanococcus jann		Retinoblastoma bin	Nucleotide sequenc	Murine LOBO homolo	Arabidopsis thalia	Human secreted exp	Borrelia burgdorfe	Plasmodium falcipa
AAF58262	AAF58262	AAF58255	AAF58255	AAF58238	AAF58238	AAX83007	AAX41515	AAC46213	AAC35071	AAC47631	AAZ23891	AAZ23896	AAC50687	AAC47245	AAT89346	AAT89345	AAQ11415	AAF26289	AAX20248	AAQ32658	AAQ55750	AAA70157	AAQ67190	AAC48719	AAV21209	AAV74906	AAZ86968	AAA64139	AAZ23895	AAC50661	AAA43753	AAX20389	AAA70212
22	22	22	22	22	22	18	20	21	21	21	20	20	21	21	18	18	12	22	20	13	15	21	15	21	19	18	21	21	20	21	21	20	21
936	936	938	938	244	244	51259	425	1120	1123	827	49999	49999	2169	2638	3211	3901	15464	5340	910715	507	1505	9408	9636	2601	1664976	1484	6002	20000	49999	1530	456	591	1998
•	5.9	•													$^{2.1}$		2.1		٠	2.1	2.1	2.1	2.1	2.1	$^{2.1}$	2.1	2.1	2.1	2.0	2.0	2.0	2.0	2.0
116.6	16.	116.6	16.	9.09	59.5	44.8	44.6	43.4	43.4	43.2	42.8	42.8	42.6	42.6	42.4	42.4	42.2	41.8	41.8	41.6	Ϊ.	•	•	41	4	0	0	0	o.	0	φ.	39.6	о О
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; lettuce; ss.
                                                                                                                                                                                                                                                                                                           /*tag= d
/note= "bases 147-149 are illegible in Fig 1"
misc_difference 186..189
                                                                                                                                                                                                                                                                                                                                         /*tag= e /note= "bases 186-189 are illegible in Fig 1" misc_difference 226..227 /*tag= f
                                                                                                                                                                                                                                                                          /*tag= c
/note= "bases 105-110 are illegible in Fig 1"
                                                                                                                                                                                                    /*tag= a
/note= "bases 26-29 are illegible in Fig 1"
                                                                                                                                                                                                                                      /*tag= b
/note= "bases 66-72 are illegible in Fig 1"
misc_difference 105..110
                                                                              Romaine lettuce violaxanthin de-epoxidase cDNA.
                                                                                                                                                                             Location/Qualifiers
            BP.
                                                                                                                                                     Lactuca sativa L. cv. romaine.
         AAT66241 standard; cDNA; 1981
                                                        28-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                               misc_difference 147..149
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                                                                                                                                                                                                                         misc_difference 66..72
                                                                                                                                                                                        misc_difference 26
                                 AAT66241;
AAT66241
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Wed Nov

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A cDNA clone (AAT66241) codes for the 55 kDa violaxanthin de-epoxidase (VDE) (AAM09874) of romaine lettuce. VDE was purified from romaine lettuce chloroplasts and 2 tryptic peptides were used to develop primers (see also AAT662445), which amplified a partial VDE sequence. The amplified sequence was then used to screen a lettuce cDNA library, and the 1981 bp DNA sequence was identified. VDE nucleic acids (see also AAT6624-43), in sense or antisense orientation, can be used in genetic constructs, pref. also contg. a plastid translocation sequence, to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases photosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding plant violaxanthin de-epoxidase - used to modify the sensitivity of a plant to light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.6%; Score 1894.6; DB 18; Length 1981; Best Local Similarity 97.4%; Pred. No. 0; Matches 1931; Conservative 0; Mismatches 49; Indels 2; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
/note= "bases 226-227 are illegible in Fig 235..1656 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1981 BP; 608 A; 337 C; 433 G; 577 T; 26 other;
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                                                                                                                                                                                                                                          96US-0023502
95US-0006315
                                                                                                                                                                                                          96WO-US18291
                                     /*tag= g
235..609
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610..1653
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                                                                                                                                                                                                                                                                                           (CALJ ) CALGENE INC.
                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-281036/25.
                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW09874.
                                                      transit_peptide
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07-NOV-1995;
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                                                                                                                                                                                                                                                             taagcnnnnaagtactccgattgtcaggtggcctttggaagcc-acnnactggctatggc 239
                              tgtgggttcgaattttacccaccacaagttttgtcctaccataattgggataaggagtct 60
2; Gaps
                                                               1 tgtgggtttgaattttacccaccacnnnntttgccctaccataattgggataaggagtct
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1200 ccgaggtcgaaacgacgcatgggatggatacggtgggtccgtgatctacacccgaagccc 1259
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                        gcttgcaaaatgtatagcaaacccatcttgtgcggcaaacgttgccgtctacagacttg
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1440 agaagaggttgaaaaagaggtggagaggttagagatactgagatgcttgtttcagag
                                    gttgcttgaagggtttaaggagttgcaacaagatgaagagaattttgtgagggagttgag
                                                                                                                                                                                   gtgataaacgtgtttgtgatttgtttattggcttaaaattgtagaatagcttttttaatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tobacco violaxanthin de-epoxidase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 42..1478 /*tag= a e 42..443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              photoprotection; transgenic plant; xanthophyll; lettuce; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana tabacum L. cv. xanthi.
                                                                                                                                                                                                                                                                                                                                                                                              AAT66242 standard; cDNA; 1589
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444..1475
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(VDE) (AAW09875), an enzyme that catalyses the de-poxidation of violaxanthin to zeaxanthin and antheraxanthin. VDE nucleic acids (see also AAT66241, AAT66243), in sense or antisense orientation, can be used in genetic constructs, pref. also contg. a plastid translocation sequence, to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                963 tcaacttcatgagtttcatatggaaaatgataaacttgttgggaacttaacatggcgcat 1022
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                                                                                                                                                                                                                                          cDNA clone (AAT66242) codes for tobacco violaxanthin de-epoxidase
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                                                                                                                                                     \mathsf{DNA} encoding plant violaxanthin de-epoxidase - used to modify the sensitivity of a plant to light
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        Query Match
        32.5%;
        Score 643.8;
        DB 18;
        Length 1589;

        Best Local Similarity 71.8%;
        Pred. No. 6.3e-154;

        Matches 862;
        Conservative 0;
        Mismatches 327;
        Indels 12;

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                                                                    Yamamoto
                                                                                                                                                                                                        Disclosure; Fig 2; 41pp; English.
95US-0006315
                                                                 Bugos RC, Rockholm DC,
                                  (CALJ ) CALGENE INC
                                                                                                 WPI; 1997-281036/25
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07-NOV-1995;
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                                                                                                                                                                                                                                                                                                   1383 tgagaaaacagcggaagaggcgagaagttgttgataaaagaagctgtagagatagaaga 1442
                                                                                                                                                                                                                                                       gcttgaagggtttaaggagttgcaacaagatgaagagaattttgtgagggagttgagtaa 1562
                                                                                                                                                                                                                                                                1563 agaagagaaggaaattctgaatgaacttcaaatggaagcgactgaagttgaaaagcttt 1622
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1083 agatetteetggageaetttataateatgaeaatgagtttetteaetaeeaagatgaetg 1142
                                   1143 gtacatattatcttcccaaatcgaaaacaaacccgatgattacatattcgtatactaccg 1202
                                                                      1263 actececegaategateateceaaacetacaaaageagecaaateegtgggtegagaett 1322
                                                                                                                           1097 tttgcctgaaagcattataccggagttgcaaaccgcagctcaaaaagttgggcgtgattt 1156
                                                                                                                                             1323 taacaatttcataacaaccgacaatagttgtgggcctgagcctccattggtggaaaggct 1382
                                                                                                                                                                                                                                     1277 agaagta------gagaaggtgagagataaagacaagtcaccttattcagtaaact 1324
                                                     977 gtatattttgtcatccaaagtagaaaatagtccagaggattacatatttgtgtgtactataa 1036
        Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; lettuce; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis violaxanthin de-epoxidase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana cv. columbia.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAT66243 standard; cDNA; 1555 BP
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                                                                                                                                                                                                                                                                                                                                                   DNA encoding plant violaxanthin de-epoxidase - used to modify the sensitivity of a plant to light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.8%; Score 610.2; DB 18; Length 1555; 72.5%; Pred. No. 2.2e-145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A cDNA clone (AAT66243) codes for Arabidopsis violaxanthin
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                                                                                                                                                                                                         Bugos RC, Rockholm DC, Yamamoto HY;
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96WO-US18291
                                                      96US-0023502
95US-0006315
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Matches 805; Conservative
                                                                                                                                                   (CALJ ) CALGENE INC.
                                                                                                                                                                                                                                                                         WPI; 1997-281036/25.
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07-NOV-1996;
                                                            06-AUG-1996;
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                                                                                    Cgaaacgacgcatgggatggatacggtgggtccgtgatctacacccgaagcccgacactc 1266
                                                                                                cccgaatcgatcatcccaaacctacaaaagcagccaaatccgtgggtcgagactttaac 1326
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aaaacagcggaagagggggaaagttgttgataaaagaagctgtagagatagaagaaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Electron-transfer group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF58252 standard; DNA; 936
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                                    The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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           Example 6; Page 127; 159pp; English.
                                                                                                            monitoring gene expression.
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                                           Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                             (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                        26-JUL-2000; 2000WO-US20476.
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                 Oligonucleotide D1835
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                                                           gene expression; ss
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                                                         1801 tttacaaaaaattgattgtctattggtagccaagaggttcacgaaaagactgaaagggt 1860
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5.9%; Score 116.6; DB 22; Length
Best Local Similarity 0.7%; Pred. No. 4.7e-20;
Matches 5; Conservative 446; Mismatches 260; Indels
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                                                                                                Example 6; Page 127; 159pp; English.
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Best Local Similarity 0.8%; Pred. No. 4.7e-20;
Matches 5; Conservative 421; Mismatches 235; Indels
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                                                                                                                    Electron-transfer group; ETM; mismatch; genotyping;
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AAF58257 standard; DNA; 936 BP
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5.9%; Score 116.6; DB 22; Length 936;

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1321 tttaacaatttcataacaaccgacaatagttgtgggcctgagcctccattggtggaaagg 1380
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                  1381 cttgagaaaacagcggaagagggcgagaagttgttgataaaagaagctgtagagatagaa
                                                               1441 gaagaggttgaaaaagaggtggagaaggttagagatactgagatgacttLgtttcagagg
                                                                                                             Electron-transfer group; ETM; mismatch; genotyping;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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               (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                         monitoring gene expression.
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Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%; Score 116.6; DB 22; Length 936;
Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
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                                                                      AAF58259 standard; DNA; 936 BP
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group, useful as labels in allowing repeat analyses on
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1681 atatatagtcatatggattatgtagatactagagaaaacccaaaaaaacttttgtatacg 1740
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                                                                                                                                                       Electron-transfer group; ETM; mismatch; genotyping;
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Query Match 5.9%; Score 116.6; DB 22; Best Local Similarity 0.7%; Pred. No. 4.7e-20; Matches 5; Conservative 446; Mismatches 260;
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1861 cttgccggtttgcgggttaggccaaattttttgggggcgggatcggtcttgatcgggtttt 1920

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1921 totttaaaaacatgtattttttataaatgatgagttattttcaatttttggctaaaaaaa 1980

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                      Example 6; Page 128; 159pp; English.
                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC
            26-JUL-2000; 2000WO-US20476.
                                              99US-0145695
                                                            17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                           monitoring gene expression.
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                                                                                                                                                                                                                                        a single surface
                                                26-JUL-1999;
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Oligonucleotide D1876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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5; Conservative 446; Mismatches 260; Indels
Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                      (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                AAF58255 standard; DNA; 938 BP
                                                                                                                                                                                                                                                                     26-JUL-2000; 2000WO-US20476.
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                                                                                                                                                          Oligonucleotide D1876
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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1691 atatggattatgtagatactagagaaaacccaaaaaaacttttgtatatacgtgataaacgt 1750
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                                                                                           1571 aggaaattctgaatgaacttcaaatggaagcgactgaagttgaaacttttgggcgcg 1630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electron-transfer group; ETM; mismatch; genotyping;
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detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                          Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
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Search completed: November 6, 2001, 02:55:37 Job time: 11196 sec

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                                                                                November 5, 2001, 23:48:41; Search time 166.68 Seconds (without alignments) 2691.702 Million cell updates/sec
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Sequence 3, Appli
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 Compugen Ltd
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US-08-74-959A-8
US-09-357-014-8
US-09-357-014-6
US-09-357-014-6
US-08-10-15-26-1
US-08-323-170B-1
US-08-781-891-208
US-08-660-309-3
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US-08-6007-005-17
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US-08-463-483A-1
US-08-471-046A-1
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US-08-405-496A-27
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-08-973-273-4
US-08-147-777-3
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                                                                                                                                                                                                                                               351203 seqs, 113238999 residues
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                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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No.
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Sequence 2, Appli
Sequence 1, Appli
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Sequence 20, Appl
Sequence 20, Appli
Sequence 1, Appli
  Sequence 1,
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Patent No. 6015939
GENERAL INFORMATION:
APPLICANT: CALGENE, INC.
TITLE OF INVENTION: METHODS RELATED THERETO
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
US-08-470-566B-1

US-08-465-334-1

US-08-460-334-1

US-08-785-420-1

US-08-78-420-1

US-08-699-103B-1

US-08-973-462-2

US-08-973-462-2

US-08-973-462-1

US-08-973-462-1

US-08-973-462-1

US-08-778-698-20

US-08-757-669A-20

US-08-446-855A-1

US-08-446-855A-1

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OPERATING SYSTEM: Macintosh 7.5
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MOLECULE TYPE: CDNA to mRNA
  6049
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                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 95616
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STRANDEDNESS:
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                                                 1141 tggtacatattatcttcccaaatcgaaaacaaacccgatgattacatattcgtatactac 1200
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US-08-747-574-2
Sequence 2, Application US/08747574
; Sequence 2, 6015939
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                 PLANT VDE GENES AND
METHODS RELATED THERETO
                                                                                                                                                                                                      Diskette, 3.50 inch, 1.40 MB
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/747,574
FLING DATE: No. 6015939ember 7, 1996
CLEASIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,502
FILING DATE: AUGUST 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,315
FILING DATE: No. 6015939ember 7, 1995
ATORNEY/AGENT INFORMATION:
NAME: Donna E. SCHAFER
REGISTRATION NUMBER: 34,719
                                                                                                                                                                                                                                      Macintosh 7.5
                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/747,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-633
                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
                                                                                 ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,
APPLICANT: CALGENE, INC.
TITLE OF INVENTION: PLANT
TITLE OF INVENTION: METHC
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1589
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Best Local Similarity 71.8%
Matches 862; Conservative
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STRANDEDNESS: single
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                        677 IGTIGGIGACTITCCIGIACCIGAICCCAGIGTICTIGICCAGAAGTITGACAIGAAAGA 736
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TITLE OF INVENTION: PLANT VDE GENES AND
TITLE OF INVENTION: METHODS RELATED THERETO
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/08747574
; Patent No. 6015939
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
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                                                                Diskette, 3.50 inch, 1.40 MB
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,502
FILING DATE: August 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,315
FILING DATE: NO. 6015939ember 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. S
                                                                                                                                     FILING DATE: NO. 6015939ember 7, 1996 CLASSIFICATION: 435
                                                                                                Macintosh 7.5
                                                                                                                 SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       36,924
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TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
                                                                               Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA to mRNA US-08-747-574-3
                                                                                                                                                                                                                                                                                                                                                                  NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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EDNESS: single
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                   OPERATING SYSTEM:
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             COUNTRY:
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1447 gttgaaaaagaggtggagaaggttagagatactgagatgactttgtttcagaggttgctt 1506
1027 actttggatggtggtttctttactcgatctgctgtgcaaacatttgttcaagatccagat 1086
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                               804 ACCCTAGACAGTGGATTCTTTACTAGGTCAGCCGTACAAAATTCGTGCAAGATCTTTACTAGG 863
                                                                                                 924 ATCCTGTCATCAAAGATAGAGAATAAACCTGAAGACTATATTTTGTATACTACCGTGGG 983
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHAINER, F. 6
APPLICANT: FALANER, F. 6
APPLICANT: FALANER, F. 6
NUMBER OF SEQUENCES: 52
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STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/232,463
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MEDIUM TYPE: Floppy
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Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Fu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
                               APPLICATION NUMBER: 26-AUG-1991
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
APPLICATION NUMBER: US/07/935,313
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                     REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                 , CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                  linear
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1446 ggttgaaaaagaggtggagaaggttagagatactgagatgactttgtttcagaggttgct 1505
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Patent No. 596224
GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
                   E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: US/08/781,891
FILLING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INPORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
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60 State Street, Suite 510
                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 51259 base pairs
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET.
CITY: Boston
...mF: Massachusetts
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CORRESPONDENCE ADDRESS:
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                                                                                      STATE: Washington
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                                                                                                                                 98104-7092
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                USA
                ADDRESSEE:
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                                                                                                              COUNTRY:
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ADDRESSEE:
STREET: 60
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TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 42.4; DB 2; Length 3211; Best Local Similarity 47.7%; Pred. No. 0.11; Matches 124; Conservative 0; Mismatches 136; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
         SOPTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                             APPLICATION NUMBER: US/08/574,959A FILING DATE: 19-DEC-95
ATTORIET/AGENT INFORMATION:
                                                                                                           NAME: Mandragouras, Amy E.
RECISTRATION INDMERS: 36,207
REFERENCE/DOCKET NUMBER: DN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-541
INFORMATION FOR SEQ ID NO: 8:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09357014 Patent No. 6291645 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                            LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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LOCATION: 439..3157
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                                                                                                                                                                                                                                                                                                                      linear
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US-09-357-014-8
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1375 gaaaagcttgagaaaacagcggaagagggcgagaagttgttgataaaagaagctgtagag 1434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1435 atagaagaagaggttgaaaaagaggtggagaaggttagagatactgagatgcttgttt 1494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 42.4; DB 4; Length 3211;
47.7%; Pred. No. 0.11;
tive 0; Mismatches 136; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFARA: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: LAHIVE & COCKFIELD 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08574959A Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                     LENGTH: 3211 base pairs
                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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Matches 124; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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us-09-075-375a-1.rni

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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
                                                                                                                                                   TELEPHONE: (617)227-7400
TELEPKX: (617)27-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            LENGTH: 3901 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/07915246
; Patent No. 5401836
                                              FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PatentIn Release #
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                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA
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Best Local Similarity 47.75
Matches 124; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-357-014-6
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US-07-915-246-1
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TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3901;
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
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2.1%; Score 42.4; DB 2;
Best Local Similarity 47.7%; Pred. No. 0.12;
Matches 124; Conservative 0; Mismatches 136;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND USES THEREFOR
                                                               APPLICATION NUMBER: US/08/574,959A FILING DATE: 19-DEC-95 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09357014 Patent No. 6291645 GENERAL INFORMATION:
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STATE: Massachusetts
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS TOCATION: 439..3847
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                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-574-959A-6
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1375 gaaaggettgagaaaacagcggaagagggcgagaagttgttgataaaagaagctgtagag 1434
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APPLICANT: Baszczynski, Chris L.
APPLICANT: Fallis, Lynne
APPLICANT: Bellmare, Guy
APPLICANT: Bolvin, Rodolphe
TITLE OF INVENTION: A BRASSICA REGULATORY SEQUENCE FOR
TITLE OF INVENTION: ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
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47.7%; Pred. No. 0.12;
tive 0; Mismatches 136; Indels 0
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION:
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STREET: 500 W. Madison St. 34th Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 439..3847
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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; LOCATION:
US-08-323-170B-1
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                                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
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APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen, Pfs230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1491 gtttcagaggttgcttgaagggtttaaggagttgcaacaagatgaagagaattttgtgag 1550
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,246
FILLING DATE: 19920716
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/08323170B
; Patent No. 5733772
                                                                                           ATJUAN...

RAME:
REGISTRATION NUMBER: 52,-
REGISTRATION NUMBER: 91 P
TELECOMOUTCATION INFORMATION:
TELEPHONE: 312 707-8889
TELEFAX: 312 707-8155
; INFORMATION FOR EQQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1611 tgaaaagctttttgggcgcgcg 1632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: Somatic
TISSUE TYPE: Root
                                                                             ATTORNEY AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica napus
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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1389 aacagcggaagagggcgagaagttgttgataaaagaagctgtagagatagaagaagaggt 1448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 2.1%; Score 41.2; DB 1; Length 9636; Best Local Similarity 51.6%; Pred. No. 0.34; Matches 94; Conservative 0; Mismatches 88; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,170B FILING DATE: 13-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                   NAME: Quine, Jonathan A. REGISTRATION NUMBER: P41,261
REFERENCE/DOCKET NUMBER: 015280-113100US
TELECOMMUNICATION INFORMATION:
                                                                                                          FILING DATE: 12 C4 1224

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409

FILING DATE: 29-7AN-1993

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 208, Application US/08781891
Patent No. 6090620
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEED and BERRY LLP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             9636 base pairs
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Yu, Chang-En
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 149..9556
                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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APPLICANT: Fu, Yir
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STREET: bocc
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CITY: San Diego
STATE: California
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US-08-460-309-3
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US-08-125-077-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 119; Indels , 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          2.0%; Score 39.6; DB 3; Length 16442; 48.3%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
                                              APPLICATION DAINS

APPLICATION NUMBER: US/08/781,891

FILING DATE: 27-DEC-1996

CLASSIFICATION: 800

ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 240052.419

FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-6031

INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid

STARANDENDENS: SINGIE
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APPLICATION NUMBER: US PCT/US 94/10730
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5837496
GENERAL INFORMATION:
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US-08-781-891-208
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1373 tggaaaggcttgagaaaacagcggaagagggcgagaagttgttgataaaagaagctgtag 1432
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Pred. No. 1.4;
0; Mismatches 89; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Engrall, Eva APPLICANT: Leivo, Ilmo TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin TITLE OF INVENTION: Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
                                                                                                                                                                           FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
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Best Local Similarity 50.89
Matches 92; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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us-09-075-375a-1.rni

US-09-007-005-17

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; Requence 17, Application US/09007005B
; Redent No. 625858
; GENERAL INFORMATION:
    APPLICANT: SCOStak, Jack W.
    APPLICANT: Scostak, Jack W.
    APPLICANT: Liu, Rihe
    TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
    TITLE OF INVENTION: FUSIONS
    FILE REFERENCE: 00786/350003
    CURRENT APPLICATION NUMBER: US/09/007,005B
    CURRENT FILING DATE: 1999 10.14
    EARLIER FILING DATE: 1999 -01-37
    EARLIER FILING DATE: 1997-01-27
    EARLIER FILING DATE: 1997-01-27
    SARLIER FILING DATE: 1997-01-6
    NUMBER OF SEO ID NOS: 33
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.9%; Score 38.6; DB 2; Length 6942; 50.8%; Pred. No. 1.4; tive 0; Mismatches 89; Indels 0.
FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN.1990

PRIOR APPLICATION NUMBER: US 07/919,951

APPLICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6942 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
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Matches 92; Conservative
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US-08-125-077-3
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                                                                                                                                                                                                                                        1512 gittaaggagitgcaacaagaigaagaaattitgigagggagitgagiaaagaagagaa 1571
                                                                                                                 46 arcrararurgrnrnsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsr 105
                                                                                                                                                                                        166 nrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrcrargr 225
                                        Gaps
                                    0;
DB 4; Length 289;
; Score 38.2; DB 4; Length 28
Pred. No. 0.55;
97; Mismatches 113; Indels
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  1.98;
6.78; P
                   Best Local Similarity 6.7% Matches 15; Conservative
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    Query Match
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November 5, 2001, 23:45:51; Search time 3841.92 Seconds (without alignments) 4874.152 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                                           OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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gb_est36:*
gb_est37:*
gb_est39:*
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em_estba:*
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em_esthum5:*
em_esthum6:*
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1981
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em_esthum8:*
em_esthum9:*
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gb_est6:*

gb_est7:*

gb_est8:*

gb_est10:*

gb_est11:*

gb_est11:*

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gb_est21:*

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em_esthum3:*
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2: gb_est2:*
3: gb_est3:*
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                                                                                                                                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                            Run on:
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44: em_esthum10:*
45: em_esthum11:*
46: em_esthum11:*
48: em_esthum11:*
48: em_esthum11:*
50: em_esthum12:*
51: em_esthum17:*
52: em_esthum17:*
53: em_esthum10:*
54: em_esthum10:*
55: em_esthum21:*
56: em_esthum21:*
57: em_esthum21:*
56: em_esthum21:*
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56: em_esthum21:*
60: em_esthup1:*
60: em_estro10:*
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118; gb_est49;*
119; gb_est49;*
121; gb_est50;*
122; gb_est52;*
123; gb_est52;*
124; gb_est52;*
125; gb_est52;*
126; gb_est55;*
127; gb_est56;*
128; gb_est56;*
139; gb_est56;*
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150; gb_est100;*
160; gb_est100;*
170; gb_est100;*
170;
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200 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	b_gss32 b_gss33 b_gss34 b_gss2i m_gss_i m_gss_r m_gss_r b_gss3r b_gss36
C	55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AW398615 AW398615 EST309115 AQ828812 AW398615 EST309115 AQ126243 AZ126934 AZ126934 BE191198 BE19111 BE1911 BE191
c.
ALIGNMENTS AV410579 427 bp mRNA BEST AV410579 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWL074g05_r 5', mRNA sequence. AV410579.1 GI:7723433 EST Lotus japonicus. Lotus japonicus. Lotus japonicus Lotus japonicus Evaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopl Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotus 1 (pases I to 427) Asamizu, E., Nakamura, Y., Sato, S. and Tabafa.S.

```
DNA Res. 7 (2), 127-130 (2000)
20277479
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Chen, J., Mondryama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,
Rosce, M., Warren, B., Ton, B., Tan, Y. K., Borillo, C., Carpio, T.,
Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L.,
Turner, C., Krikorian, S., Elder, L. and Hanson, D.
                                                                                                                                                                                                                  /organism="Lotus japonicus"
/db_xref="taxon:34305"
/db_xref="taxon:34305"
/clone="wwL074905_"
/clone=lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="vector: pBluescriptII SK-; Site_1: BcoRI; Site_2:
%hol: solte=whyakojima MG-20"
a 85 c 102 g 128 t
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1994713 483 bp mRNA EST 08-SEP-1999 701499353 A. thaliana, Ohio State clone set Arabidopsis thaliana cDNA clone 701499353, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 tcatacaattggctatcgtattggtttgcacatttgttatcgttcccagagttgatgccg 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611 ttgatgetettaaaaettgtgettgtttaeteaaagaatgeaggattgagettgeaaaat 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   791 aattcaacgagtgtgcggtttcccgaaagaaatgtgtgccccggaaatcggatgtgggtg 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          851 aattocoggttocogatogtaatgoagtggttoaaaattttaacatgaaagactttagtg 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 AATTTAATGAGTGTGCAGTCTCCCGGAAGAAATGTGTACCTAAGAAATCTGACGTGGGAG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.9%; Score 254.6; DB 30; Length 427; Similarity 77.6%; Pred. No. 1e-51; D8: Conservative 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           911 ggaagtggtatataacaagtggtttaaatcctacatt 947
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AUTHORS
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                                                                                                                                                                                                                                                                          /clone_lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clones from the
Arabidopsis thaliana Ohio State clone set."
1 112 c 110 g 125 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Glycine.
1 (bases 1 to 515)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            952 gcatttgattgtcaacttcatgagtttcatatggaaaatg---ataaacttgttgggaac 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1009 ttaacatggcgcataaaaactttggatggtggtttctttactcgatctgctgtgcaaaca 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      652 aggattgagcttgcaaaatgtatagcaaacccatcttgtgcggcaaacgttgcctgtcta 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 CAGACCTGCAATAACCGTCCAGATGAAACCGAGTGCCAGATTAAATGTGGGGGATCTGTTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 GAGAACAGTGTTGTTGATGAGTTCAACGAGTGTGCTGTGTCGAGAAAAAAAGTGTGTTCCT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   832 cggaaatcggatgtgggtgaattcccggttccggatcgtaatgcagtggttcaaaatttt 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 AGAAAATCTGGATCTCGGAGAATTTCCTGCCCCAGACCCTTCTGTTCTTGTACAGAACTTC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               892 aacatgaaagactttagtgggaagtggtatataaacaagtggtttaaatcctacatttgat 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 AGGATAGAACTCGCGAAGTGCATTGCCAACCCTGCCTGTGCAGCCAATGTCGCGTGCCTT 73
                                     Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 249.2; DB 104; Length 483; nilarity 72.1%; Pred. No. 2.2e-50; Conservative 0; Mismatches 128; Indels 3;
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  Arabidopsis thaliana Gene Expression MicroArray
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                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    110 g
                                                                                                                                                                                                                                                         /clone="701499353
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                      (1999)
                                                                                                                                     Fax: 314-427-3324
                                                                                                                    Tel: 877-577-2733
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/note="Vector: pBluescript II SK+; Site_I: EcoRI; Site_2:
Xho1; The CDNA library was constructed from mRNA isolated
from germinating shocts of 3 day old seedling for the
cultivar Williams B2. The seedlings were germinated in a
growth chamber using germination paper in a solution
containing 100pm auxin. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT) sequence
with a XhoI restriction site. EcoRI adapters were ligated
to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoRL). This library was constructed
in the laboratory of Dr. Randy Shoemaker."
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Stepfoce,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Bowers,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Germinating shoot, 3 day old seedling, auxin treatment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watcon.wustl.edu

Email: est@watcon.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World

This clone is available through: Galsa For further information

Parkway Circle St. Louis, Missouri 63134 For further information

call: (800) 430.0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)

427-3324 or contact: clones@genomesystems.com or

info@genomesystems.com web site: www.genomesystems.com

High quality sequence stop: 421.
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                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Pred. No. 2.5e-48;
0; Mismatches 157; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1067-1991"
                                                                                                                                                                                                                                                                                                              Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Gm-c1067'
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67.9%;
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314 286 1810
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1 (bases 1 to 400)
Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of CDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Fes. 7, 175-180 (2000)
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/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                       AV440942 Arabidopsis thaliana above-ground organ two to six-week old Arabidopsis thaliana cDNA clone AP216c07_f 3', mRNA sequence.
                                                            tttgtttcagaggttgcttgaagggtttaaggagttgcaacaagatgaagagaattttgt 1547
                                                                                                                                       1548 gagggagttgagtaaagaagaaggaagtctgaatgaacttcaaatggaagcgactga 1607
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410 AAGAAGGTTATCAAAACAAGAAATGGAAATTCTTTATAGGCTCAAAATGGAAACCCAGTG 469
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
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/db_xref="taxon:3702"
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/clone_lib="Lambda-PRL2"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_l: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were l)
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 438)
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18839 Lambda-PRL2 Arabidopsis thaliana cDNA clone 207C23T7, mRNA
                                                                                                                                                                                                 1588 cttcaaatggaagcgactgaagttgaaaagctttttggggcgcggttaccgattaggaaa 1647
                                                                                               1468 gttagagatactgagatgactttgtttcagaggttgcttgaagggtttaaggggtttaaggagttgcaa 1527
                       160 CAAGACGAGAGATTTCGTGAGAGTTAAGTAAAGAAGAGATGGAGTTTTTGGATGAG 101
                                                                                                                                                                                                                                 100 ATCAAAATGGAAGCAAGTGAGGTTGAAAAATTGTTTGGGAAAGCTTTGCCAATCAGGAAG 41
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/db_xref="taxon:3702"
/clone="207C23T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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Fax: 517-353-9168
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DB 159; Length 438;

Query Match 9.1%; Score 181.2; DB 159; Lengt Best Local Similarity 72.5%; Pred. No. 9e-34; Matches 245; Conservative 0; Mismatches 92; Indels

652 aggattgagcttgcaaaatgtatagcaaacccatcttgtgcggcaaacgttgcctgtcta 711

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Wed Nov

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212;
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lotus japonicus.
Lotus japonicus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MWL079b09_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Yector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note="Wector: pBluescriptII SK-; Site_1: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 248)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a logume. Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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                                                     cagactigcaacaatcgtcctgacgagaccgaatgtcagataaaatgtggtgacttgttc 771
                                                                        74 CAGACCTGCAATAACCGTCCAGATGAAACCGAGTGCCAGATTAAATGTGGGGATCTGTT 133
                                                                                                                             134 GAGAACAGTGTTGTTGATGAGTTCAACGAGTGTGCTGTGGGAGAAAAAAGTGTGTTCCT 193
                                                                                                                                                                                                 832 cggaaatcggatgtgggtgaattcccggttccggatcgtaatgcagtggttcaaaatttt 891
                                                                                                                                                                                                                                   194 AGAAAATCTGATCTCGGAGAATTTCCTGCCCCAGACCCTTCTGTTCTTGTACAGAACTTC 253
                                                                                                                                                                                                                                                                      892 aacatgaaagactttagtgggaagtggtatataacaagtggtttaaatcctacatttgat 951
                                                                                                                                                                                                                                                                                                        254 AACATCTCGGACTTTAACGGGAAGTGGTACATTACAAGTGGCTTGAATNCAACCTTTGAT 313
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                  14 AGGATAGAACTCGCAAAGTGCCATTGCCAACCCTGCCTGTGCAGCCAATGTCGCGTGCCTT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV410854 Lotus japonicus young plants (two-week old) Lotus paponicus cDNA clone MWL079b09_r 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                314 GCCTTCGNCTTGCCANCTGCATGGGTTTCCNACAGGAA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Lotus japonicus"
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/clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/dev_stage="mixed stages"
/lab_host="SOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
a 115 c 142 g 190 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EST309115 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT4A14 5', mRNA sequence.
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747 tcagataaaatgtggtgacttgttcgaaaacagtgtggtggaccaattcaacgagtgtgc 806
                                                                                                                                      185 CCAAATTAAATGCGGGGCACCTGTTTGAAAACAGTGGTGGTTGATCAATTTAATGAGTGTGC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/db_xref="taxon:28526"
/clone="CLPT4A14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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/tissue_inpe="leaf" title bat Library (ECORI)"
/tissue_inpe="leaf" title bat Library (ECORI)"
/lab host="E. coli DH10B"
/note="vector: pacIndigo; Site_1: ECORI; Site_2: ECORI;
Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the hunid tropics and subtropics, rely on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumqamathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones
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Midy.R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUBSB12 871 bp DNA GSS 03-NOV-1999
nbeb0002N20r CUGI Rice BAC Library (ECORI) Oryza sativa genomic
clone nbeb0002N20r, DNA sequence.
                                                                                                                                                                                                               tgatgccgttgatgctcttaaaacttgtgcttgtttactcaaagaatgcaggattgagct 662
                                                                                                         tgcaaaatgtatagcaaacccatcttgtgcggcaaacgttgcctgtctacagacttgcaa 722
                                                                                                                                   /db_xref="taxon:4530"
/clone="nbeb0002N20r"
/clone_lib="cuGI Rice BAC Library (EcoRI)"
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Tel: 864 656 7288
Fax: 864 656 4293
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High quality sequence stop: 503.
Location/Qualifiers
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/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: GGAAACAGCTATGACCATG
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(doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                               347 ATTGTAGATCAAATGTGGAGATCTGTTTGAGAACACTGTGGTCGATGAGTTCAACGAGTG 288
                                                                                                                                                                                                                                                                                                                           864 ggatcgtaatgcagtggttcaaaattttaacatgaaagactttagtgggaagtggtatat 923
                                                                                                                                                                                                                                                                                                                                                                                                                          227 TGATCCATCCGCCCTTGTCAAGAACTTCAACATGGCTGATTTCAACGGCAAGTGGTATAT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                               924 aacaagtggtttaaatcctacatttgatgcatttgattgtcaacttcatgagtttcatat 983
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                                                                                                                                                                                                                                                                                                       804 tgcggtttcccgaaagaaatgtgtgccccggaaatcggatgtgggtgaattcccggttcc 863
                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 CGAGAGACAAAACTTATAGGGAACTTGACATGGAGAATTCGAGCTGGTACCCGGGGAT 48
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Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                    Query Match 7.8%; Score 154.2; DB 234; Length 871; Best Local Similarity 69.3%; Pred. No. 4.1e-27; Matches 210; Conservative 0; Mismatches 93; Indels 0;
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="OSJNBb0075L17f"
/clone_lib="CUGI Rice BAC Library (ECORI)"
/tissue_type="Leaf"
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Tel: 864 656 7288
Fax: 864 656 4293
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High quality sequence stop: 642.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seq primer: GTAAAACGACGGCCAGTG
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AZ126249.1 GI:8200598
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Anote="Vector: pasternation; Site_1: ECORI; Site_2: ECORI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumyanathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa. Nipponbare variety using ECORI as the cloning enzyme. The library contains 55,296 clones with an average insert size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 121 Kb providing approximatiby 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 % Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 411)
Ning, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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Rice BAC Library (EcoRI) Oryza sativa genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                864 ggatcgtaatgcagtggttcaaaattttaacatgaaagactttagtgggaagtggtatat 923
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161 c 182 g 227 t 8 others
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7.6%; Score 149.8; DB 238; Length 812;
Best Local Similarity 69.0%; Pred. No. 4.8e-26;
Matches 205; Conservative 0; Mismatches 92; Indels 0;
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Tel: 864 656 7288
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/lab_host="E. coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4530"
/clone="0SJNBb0079L12r"
                                                                                                                                                                          High quality sequence start: 37
High quality sequence stop: 374.
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                           /strain="Japonica"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                             Location/Qualifiers
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Shomaker, R., Keilm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M. Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Thalsing, B., Allen, M., Bowers, Y. Person, B., Saaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pT7T3Pac (pT7T3, Pharmacia); Site_1: EcoRI; Site_2: HindIII; This cDNA library was constructed from mRNA isolated from the senescing leaf tissue of mature greenhouse grown plants of the cultivar Williams 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                     Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementary DAM was synthesized from mRNA using a 3' anchored poly(dT) primer. EcoRI adapters were ligated to the blunt ended CDNA fragments followed by digestion with EcoRI and HindlII. The CDNA framents were directionally cloned into the EcoRI-HindlII restriction site of the [T7T3-Pac vector. The ligated CDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available through: Genome Systems, Inc. 4633 World
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 agacaattcatacaattggctatcgtattggtttgcacatttgttatcgttcccagagtt 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 ATACGCATCACGCCAGTAGCTGCCATATTGGTATCCATTTTAATGATCATTCCACCAGCT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 gatgccgttgatgctcttaaaacttgtgcttgtttactcaaagaatgcaggattgagctt 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/dev_stage="mature plants"
/lab_host="DH10B"
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1038-2146"
/clone_lib="Gm-c1038"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  info@genomesystems.com web site: www.genomesystems.com
Possible reversed clone: similarity on wrong strand
Insert Length: 978 Std Error: 0.00
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Best Local Similarity 75.1%; Pred. No. 1.6e-25;
Matches 184; Conservative 0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                      Public Soybean EST Project
Unpublished (1999)
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       GI:8670091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
BE191198.1
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A1668224 602 bp mRNA EST 02-FEB-2000
605018D09.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
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/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1272 atcgatcatcccaaacctacaaaaagcagccaaatccgtgggtcgagactttaacaattt 1331
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63.5%; Pred. No. 6.1e-25;
tive 0; Mismatches 128; Indels 12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize ESTs from various cDNA libraries sequenced at Stanford
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/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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/cultivar="Ohio43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: walbot@stanford.edu
Plate: 605018 row: D column
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                              cDNA, mRNA sequence.
AI668224
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Walbot, V.
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/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII; Produced by Rod Wing" 130 c 111 g 163 t
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Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a BAC End Sequence Database To Identify Minimal Overlaps for
                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                            1572 ggaaattetgaatgaaettcaaatggaagegactgaagttgaaagetttttgggeegeg 1631
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                                                                 372 TCTCATGGAGGTGAAACAGGATTTCATGAACTTCTTGCAGGGGCTGAGCAAGGAGGAGT 313
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                                                                                                                                                                                                                                                                                       13-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                           B28051 599 bp DNA GSS 13-OCT-199
T27G7TFB TAMU Arabidopsis thaliana genomic clone T27G7, DNA
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Tel: 301 838 0200
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0; Mismatches 68
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The Institute for Genomic Research
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Unpublished (1997)
Other_GSSs: T27G7TR
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/sex="hermaphrodite"
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Seq primer: M13-21
Class: BAC ends
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Fax: 301 838 0208
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Assumizu, E., Nakamura, Y., Sato, S. and Tabata, S. Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. A large scale analysis of CDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and Size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                      AV521985 335 bp mRNA EST 07-SEP-2000 AV521985 Arabidopsis thaliana aboveground organs two to six-week
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                                                                                                                                                                                                                                                                       old Arabidopsis thaliana cDNA clone APZ70c09F 3', mRNA sequence.
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80 TACAAGTGGCTTGAATCCAACCTTTGATGCCTTCGACTGCCAGCTGCATGAGTTCCACAC 21
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Local Similarity 76.5%; Pred. No. 5.2e-24;
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/db_xref="taxon:3702"
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AV521985.1 GI:8681512
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/clone_Trzww
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; Produced by Rod Wing"
a 366 c 195 g 357 t 25 others
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1147)
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
                                                                                                                                                                                                                                                                                         University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
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                                                                                                                                                                                                                  Unpublished (1997)
Other_GSSs: T27M8-Sp6.1, T27M8-Sp6, T27M8-T7
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                         Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 110
High quality sequence stop: 594.
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/db_xref="taxon:3702"
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         B08217.1 GI:2089494
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Best Local Similarity 71.8%
Matches 181; Conservative
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Search completed: November 6, 2001, 00:54:03 Job time: 4092 sec

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: November 6, 2001, 02:52:36; Search time 93.61 Seconds (without alignments) 914.444 Million cell updates/sec 7495

Perfect score: 7495
Sequence: 1 MALSLHTVFLCKEBALNLYA......MEASEVEKLFCKALPIRKVR 1412

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Total number of hits satisfying chosen parameters: 4126 Minimum DB seq length: 0 Maximum DB seq length: 2000000000

412676 seqs, 60623988 residues

Searched:

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Listing first 45 summaries

A_Geneseq_0601:*

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: SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*

: SIDS1/gcgdata/geneseq/geneseqgp/AA1991.DAT:*

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: SIDS1/gcgdata/geneseq/geneseqgp/AA1991.DAT:*

: SIDS1/gcgdata/geneseq/geneseqgp/A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Tobacco violaxanth	Romaine lettuce vi	Arabidonsis violax	Arabidopsis thalia	Arabidonsis thalia	Arabidopsis thalia	Arabidonsis thalia	Arabidopsis thalia	Arabidonsis thalia	Arabidopsis thalia	P. falciparum live
		ID	AAW09875	AAW09874	AAW09876	AAG49996	AAG49997	AAG06331	AAG06330	AAG49998	AAG06332	AAY44787	AAW24790
		DB	18	18	18	21	21	21	21	21	21	21	18
		e Match Length DB 1	478						526				
ď	Query	Match	34.1	33.3	32.2	2.8	2.8	2.8	2.8	2.8	2.7	2.0	2.0
		Score	2554	2498	2417	212.5	210	209	209	207	206	151	147.5
	Result	No.	1	7	æ	4	Ŋ	9	7	8	o	10	11

mitos milos odium sabba-gr homol homol homol cilm cilm cilm cilm cilm cilm cilm cil	Human p160 polypep Human p160 polypep Erysiphe graminis Potato starch synt P. falciparum FCR3
AAR7282 AAW2399 AAW220129 AAW220129 AAW250129 AAR6017 AAR9526 AAR9526 AAR95077 AAG3621 AAG3622 AAG3621 AAG362 AAG3621 AAG362 AAG362 AAG362 AAG362 AAG362 AAG362 AAG362 AAG362	8 AAW31186 8 AAW31185 7 AAR98811 1 AAB49306 2 AAB62142
100 100 100 100 100 100 100 100 100 100	905 18 1135 18 2273 17 1230 21 3542 22
147 147 147 135:55 135:55 135:55 137:55 128:	119 118.5 117.5 117.5
11111111111111111111111111111111111111	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; tobacco.
                                                                                                                                                                                                                                                                                                           /note= "conserved Cys residue"
Misc-difference 155
                                                                                                                                                                                                                                                                           'note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                               'note= "conserved Cys residue"
                                                                                                                                                                                                                                             385.478
/label= Highly-charged_domain
                                                                                                                                                                                                                          135. 206
/label=_Cys-rich_domain
                                                                                                                                                                            /label= Transit_peptide
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                /label= Mat_protein
                   AAW09875 standard; Protein; 478 AA.
                                                                            Tobacco violaxanthin de-epoxidase.
                                                                                                                                                                                                                  "Claim 8"
                                                                                                                                     Nicotiana tabacum cv. xanthi.
                                                        28-JUL-1997 (first entry)
                                                                                                                                                                                     ..478
                                                                                                                                                                                                        135..147
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                                                                                                                                                                                                                                                                                    Misc-difference 143
                                                                                                                                                                                                                                                                  Misc-difference 141
                                      AAW09875;
                                                                                                                                                                   Peptide
                                                                                                                                                                                      Protein
                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                               Domain
RESULT
AAW09875
                                                                                                                                                         Key
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The 55 kDa violaxanthin de-epoxidase (VDE) (AAW09875) of tobacco catalyses the de-epoxidation of violaxanthin to zeazanthin and antheraxanthin. This system, termed energy dependent non-radiative antheraxanthin. This system, termed energy dependent non-radiative cenergy dissipation or non-photochemical fluorescence quenching, reduces the quantum efficiency of photosystem II [PSII), helping to prevent PSII over-reduction and photoinhibitory damage. The amino acid sequence of the VDE was deduced from an isolated CDNA clone (AAM566242). VDE nucleic acids (see also AAT66241, AAT66243), in sense or antisense orientation, can be used in genetic constructs to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases contends lower in the photosensitivity of a range of crops, trees and ornamentals can be modified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 RICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAI 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 VAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETEC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 MALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSP 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding plant violaxanthin de-epoxidase - used to modify the sensitivity of a plant to light
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                                                                                                                                                                                                        /note= "conserved Cys residue"
252
                                                                                           'note= "conserved Cys residue"
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/note= "conserved Cys residue"
                              'note= "conserved Cys residue"
                                                            'note= "conserved Cys residue"
                                                                                                                          'note= "conserved Cys residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bugos RC, Rockholm DC, Yamamoto HY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                            96WO-US18291.
                                                                                                                                                                                                                                                                                                                                                                                                            96US-0023502.
95US-0006315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CALJ ) CALGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-281036/25
                                                                                                            Misc-difference 180
                                                                                                                                          Misc-difference 184
                                                                                                                                                                          Misc-difference 190
                                                                                                                                                                                                        Misc-difference 206
                                                                                                                                                                                                                                                                    Misc-difference 382
                                              Misc-difference 167
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                                                                            Misc-difference 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 AA;
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               Misc-difference
                                                                                                                                                                                                                                     Misc-difference
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07-NOV-1995;
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241 rglnptfdafdcqlhefhteenklygnlswrirtpdggfftrsavgkfvgdpkypgilyn 300
                                                                                                                    121 vaifilsvaskadavdalktctcllkecrlelakcisnpacaanvaclqtcnnrpdetec 180
                    654 QIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT 713
                              714 RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773
                                                                                                         HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 833
                                                                                                                                                  834 LQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDK 893
                                                                                                                                                              Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; lettuce.
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/label= Highly-charged_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Tryptic_peptide-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= Tryptic_peptide-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Tryptic_peptide-21
                                                                                                                                                                                                                                                                                                                                   Romaine lettuce violaxanthin de-epoxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Cys-rich_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= Transit_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "conserved Cys
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= Mat_protein
                                                                                                                                                                                                                                                                      AAW09874 standard; Protein; 473 AA
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                                                                                                                                                                                                                                                                                                                                                                                                   Lactuca sativa L. cv. romaine
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361 RDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLF

421 QRLLEGFKELQQDEENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLR 473

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The 55 kDa violaxanthin de-epoxidase (VDE) (AAW09874) of romaine lettuce catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. This system, termed energy dependent non-radiative energy dissipation or non-photochemical fluorescence quenching, reduces the quantum efficiency of photosystem II (PSII) the print to prevent PSII over-reduction and photoinhibitory damage. The amino acid sequence of the VDE was deduced from an isolated CDNA clone (AAT66241). VDE nucleic acids (see also AAT66242-43), in sense or antisense orientation, can be used in genetic constructs to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underspression of VDE increases photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding plant violaxanthin de-epoxidase - used to modify the sensitivity of a plant to light
   'note= "conserved Cys residue"
                              'note= "conserved Cys residue"
                                                                /note= "conserved Cys residue"
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                                                                                                                                                                                                                                                                                                                                                                            Yamamoto HY;
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95US-0006315
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                                             Misc-difference 190
                                                                                                                                                                                                                                                                                                                                          (CALJ ) CALGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 AA;
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               Misc-difference
                                                                              Misc-difference
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Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin;
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/label= Transit_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana var. columbia.
                                                                                                                                           AAW09876 standard; Protein; 462 AA
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                                                                                                                                                                                                                                           (first entry)
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/label= Cv
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Pred. No. 9.2e-187;
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99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. This system, termed energy dependent non-radiative energy dissipation or non-photochemical fluorescence quenching, reduces the quantum efficiency of photosystem II (PSII), helping to prevent PSII over-reduction and photoinhibitory damage. The amino acid sequence of the VDE was deduced from an isolated cDNA clone (ART66241). VDE nucleic acids (see also AAT66241-42), in sense or antisense orientation, can be used in genetic constructs to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases a photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding plant violaxanthin de-epoxidase - used to modify the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 32.2%; Score 2417; DB 18; Length 462; Local Similarity 99.8%; Pred. No. 1.9e-180; es 461; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The violaxanthin de-epoxidase (VDE) (AAW09876) of Arabidopsis
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                                                                                                                                                                                                                            Yamamoto HY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         sensitivity of a plant to light
96WO-US18291
                                                                                           95US-0006315
                                                            96US-0023502
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                                                                                                                                                           (CALJ ) CALGENE INC.
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07-NOV-1996;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 63310.
                AAG49996 standard; Protein; 525 AA.
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99US-0130891.
99US-0131449.
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990S-0135124.
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                                                   18-OCT-2000 (first entry)
                                                                                                        termination sequence.
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07-JUN-1999;
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270 FFTRSAVQTFVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAW 329
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20.2%; Pred. No. 4.5e-08;
:1ve 98; Mismatches 215; Indels 235; Gaps
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                     ||| ::| | :|| | :|| 492 cenppl----gipqgsrlhsrisiieepdseek 520
                                                     --WEITRGLNPTFDAFDCQLHEFHTEENK
                                                                                                                                                                         856 GPEPPLVERLEKKVEEGER----TIIKEVEEIEE 885
                                                                                                                                                                                                                                              AAG06330 standard; Protein; 526 AA
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99US-0132487.
99US-0132863.
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990S-0134218.
990S-0134219.
990S-0134221.
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99US-0130891.
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99US-0126264
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09-MAR-1999;
23-MAR-1999;
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16-APR-1999;
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28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCG 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76; Mismatches 191; Indels 186; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%; Score 209; DB 21; Length 522; 11.2%; Pred. No. 8.4e-08;
990S-0151080.
990S-0151303.
990S-0151438.
990S-0151930.
                                                99US-0153070.
99US-0153758.
99US-0154018.
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99US-0155139.
99US-0155486.
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99US-0156458.
99US-0156596.
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99US-0157865
99US-0158029
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99US-015823
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99US-0160741.
99US-0160767.
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99US-0160770.
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990S - 0160981
990S - 0160404
990S - 0161405
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990S - 0161361
990S - 0161361
990S - 0161920
990S - 0161932
                                                                                99US-0154039
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Matches 122; Conservative
                                                10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
                                                                            16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
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14-0CT-1999;
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28-0CT-1999;
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07-SEP-1999;
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13-OCT-1999;
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UUS-0146386 UUS-0146388 UUS-01470389 UUS-01470204 UUS-0147302 UUS-0147302 UUS-0147302 UUS-0147260 UUS-0147260 UUS-0147303 UUS-0147303 UUS-0147303 UUS-0147303 UUS-0147303 UUS-0147303 UUS-0147303 UUS-0147303 UUS-0147303 UUS-0147303	0125 0148565 015 0148684 015 0148684 015 0149725 016 0149723 017 0149929 018 0149929 018 0149929 018 0149929 018 0150866 018 0150866 018 0150866 018 0150866 018 0151086 018 0151308 018 0151308 018 0151308 018 015308 018 0153758	990x - 015473 990x - 0155486 990x - 0155486 990x - 0155486 990x - 0155686 990x - 015753 990x - 015753 990x - 015723 990x - 0159293 990x - 0159293 990x - 0159293 990x - 0159284 990x - 0159284 990x - 0159638 990x - 0159638 990x - 0159638 990x - 016969 990x - 016969 990x - 0160961 990x - 0160961
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23-APR-1999;
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12-JUL-1999;
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    29;
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                                                                                 375 PEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDE 434
                                                                                            435 ENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVG 494
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Best Local Similarity 21.2%; Pred. No. 8.5e-08;
Matches 122; Conservative 76; Mismatches 191; Indels 186; Gaps
                                                                                                                              745 IRTPDGGFFTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVENSPE 797
                                                                                                                                                                                                                            495 SKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNL
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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99US-0142920
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les 86; Conservative
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25-OCT-1999
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26-0CT-1999
                                                                                                                      28-SEP-1999,
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The present sequence is a MIM protein from Arabidopsis thaliana, which contributes to recombination repair of DNA damage in plant cells. The protein was tracked down with the help of a T-DNA tagged Arabidopsis mutant showing hypersensitivity to methyl methanesulphonate (MMS). It shows homology to a member of SMC (Structural Maintenance of Chromosomes) protein family and confers hypersensitivity to treatment with MMS, X-rays, UV light or mitomycin C. The present sequence is useful for DNA repair in plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= DA-box
/note= "conserved motif which harbours a Walker B type
NTP binding domain"
                                                                                  372 ekerlqsalekcgikewelf-avdncscenppl----gipqqsrlhsrisiieepdse 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Arabidopsis polynucleotide encoding protein useful for assisting recombinant repair of DNA damage in plants \,^{\circ}
830 IIPELQTAAQKVG-RDFNTFIKTDNTCGPEPPLVERLEKKVEEGER-----TIIKEVEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM: recombination; plant; DNA repair; hypersensitivity; SMC protein family; Structural Maintenance of Chromosomes; MIM; methyl methanesulphonate; irradiation; mitomycin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana recombination repair protein, MIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Coiled_coil_region-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Coiled_coil_region-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49..56
/label= NTP_binding_domain
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/label= Hinge/spacer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY44787 standard; Protein; 1055 AA.
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1055 AA;

Sequence

S

AAW24790

43; 128 ALKTCACLLKECRIE-----LAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFEN 181 57 ailtalciafgcrargtgraatlkdfiktgcsyavvqvemknsgedafkseiyggviile 116 SVVDQFNECAVSR----KKCVPRKSDVGEFPVPDRNAVVQNFNM------KDFSGK 227 WYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPG 287 169 syi-----leck-----gn----ssflrnllg---qvndllg 194 195 siyehltkataivd-----elentikpiekeiselrgk------iknmegv 234 397 eeiaqrlqqlkkklawswvydvgrq------lqeqtekivklkeriptcq 278 ---EENFVRELSKEEKEILNELQMEATEVEKLFGRALP 468 449 570 GCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCI 629 689 FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTF-----DAFDCQLHEFHTEENKLV--- 738 594 krlsnik-evytldgykmffrgpvqttlpplsrrpsrlcasfddgi---kdleieaskeg 649 650 ne----ingcmrrkreaeenleelelkvrglkkhrsqaekvlttkelemhdlk-----n 699 854 TCGPEPPLVERL-EKKVEEGERTIIKEVEEIEEE---VEKVRD--KEVTL----FSKLFE 903 ---GNLSWRIRTPDG-GFFTRSAVQKFVQD-PKYPGILYNHDNEYLLYQDDWYILSSKVE 793 794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDN 853 700 tvaae---ieslpsssvnelgreimkdleeidekeafleklgnclkeaelkankltalfe 756 288 ALYNHDNEFLHYQDDWYILSSQIEN--KPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLP ESIIPNLQKAAK -----SVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKE ----EMTLFORLLEGFKE------LQQD 390 vetirsikeeencflekafegrkkmehiedmiknhqkrqrfitsnindlkkhqtnkvta 511 FGSIVVAKICSS-RRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNS -----tlrgcaneanyrnlki-----iiydfsrprlniprhmvpqtehpti 555 fsvidsd-------nptflnvlvdqsgverqvlaenyeegkavafg 337 fnhkcnyvqkikdrvrrlerqvgdineqtmkntqaeqseieeklkylerevek-----IRKLRMALAPHSN---------FLANHETIKYYVGSKLPGHKRFSWGWEDY 450 fggdrvinllgaiernhrrfrkpp------igpigs-----630 SNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVS-RKKCVPRKSDVGD Query Match 2.0%; Score 151; DB 21; Length 1055; Best Local Similarity 19.3%; Pred. No. 0.0084; Matches 182; Conservative 119; Mismatches 306; Indels 334 ----hvtlvngnkwassveqalgt--llnafivtdhkdsl-----904 GFKELQRDE----ENFLRELSKEEMDVLDGLKMEATEVEKL 940 AVEIEEEVEKEVEKVRDT-----Query Match Best Local 182 228 346 235 398 434 469 739 g g g 셤 ò ò ŏ ò ð a 염 ò ŏ g οχ a ò g à q ò 셤 ò qq ŏ g g δ

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This sequence corresponds to a Plasmodium falciparum strain K1

pre-erythrocytic liver stage antigen 3 (LSA-3) protein. The encoding
gene sequence was isolated by screening a P. falciparum strain T9/96
library with serum from a missionary treated by prophylaxis (for strain
T6/96 see FR9101286). Of 20 clones isolated, clone 7295 was used to
screen a library generated from Thai strain K1. One clone contained a
6.85 kb insert including the genomic sequence AAT78667. The gene
comprises a 1.8 kb region encoding 3 major blocks of tetrapeptide
comprises a 1.8 kb region encoding 3 major blocks of tetrapeptide
comprises a 1.8 kb region encoding 3 major blocks of tetrapeptide
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comprises a 1.8 kb region encoding 4 major blocks and as vaccines for menuncherapy of malaria.
                                                                                                                                                                                  Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum; prophytyaxis; Thai strain; gene organisation; exon; intron; hydrophobic; glycosyl-phosphatidylinositol membrane anchoring sequence; antibody; vaccine; immunotherapy; malaria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 409; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum poly:peptide(s) and related nucleic acids -derived from the liver stage antigen-3, useful for malaria vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18; Length 1786;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 SIIPNLQK-AAKSVGRDFN-----NFITTDNSCGPEPPLVE-
                                                                                                                                                                                                                                                                                                                                                                                              "repeat region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "repeat region
1537..1576
                                                                                                                                         P. falciparum liver stage antigen-3,
AAW24790 standard; Protein; 1786 AA.
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                                                                                           (first entry)
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/note= "r
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                                                                                                                                                                                                                                                                                                     Plasmodium falciparum,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9641877-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUN-1996;
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                                                                                         08-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-DEC-1996.
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Region
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1678 vvgff 1682

QQ	915	::: ::
οy	442	SKEEKEIINELOMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHK 501
qq	972	: : : : : :
Οy		557
ор	1025	mfrsietsivigseekvdlnenvvssildnienmkegllnklenisst 1072
Oy Op	558 1	HSINQNVPKG-NSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTC 616
δy	617	LLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECA 673
qq	1110	esdvit
Oy Op	674	VSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH 731
75 67	732	TEENKLYGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSK 791 :: : : :
0	. ~	AVLPESI IPELQTAAQKVGRDFNTF 848
- Q	1243	: : : eklkelekalsedskei 12
Qγ	849	ICGPEPPLVERLEKKVEEGERIIKEVEEIEEEVEKVRD
qq	1279	vieeehditttld
Oy Dp	1330	EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRAL 945
Οy	946	PIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL 994
qq	1390	sleveeekkleevhelkeevehiisgdahikg 1421
ΟŸ	995	VPL
qq	1422	-:leeddleevddlkgsildmlkgdmelgdmdkesledvttkl1462
ΟŸ	1055	IVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLOTCNNRPDETECQIK
qq	1463	150
0.y	1113	CGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGL 1172
3 8	1173	OLHEFHTEGDNKLVGNISMRIKTLDSGFFTRSAVOKFVODPNOPGVLYNHD 123
연	1525	
οy	1233	NEYLHYODDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELE 1292
QQ	1552	
δλ	1293	FSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEBEVE
QQ	1584	kakkklekveegvsglkhvdevmkyvqkidkevd 1
δλ	1346	QRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEASE 1
go.	1627	rskaleskndvtnvlkqnqdffskv
δλ	1398	VEKLF 1402

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ARR72829 is human mitosin. Mitosin is involved in the regulation of the mammalian mitotic cell cycle. Mitosin as with E2F-1 (see AAR72824) interacts with the retinoblastoma brotein (the retinoblastoma tumour suppressor gene product). Mitosin is first synthesised at the G1/S boundary, it is then phosphorylated from S through M phase, and during mitosis, is closely associated with the centromeres/Kinetochores at the mitosic spindle poles. Mitosin is necessary for a everyvoic cell to enter the M phase of the mitotic cell cycle and its degradation is necessary for a cell to advance on to the next stage. Mitosin is thus useful for controlling cell growth as overexpression of mitosin prevents cell from exiting the M phase.

An anti-mitosin antibody, antibody fragment or a phosphorylated mitosin mutein ( or nucleic acid encoding it) can also be used to inhibit cell division which is particularly useful for the study of the cell cycle. A further use is to control hyperproliferative cells, and so control diseases such as psoriasis and breast cancer. It can also be used to block gametogenesis of an immature gamete.
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Best Local Similarity 18.4%; Pred. No. 0.064;
Matches 240; Conservative 188; Mismatches 443; Indels 434; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | | : | | : | | | | 315 lsetlslekkemssilslnkreieeltqengtlkeinaslnqekmnligk-sesfanyid 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purified mammalian protein mitosin and agents that bind it and inhibit its action – used to promote cell growth or to inhibit cell division, and/or proliferation
                                                                                                                                                                       Cell cycle; M phase; mitosin; retinoblastome; mitosis; cell growth; inhibition.
                                                                                                                                                                                                                                                                 Location/Qualifiers
1480..1659
/label= internal_repeat
1660..1839
                                                                                                                                                                                                                                                                                                                                          /label= internal_repeat
                                 AAR72826 standard; Protein; 2482 AA.
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                                                                                                         (first entry)
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                                                                                                                                             Human mitosin.
                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                              WO9511309-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1993;
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                                                                       AAR72826;
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RESULT 1
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449 1ce 433 500 nns 489 HGK 551		nah 656 DF- 689 Kll 711	76 78 78 81	WL 826 : 868 868 	SKE 922 SS 984 SS 960 SKE 1044	1002 nye 1100 1033 ed 1160	KC 1084 	GN 1197 1 1258 1 1252 1 1310
kaaqeknskleclinectslce LANHETIKYYVGSKLPGH : : : : : : : : :	EKWGÇFAKTALIVALETLEVASKADAV ELST GENERALI GENERA	daeekyisgphelstsqndnah AVSRKKCVPRKSDVGDF- : : : srsecitatrkmaeevgkll	fgeqpneqhpvslapldesnsyehltlsdkev GFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQD : : -flslqsehkilhdqhcqmsskmselqtyvdsl	AWDGYGGSVLYTRSAVL :	FKELQRDEENFLRELSKE	LKILPPIQSADL- 	VDALKTCACLLKGCRIELAKC	FDCQLHEFHTEGDNKLVGN ::
gky SNE qnll	HNLSPAHSINONVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDAL	Kekeciqhelqtirgdletsnlqdmqsqelsglkdceidaeekyis; VAC-LQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSKKKV	: : .:	DWYILSSKVENSPEDYIFVYYKGRND	RTIIKEVEEIEEEVEKVRDKEVTLESKLFEGFKELQRDEENFLRELSKE :: :: ::	htsettertpkhd-vhqicdkdaqqdlnldiekitetgalkptgecsqqspdtnye htsettertpkhd-vhqicdkdaqqdlnldiekitetgalkptgecsqqspdtnyeSRPLSAFRSGFSKGIFDIVPLPSK	NELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKC	FNGKWYITSGLNPTEDA
DEENFVRELSKEEKEIL	HNLSPAHSINONVPKGNSG : : : : : : : : nsvkeresernq-	Kekeclqhelqtirgdlet VAC-LQTCNNRPDETEC : lqcslqttmnklnelekic	nevkilnddsgllhgelve QLHEFHTEENKLVGNLSWR : qmhfaelgek	DWYILSSKVENSPEDYIEVYYKGRND : : : :	RTIIKEVEBIEEBVEKV ::: :: :: qslekleekmesqgim EMDVLDGIKMEATEVEKLF- ::: : : tlemesklaaekkqteqIsl	htsettertpkhd-vhqic	rdrkveslinemkeldskihlgevglmt rdrkveslinemkeldskihlgevglmt IANPACAANVACLQTCNNRPDETECQIK	EFPAPDPSVLVQNFNISD : : : : : : : : : : dswkerfldven
433 450 434 501 490	552 544 612	597 638 657 690	712 726 769	784 811 827 869	874 929 923 985	961 1045 1003 1101	1034 1161 1085 1200	1144 1213 1198 1259
	o a o	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 6 B	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	oy Oy	0y 0y 0b	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00 00 00 00 00 00 00 00 00 00 00 00 00

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| ::| ::|: ::|: 14: | ::| 1368 hciqvaeaevkektellqtlssdvsellkdkthlqeklqslekdsgalsltkcelengia 1427
1253 P-----EDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFI 1306
                                             1307 RIDNICGPEPALVERIEKTVEEGERIIVKEVEEIEEE---VEKEVEKVGRTEMTLFQRLA 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence for mitosin, a phosphoprotein necessary for the cell to ente mitosis. The protein's degradation is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated mitosin protein and gene - useful for, e.g. developing products for therapy and diagnosis of hyper-proliferative disorders such as cancers or psoriasis
                                                                                                                                                                                                                                                                             Mitosin; phosphoprotein; mitotic cell cycle; antibody; analogue; inhibition; M phase; Antagonist; hyperproliferative cell; cancer; leukaemia; lymphoma; chromosome segregation.
                                                                                           1364 EGFNELKQDEENFVRE-----LSKEEMEFLDEIK-MEASEVEK 1400
                                                                                                            :| :::| |:| || 1128 ----qlnkekellvkeseslqarlsesdyeklnvskaleaalvek 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= "Bipartite targeting motif"
/note= "Optionally C or G"
2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= "Bipartite targeting motif"
/note= "optinally A or T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "leucine heptad repeat"
Misc-difference 2188
                                                                                                                                                                                                                                                                                                                                                                  258..280
/note= "leucine heptad repaet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 40-52; 43pp; English.
                                                                                                                                                                               AAW23996 standard; Protein; 2482 AA.
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                      Human mitosin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0328254,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0328254.
93US-0141239.
                                                                                                                                                                                                                                                                                                                                                                                     340..362
564..593
1387..1443
1885..1962
2146..2188
                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-109817/10.
N-PSDB; AAV09076.
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Misc-difference 2
Misc-difference 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee W, Zhu X;
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-1994;
                                                                                                                                                                                                                             28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5710022-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JAN-1998
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Domain
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Domain
                                                                                                                                                       RESULT 13
AAW23996
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                                                                                                                                                                                            δ
                                                                    Dp
                                                                                              δŏ
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The mitosin protein, can be used to control the growth of cells. An antiosin protein, can be used to control the growth of cells. An can initosin antibody, a mutant or a non-functional analogue of mitosin can inhibit the mitotic cell cycle by preventing the cells from entering the M phase, and over expression of mitosin or its functional equivalent, would inhibit the cycle by preventing cells from entering the M phase. Antagonists to this protein can be used to control hyperproliferative cells in, (e.g. thyroid hyperplasia, Grave's disease, psoriasis, benign prostatic hypertrophy, Li-Fraumeni syndrome, breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, supplementation of lost mitosin function by introduction of the protein or nucleic acid encoding the protein into a cell can restore defective chromosome segregation, which is a marker of progressing malignancy. Malignant proliferation of cells can then be halted. The protein can also be used for the detection and diagnosis of hyperproliferative

2482 AA; Seguence

90; VAC-LQTCNNRPDETE--CQIKCGDLFENSVVDEFNECAVSRKKCV--PRK--SDVGDF- 689 769 qmhfaelqek------flslqsehkilhdqhcq--msskmselqtyvdsl 810 : |:: |: | | | | : :::| | | eqtgdmsllsnlegavsanqcsvdevfcsslqeenltrketpsapakgveeleslcevyr 928 ::: |::||::| :::|: ;| ds1----ekleekmesqgimknkelqeleq1|sserqeldc1rkqylseneqwqqkltsv 984 374 ereksiselsdgykgeklillgrceetgnayedlsgkykaageknsklecllnectslce 433 612 KTCTCL------ACAAN 637 597 kekeclqhelqtirgdletsnlqdmqsqeisglkdceidaeekyisgphelstsqndnah 656 57 lqcslqttmnklnelekiceilqaekye--lvtelnd---srsecitatrkmaeevgkll 711 ----PVPDPSVLVQKFDMKDFSGKWFITRGLNP---------TFDAFDC 725 726 QLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQD-- 783 784 --DWYILSSKVENSPEDYIFVYYKGRND------AWDGYGGSVLYTRSAVL 826 RTIIKEVEEIEEEVEK---VRDKEVTLFSKLFEG-----FKELQRDEENFLRELSKE 922 379 LVERLEKTAEEGEKLLIKEAVEIEEEVE----KEVE-KVRDTEMTLFQRLLEGFKELQQ 432 434 nrknele----q1keafakehqef1tklafaeernqn1m1e1etvqqa1rsemtdnqnns 489 552 HNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDAL 544 -----nsvkereserng-cnfkpgmdlevkeisldsynaglvgleamlrnkelklgese PE----SIIPELQTAAQ----KVGRDFNTFIKTDNTCGPEPPL----VERLEKKVEEGE ---NELQMEATEVEKLFGRALP--IRKLRMALAPHSNFLANHETIKYYVGSKLPGH----501 KRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRI------CCGLDSRGLQLFSHGK 811 kaenlvistnirnfqqdlvkemqlqleeqlvpslssscvpdssslsslgdssfy--rall Query Match 2.0%; Score 147; DB 19; Length 2482; Best Local Similarity 18.4%; Pred. No. 0.064; Matches 240; Conservative 188; Mismatches 443; Indels 434; 433 DEENFVRELS --- KEEKEIL --450 qq Q Dp δ οg g ò g q δ qq g δ g δ ŏ a δ ŏ ò δ Qγ

WPI; 2000-365347/31.

985 tlemesklaaekkgteglslelevarlglggldlssrsllgidtedaiggrnescdiske 1044 ------PCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPI-----QSADL--- 1002 ----RITGGRS-----SRPLSAFRSGFSKGIFDIVPLPSK-------1033 1101 ppgedktggsseciselsfsgpnalvpmdflgngedihnlglrvketsnenlrllhvied 1160 -----NELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKC 1084 1161 rdrkvesllnemkeldsklhlgevglmt------kieac----ieleki 1199 1085 IANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLG- 1143 ----kk---ensdlse 1212 1144 --EFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTE----GDNKLVGN 1197 1213 kleyfscdhqellqrvetse-----glns----dlemhadkssredigdnvakvn 1258 ISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLH-----YQDDWYILSSKIENK 1252 1253 P-----EDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFI 1306 1307 RTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEE---VEKEVEKVGRTEMTLFQRLA 1363 1368 hoigvaeaevkektellgtlssdvsellkdkthlgeklgslekdsgalsltkcelengia 1427 923 EMDVLDGLKMEATEVEKLF-----GRALPIRKLMAVATH------CFTS-- 960 Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide. 1259 dswkerfld-----venelsrirsekasiehealyleadlevvgteklclekdnenk Plasmodium falciparum chromosome 2 related protein SEQ ID NO:182. 1428 ----qlnkekellvkeses1qar1sesdyek1nvskaleaalvek 1468 1364 EGFNELKQDEENFVRE-----LSKEEMEFLDEIK-MEASEVEK 1400 Venter JC; AAB18324 standard; Protein; 1558 AA. Gardner M, 99WO-US26796. 98US-0107131. (first entry) Hoffman S, Carucci D, Plasmodium falciparum (VENT/) VENTER J C. (HOFF/) HOFFMAN S. (CARU/) CARUCCI D. GARDNER M. WO200025728-A2. 05-NOV-1998; 05-NOV-1999; 07-NOV-2000 11-MAY-2000 AAB18324; GARD/) 1034 AAB18324 RESULT g g δλ qq g οy Ω δy q ŏ g οy δy δ

Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -

Disclosure; Page 410-414; 577pp; English.

by chromosome 2 of the human malarial parasite, hasmodium falciparum.

Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequenced by its will help to expand our understanding of parasite biology, a process hampered by the cumberate drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new cuts. AAA70078 to AAA70278 and AAB1814 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. proteins and their fragments (I) encoded present invention describes

1558 AA; Sequence

50; Ouery Match 1.9%; Score 143.5; DB 21; Length 1558; Best Local Similarity 17.9%; Pred. No. 0.059; Matches 206; Conservative 153; Mismatches 377; Indels 413; Gaps 391 EKLLIKEAVEIEEEVEKEV----EKVRDTEMTLFQRLLEGFKELQQD----EENFVREL 441 347 SIIPNLQK-AAKSVGRDFN-----NFITTDNSCGPEPPLVE-----RLEKTAEEG 390 502 RFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHG----KHNLSPA 557 ------mfrsietsivigsee--kvdlnenvvssildn--ienmkegllnklenisst 840 558 HSINQNVPKG-NSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTC 616 617 LIKECRLELAKCISNPACAANVACLQTCNNRPDETECQ---IKCGDLFENSVVDEFNECA 673 674 VSRKKCVPRKSDVGD--FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH 731 TEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSK 791 -VENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESI--IPELQTAAQKVGRDFNTF 848 442 SKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHK 841 egvqetvtehveqnvyvdvdvpamk----dqf-----lgilneagg-----IKTDNTCGPEPPLVERLEKKVEEGE--RTIIKEVEEI----EEEVEKVRD-------ekedltdkmidaveesieiss-dskeet-------Query Match Best Local 878 932 732 à qq ò a ò g ò 셤 δ q δ g δλ g ŏ ò

WPI; 1997-393672/36. N-PSDB; AAT75237

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qq	1047	idakddtlekvieeehditttldevvelkdveedkiekvsdlkdleedilk 1097
Qy	894	EVTLFSKLFEGFKELQRDEBNFLRELSKEEMDVLDGLKMEATEVEKLFGRAL 945
qq	1098	evkeikeleseiledykelktietdileekkeiekdhfekfeeeaeeikdleadilkevs 1157
Qy	946	PIRKIMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL 994
Op	1158	sleveeekkleevhelkeevehiisgdahikg 1189
δy	995	PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACA 1054
q	1190	leeddleevddlkgsildmlkgdmelgdmdkesledvtakl 1230
Οy	1055	FLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIK 1112
qq	1231	
οy	1113	DPSVL
q	1270	k 1292
οy	7	NPTEDAEDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLXNHD 1232
qq	1293	epkdeivevemkdedided 1319
Oy	1233	VLPNSIIPELE 129
o o	1320	7
0y	1293	KAAKSIGRDSTFIRTDNTCGPEPALVERIEKTVEEGGRIIVKEVEEIE 1341
3	,	
Oy Op	1342	EEVEKEVEKVGRIEMILFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKM 1393 : : : : : :
οy	1394	
QQ	1446	
RESULT AAW227 ID A	JLT 15 22775 AAW22775	775 standard; Protein; 1312 AA.
AC X	AAW22775	775;
X L	21-DE	-DEC-1998 (first entry)
S E X	Нитар	Human RAD50.
XXX	Human	Human; RAD50; DNA repair; tumour suppression; cancer; Septin-2; central nervous system.
SO.	Ното	Homo sapiens.
N N	W0972	WO9727284-A2.
X E :	31-10	31-JUL-1997.
Y P.	24-JA	24-JAN-1997; 97WO-US01299.
8 K K K	17-JU 26-JA	17-JUL-1996; 96US-0687080. 26-JAN-1996; 96US-0592126.
AA Y	(GENE	(GENE-) GENELABS TECHNOLOGIES INC.
PI X	Dolganov	nov G;
DR DR	WPI; N-PSD	; 1997-393672/36. SDB; AAI75237.

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The human RAD50 (hRAD50) is involved in DNA repair and has tummour suppression activity, can be used to detect predisposition to, decrease the risk of or treat cancers, e.g. acute myeloid leukeamia, myeloid splastic syndrome, therapy related myelodysplastic syndrome, therapy related myelodysplastic syndrome, therapy related acute myeloid leukaemia, refractory anaemia or refractory anaemia with excess blasts. Also disclosed in this invention is Human Septin-2 homologues of which may be used as targets for cancer therapies and central nervous system directed treatment methods, and to measure the proliferative potential of selected cell types.
                                         predisposition to, decrease risk of and treat cancer, also Septin-2
                     Human tumour suppressor gene RAD50 - useful to detect
                                                                                                                           Claim 5; Page 82-86; 195pp; English.
                                                                         homologues
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24;
                                                                                                                               -----adldrtlrk-----1dgemegl-nh-- 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 KTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIK-----CGDLFE 662
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                                                                                                                                                                                                 438 VRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFL-----ANHETIKY 491
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Ouery Match 1.8%; Score 135.5; DB 18; Length 1312; Best Local Similarity 19.7%; Pred. No. 0.19; Matches 124; Conservative 95; Mismatches 218; Indels 191; Gaps
                                                                                                                                                                                                                                                                                                492 YVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGK 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      815 klagidldrtvagvngekgekghkldtvsskielnrkligdagegighlksttnelksek 874
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^{*}Search completed: November 6, 2001, 04:59:28 Job time: 7612 sec

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: November 6, 2001, 02:56:11; Search time 90.8 Seconds (vithout alignments) 349:941 Million cell updates/sec

Title: US-09-075-375A-2

Perfect score: 7495
Sequence: 1 MALSLHTVFLCKEEALNLYA......MEASEVEKLFGKALPIRKVR 1412

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
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7 /cgn2_6/ptcdata/2/iaa/PcTuS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. 1 2 3 4 4 6 6	Score 147.5 135.5 135.5 132.5	% Match Match 2.0 2.0 1.8 1.8 1.8 1.8	Length 1786 2482 1312 1312 776	DB 17 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	US-08-973-462-8 US-08-328-254-6 US-08-592-126-148 US-08-687-080-51 US-08-021-601-2 US-08-08-849B-2	on 8, 6, 148 51, 2,
10 11 12 13 14 15	124 124 124 1124 1119		14498 14498 1581 1581 1581 9055	144444444444444444444444444444444444444	US-08-4404-531B-28 US-08-476-900A-28 US-08-488-546A-28 US-08-404-531B-6 US-08-476-900A-6 US-08-476-900A-6 US-08-574-959A-9 US-08-574-959A-9	99,000
10 11 11 11 12 13 13 14 14 15 16 17 18 17 18 17 18 17 18 17 18 17 18 17 18 18 18 18 18 18 18 18 18 18 18 18 18	119 117.5 1117.5 1115.5 1115.5 1115.5 1115.1 114.5		1135 1135 1135 1130 11130 3111 3411 14435 1579	u 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	US-08-574-959A-7 US-08-357-014-7 US-08-968-567-12 US-08-460-309-2 US-08-460-309-4 US-08-125-077-2 US-08-125-077-4 US-08-568-459A-4 US-08-568-459A-4 US-08-555-587-184 US-08-482-728A-19	7, 12, 12, 22, 44, 184,

Sequence 4, Appli	Sequence 1, Appli	Sequence 1, Appli	4	Patent No. 5444158	Sequence 16, Appl		Sequence 4, Appli	Sequence 4, Appli	9	7	7	7	8	7	7	Sequence 9, Appli	Sequence 9, Appli			
US-09-028-366-4	US-08-353-700-1	PCT-US95-16216-1	US-08-923-992A-4	5444158-2	US-08-755-587-16	US-08-603-753D-4	US-09-099-753-4	US-08-986-106-4	US-08-923-992A-6	US-08-923-992A-2	US-09-177-249-2	US-09-061-769A-2	US-08-923-992A-8	US-08-986-963-2	US-08-323-170B-2	US-08-946-475-9	US-09-340-479-9		ALIGNMENTS	
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523	3248	3248	1104	1130	2329	3418	3418	3418	1128	1164	689	689	1098	425	3135	711	711			
1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.4	1.4			
114	112.5	112.5	111.5	111.5	111.5	111.5	111.5	111.5	110.5	110.5	110	110	109.5	109	109	108.5	108.5			
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45			

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1422 -- LEEDDLEEVDDLKGSILDMLKGDMELGDMD-----KESLEDVTTKL----- 1462
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                                                                                                 1110 -LKEMFFNLEDVFKS---ESDVITVEEIKDEPVQKEVEKETVSIIEEMEENIVDVLEE-- 1163
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617 LLKECRLELAKCISNPACAANVACLQTCNNRPDETECQ---IKCGDLFENSVVDEFNECA 673
                                                                                                                                                                                                        674 VSRKKCVPRKSDVGD--FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH 731
                                                                                                                                                                                                                                                                                                                                                                                                                     732 TEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSK 791
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APPLICANT: Zhu, Xuellang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    1164 -----EKEDLTDKMIDAVEESIEISS-DSKEET------
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STREET: 4370 La Jolla Village Drive, Suite 700
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657 LQCSLQTTMNKLNELEKICEILQAEKYE--LVTELND---SRSECITATRKMABEVGKLL 711
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                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         PC-DOS/MS-DOS
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                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2482 amino acids
                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                      California
                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
San Diego
                                                                            92122
                                                                                                                                                                  COMPUTER:
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                                                                                                                                                                                                                     SOFTWARE:
                                                   COUNTRY:
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1161 RDRKVESLLNEMKELDSKLHLQEVQLMT------KIEAC-----IELEKI 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1045 HTSETTERTPKHD-VHQICDKDAQQDLNLDIEKITETGALK---PTGECSGEQSPDTNYE 1100
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874 RTIIKEVEEIEEEVEK---VRDKEVTLFSKLFEG-----FKELQRDEENFLRELSKE 922
                                                                                                                                                                                                                                                                                                   923 EMDVLDGLKMEATEVEKLF-----GRALPIRKLMAVATH-----CFTS-- 960
                                                                                                                                  369 EQTGDMSLLSNLEGAVSANQCSVDEVFCSSLQEENLTRKETPSAPAKGVEELESLCEVYR 928
                                                                                                                                                                                                                                          929 QSL----EKLEEKMESQGIMKNKEIQELEQLLSSERQELDCLRKQYLSENEQWQQKLTSV 984
                                                                              827 PE----SIIPELQTAAQ----KVGRDFNTFIKTDNTCGPEPPL----VERLEKKVEEGE 873
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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Sequence 148 Application US/08592126
Fatent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encorring File For INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
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CITY: Palo Alto
STATE: CA
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19.7%; Pred. No. 0.02;
tive 95; Mismatches 218; Indels 191; Gaps
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                                               APPLICATION NUMBER: US/08/592,126
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Challes K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
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Best Local Similarity
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                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 VRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFL-----ANHETIKY 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 135.5; DB 2; Length 1312;
19.7%; Pred. No. 0.02;
tive 95; Mismatches 218; Indels 191; Gaps
                                                                                   APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: TRANS. OF RAD50 cDNA (SEQ. 54), NT INDIVIDUAL ISOLATE: 389 TO 4324
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPA: (415) 324-0960
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTONEY/AGENT INFORWATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
            Sequence 51, Application US/08687080; Patent No. 5965427
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1312 amino acids
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STRANDEDNESS: sin
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                               USA
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US-08-687-080-51
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                                                                                                                                                                                                                                                    STATE:
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Best Local Similarity 17.2%; Pred. No. 0.017;
Matches 139; Conservative 117; Mismatches 254; Indels 300; Gaps
669 FITQL----TDENQSCCPVCQRV-----FQTEAELQEVISD-----TDENGSCCPVCQRV-----700
                                                                                                                                                    783 DDWYILSSKVENSPEDYIFV--YYKGRNDAWDGYGGSVLYTRSAV-LPESIIPELQTAAQ 839
                                                                                                                                                                                               701 ----LOSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPMRQSIIDLKEKEIPELRNKLQ 755
                                                                                                                                                                                                                                               723 FDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQ 782
                                                                                                                                                                                                                                                                                                                                      880 ------VEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENF-----LRELSKEE 923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND TITLE OF INVENTION: RELATED METHODS
OWNERS OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Needle & Rosenberg, P.C. STREET: 133 Carnegie Way, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                 924 MDVLDGLKME------ATEVEKLF 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.057
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/021,601
FILING DATE: 19930212
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Patent No. 5591631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leppla, Stephen H.
Klimpel, Kurt R.
Nichols, Peter J.
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Singh, Yogendra
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639 ESDLDRLKE-
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APPLICANT:
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951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
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                                        72 EMYKAIGG---KIYIVDGDITKHISLEALSEDKKKIKDIYGKDALLHEHYVYAKEGYEPV 128
                                                                                                                                                                                                                                                                                                                                                                                        908 ---LQRDEENFLRELSKEEMDVLDGLKMEATEV----EKLFGRALPI------RKL 950
                                                                                                                                                                                                                                                                                                                                                                                                                       397 GLIDSPSINLDVRKOYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATL---- 450
733 EENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHD---NEYLLYQDDWY--I 787
                                                                                                                                                                                                                                                                                                                                          237 APEAFNYMDKFNEQEINLSLEELKDQRMLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 ----IIKQSEKEYIRI-DAKVVPKSKIDTKIQE----AQLNINQEWNKALGLPKYTKLIT 584
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                                                                                                                                       129 L---VIQSSEDYVENTEKALN------VYYEIGKILSRDILSKINQPYQKFLDVLNT
                                                                                              LSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNT
                                                                                                                                                                                                                                         177 IKNASDSDGODLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLY
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TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
TITLE OF INVENTION: Related Methods
                                                                                                                                                                                                                                                                                            879 ------EVEEIEEEVEKVRDKEVTLFSKLFEGFKE------
                                                                                                                                                                                          848 FIKTDNTCG------PEPPLVERLEKKVEEGERTIIK
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ADDRESSEE: Townsend
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Sequence 2, Application US/08082849B
Patent No. 5677274
GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Rlimpel, Kurt R.
APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogendra
US-08-082-849B-2
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1110 QIKCGDLFENSVVDE--FNECAVSRKKCVPRK---SDLGEFPAPDPSVLVQNFNISDFNG 1164

459 ------DNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDNERLKWRIQLSPDTR 510

1165 KWYITSGLNPTFDAFDCQLHEFHTEGDNKLV--GNISWRIKTLDSGFFTRSAVQKFVQDP 1222

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951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
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237 APEAPNYMDKFNEQEINLSLEELKDQRMLSRYEKWEKIKQHYGHWSDSLSEEGRGLLKKL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908 ---LQRDEENFLRELSKEEMDVLDGLKMEATEV----EKLFGRALPI------RKL 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    788 LSSKVENSPEDYIFVYYKGRNDAWDGYGGSVI,YTRSAVLPESIIPELQTAAQKVGRDFNT 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 L---VIQSSEDYVENTEKALN------VYYEIGKILSRDILSKINQPYQKFLDVLNT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 IKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 L------NRIQVDSSNP-----LSEK--EKEFLKKLKLDIQPYDINQRLQDTG 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8%; Score 132; DB 1; Length 776; Best Local Similarity 17.2%; Pred. No. 0.017; Matches 139; Conservative 117; Mismatches 254; Indels 300;
                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-JUN-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879 ----EVEEIEEEVEKVRDKEVTLFSKLFEGFKE----
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                                                                                                                                                                                                                                                                                                                                                                              NAME: Weber, Kenneth A. REGISTRATION NUMBER: 31,677 REFERENCE/DOCKET NUMBER: 15280-161-1
                                                                                                                                                                                                                              FILING DATE: 25-JUN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENTH: 776 amino acids
TYPE: amino acid
                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 ------GADLVDST---
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                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
California
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                                            94111-3834
                           USA
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                        COUNTRY:
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us-09-075-375a-2.rai

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Sequence 28, Application US/08404531B Patent No. 5863724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                    1223 NQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTR--S 1280
                                                                                                         1281 SVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE-RIIVKEV-- 1337
                                                                                                                                                                                  1338 ------EEIEEEVEKEVEKTEMTLFQRLAAGFNELKODEENFVRE------ 1379
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                                                                    534 ----IIKQSEKEYIRI-DAKVVPKSKIDTKIQE----AQLNINQEWNKALGLPKYTKLIT 584
                                                                                                                                                                                                                  637 PNIAEQYTHQDEIYEQVHSKGLYVPESRSILLHGPSKGV-ELRNDSEGFIHEFGHAVDDY 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8%; Score 132; DB 5; Length 776; Best Local Similarity 17.2%; Pred. No. 0.017; Matches 139; Conservative 117; Mismatches 254; Indels 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW STREET: Steuart Street Tower, 20th Floor, One Market STREET: Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: RELATED METHODS
TITLE OF INVENTION: RELATED METHODS
-----KLILQRNIGLEIKDVQ----
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NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         1380 ----LSKEEME-----FLDEIKMEASEV 1398
                                                                                                                                                                                                                                                                              696 AGYLLDKNQSDLVTNSKKFIDIFKEEGSNL 725
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9401624 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Leppla, Stephen H. APPLICANT: Klimpel, Kurt R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US FILING DATE: June 25, 1993 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 amino acids
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ADDRESSEE: TOWNSEND
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     511 AGYLENG---
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         951 MAVATHCFISPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1007 GRSSRPL------SAFRSGFSKGIFDIVPLPSKNELKELTAPLLIKLVG 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1110 QIKCGDLFENSVVDE--FNECAVSRKKCVPRK---SDLGEFPAPDPSVLVQNFNISDFNG 1164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 QIPIEPRKUDIIHSLSQEEKELLKRIQIDSSDFLSTEEKEFLKKLQIDIRDSLSEEEKEL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 L------NRIQVDSSNP----LSEK--EKEFLKKLKLDIQPYDINQRLQDTG 396
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788 LSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNT 847
                                                                                       129 L---VIQSSEDYVENTEKALN-----VYYEIGKILSRDILSKINQPYQKFLDVLNT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                       237 APEAFNYMDKFNEQEINLSLEELKDQRMLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908 ---LQRDEENFLRELSKEEMDVLDGLKMEATEV----EKLFGRALPI------RKL 950
                                                                                                                                                                                                                                                                      177 IKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLY 236
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                                                                                                                                                                              848 FIKTDNTCG------PEPPLVERLEKKVEEGERTIIK-----
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                                                                                                                                                                                                                                                                                                                                                                  ------EVEEIEEEVEKVRDKEVTLFSKLFEGFKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Liberty Place 46th, Floor CITY: Philadelphia
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MEDIUM TYPE: Floppy disk
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
TITLE OF INVENTION: and Method of Detecting Persistent Hyperinsulinemi
TITLE OF INVENTION: Infancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.7%; Score 124; DB 3; Length 1498;
18.8%; Pred. No. 0.24;
tive 72; Mismatches 221; Indels 17
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                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NA/~
                                                                                                                                                                        ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 6031150ris
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BYLR-0027
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995
NI: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 18.88 Matches 109; Conservative
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                                                                                                                            NUMBER OF SEQUENCES: 4:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-476-900A-28
                                                                                                                                                                                                                                             Philadelphia
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Similarity 18.8%; Score 124; DB 2; Length 1498;
Similarity 18.8%; Pred. No. 0.24;
09; Conservative 72; Mismatches 221; Indels 178; Gaps
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                        UMBER: US/08/404,531B
15-MAR-1995
                                                                                                                                                                                  NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0003
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
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                                                                                                                                                                                                                                                                                                     TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                           CLASSIFICATION:
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                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-404-531B-28
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
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NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,2
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
                                       1248 KIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIR 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 EMTSLRAFAVYTSISIFMNTAIPIAAVLITFV-----GHVSFFKESDFSPSVAFASL 580
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Similarity 18.8%; Pred. No. 0.24;
99; Conservative 72; Mismatches 221; Indels 178; Gaps
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                                                                               -----ETVME 946
846 STPMIVFLDDPFSALDVHLSDHLMQAGILELLRDDKRTVVLVTHKLQYLPHA-DWIIAMK 904
                                                                                   905 DGTIQREGTLKDFQRSECOLFEHW-----KTLMNRQDQELEK-
                                                                                                                           1308 TDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKE 1347
                                                                                                                                                   947 RK---APEPS--QGLPRAMSSRDGLLLDEDEEEEEAAESE 981
                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6054313
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60543131is
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
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REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
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APPLICATION NUMBER: US/08/488,546A
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                                                                                                                                                                                                                                                             Sequence 28, Application US/08488546A Patent No. 6054313
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CLASSIFICATION: 800
PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
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TELEPHONE: 215-568-3100
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INFORMATION FOR SEQ ID NO: 28:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1498 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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; MOLECULE TYPE: protein
US-08-488-546A-28
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                                                                                                                                                                                                                                                                               ; Sequence 28,
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor tent No. 5863724
1024 IFDIVPL-----PSKNELKELTAPLLIKLVGVLACAFLIVPSADAVDALKTCACLLKG 1076
                                                                                                                                            --RIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLF 1117
                                                                                                                                                                                                                                                                                            -----SVLVQNFNI-SDF 1162
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                                                                                                                                                                                                                                                                                                                                                                739 WNSLPD----SEGRRPQQPRAGDSGRFGCQEQRPCGYASQKPWLLNATVEENITFESPF 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ETVME 946
                                             685 FFTWTPDGIPTLSNITIRIPRGQLTMIVGQVGCKSSLLLATLG-----EMQKVSGAVF 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         794 NKORYKMVIEACSLOPDIDIL------PHGDQTQIGERGINLSTGGQRPDQCRPEPST 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     846 STPMIVFLODPFSALDVHLSDHLMQAGILELLRDDKRTVVLVTHKLQYLPHA-DWIIAMK 904
                                                                                                                                                                                                                                                                                                                                                                                                                                        1163 NGKWY----ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKT------
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STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1308 TDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKE 1347
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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979 GITRKRINGTFLL-----KILPPIQ-----SADLRTTGGRSSRPLSAFRSGFSKG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SVLVQNFNI-SDF 1162
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18.8%; Pred. No. 0.26;
tive 72; Mismatches 221; Indels 178;
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                             NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/POCKET NUMBER: BYLR-0027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08488546A
Patent No. 6054313
                                                                                                                                                                                                                                          1581 amino acids
             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.7%
Best Local Similarity 18.8%
Matches 109; Conservative
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-476-900A-6
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CORRESPONDENCE ADDRESS:
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US-08-488-546A-6
                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                  TYPE:
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TITLE OF INVENTION: Infancy
NUMBER OF SEQUENCES: 49
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TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
                                                                                                868 KVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFK--ELQRDEENFLRELSKEEMD 925
                                                                                                                                     581 SLFHILVTPLFLLSSVVRSTVKALVSVQKLSEFLSSAEIREEQCAPREPAPQGQA----G 636
                                                                                                                                                                                                                                                                                                                                                                                                                                           685 FFTWTPDGIPTLSNITIRIPRGQLTMIVGQVGCGKSSLLLATLG-----EMQKVSGAVF 738
1.7%; Score 124; DB 2; Length 1581;
18.8%; Pred. No. 0.26;
tive 72; Mismatches 221; Indels 178; Gaps
                                                                                                                                                                                                     926 VLDGLKMEA--TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDD-----GIGRL 978
                                                                                                                                                                                                                                                     529 EMTSLRAFAVYTSISIFMNTAIPIAAVLITFV-----GHVSFFKESDFSPSVAFASL 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      794 NKQRYKMVIEACSLQPDIDIL------PHGDQTQIGERGINLSTGGQRPDQCRPEPST 845
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STREET: One Liberty Place 46th, Floor
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                Matches 109; Conservative
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Query Match
Best Local Similarity
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905 DGTLQREGTLKDFQRSECQLFEHW------KTLMNRQDQELEK-----ETVME 946

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979 GITRKRINGTFLL-----KILPPIQ----SADLRTTGGRSSRPLSAFRSGFSKG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1163 NGKWY----ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKT------ 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1205 -----LDSGF-----FTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSS 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739 WNSLPD-----SEGRRPQQPRAGDSGRFGCQEQRPCGYASQKPWLLNATVEENITFESPF 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          685 FFTWTPDGIPTLSNITIRIPRGQLTMIVGQVGCGKSSLLLATLG-----EMQKVSGAVF 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      794 NKQRYKMVIEACSLQPDIDIL------PHGDQTQIGERGINLSTGGQRPDQCRPEPST 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 KLSQAQRTTL------EYSNERLKQT----NEMLRGIKLLKLYAWENIFCSRVEKTRRK 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         926 VLDGLKMEA--TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDD-----GIGRL 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 EMTSLRAFAVYTSISIFMNTAIPIAAVLITFV-----GHVSFFKESDFSPSVAFASL 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868 KVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFK--ELQRDEENFLRELSKEEMD 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 1.7%; Score 124; DB 3; Length 1581; Best Local Similarity 18.8%; Pred. No. 0.26; Matches 109; Conservative 72; Mismatches 221; Indels 178;
                                                                                                                                                                                                                                                      OFERALING SIGHER: FC JOS/MS DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
FILING DATE: OF-JUNE-1995
CLASSIFICATION: 800
SEE: No. 6054313ris
: One Liberty Place 46th. Floor
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMMUNICATION INFORMATION:
TELEPEAX: 215-568-3439
FORMATION FOR SEC. 1
                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA.
PPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1581 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                         USA
                                                                                                                               19103
     ADDRESSEE:
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                                                                             STATE: P
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1335 KEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKME 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               623 PPQLVPE-----GTPGGGGP-PALEEDLTVININSSDEEEEEGEEEE 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Indels 38; Gaps
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                                                                                                                                                                                                                                 APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.6%; Score 119; DB 2; Length 905; Best Local Similarity 31.0%; Pred. No. 0.28; Matches 39; Conservative 15; Mismatches 34; Indels
1308 TDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKE 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
                                947 RK---APEPS--QGLPRAMSSRDGLLLDEDEEEEEAAESE 981
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/574,959A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFN-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             Sequence 9, Application US/08574959A Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09357014 Patent No. 6291645 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 905 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                              US-08-574-959A-9
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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sw model using protein search, OM protein

(without alignments) 1309.294 Million cell updates/sec 6, 2001, 03:10:56; Search time 82.15 Seconds November Run on:

US-09-075-375A-2 7495 Perfect score:

..... MEASEVEKLFGKALPIRKVR 1412 1 MALSLHTVFLCKEEALNLYA... Sequence:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

summaries Maximum Match 100% Listing first 45 su PIR_68:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	violaxanthin de-ep	violaxanthin de-ep	hypothetical prote	Ψ.		hypothetical coile	1mpl protein - Mvc	rved hyp	reticulocyte-bindi	hypothetical prote	repeat organellar	myosin heavy chain	myosin beta heavy	nuclear migration	DNA topoisomerase	hypothetical prote	RESA-H3 antiden PF	conserved hypothet	hypothetical prote	-	myosin beta heavy	hypothetical prote	ເວ	surface-located me	hypothetical prote	probable membrane	hypothetical prote	. myosin-like protei	phosphoprotein pho
	;	ID	T03750	T00708	A84606	T28677	T28676	T38077	T30822	Н69378	A42771	H36812	T18372	A59286	A37102	857976	S54174	G70163	B71603	F75103	T29145	A71928	900908	T32650	C70319	JC6009	F64508	S54044	T05113	S38173	A40801
		HG :	~	~	7	7	7	7	7	~	7	7	~	~	Н	~	7	7	7	7	7	7	-	7	7	-	~	~	~	7	~
	1	Match Length DB	478	462	522	2269	2401	1957	1365	886	2829	2469	1939	1935	1935	2748	839	2166	1558	880	1199	1819	1935	5105	1002	1302	800	1025	2712	1875	1109
æ	Query	Match	34.1	2	2.8	5.6	2.2	2.1	2.1	2.1	2.1	2.1	2.0	2.0	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	.1.8	1.8
	1	score	2557	2430	210	194.5	167.5	158.5	156	155.5	155.5	155	151	148.5	146	146	144.5	144	143.5	142.5	142.5			142.5		140.5	140	139.5	139	137.5	137
	Result		1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

probable centromer hypothetical prote	OKF MSV130 HYPOLNE dystrophin, muscle myosin heavy chain conserved hypothet	major merozoite su hypothetical prote	hypothetical prote hypothetical prote chromosome assembl	anthrax toxin leth hypothetical prote chromosome segrega	major merozoite su
371410 118427	12831/ 502041 138055 170387	105603 120978 148153	725592 271622 370356	Q0032 72287 69444	AZOK1
M H F	2000 2000	25.5	M CH	E 8 G	1 S/
1676 3724 1127	3660 1937 978	1639 2261 1934	1624 1979 1156	809 1170 1156	1631
8.89	. 6. 6. 6. 6. 6. 6. 6.	111 8.8.8	8.8.8	1.8	1.7
136.5	134 134 134	134 134 133.5	133 133 132.5	132 131.5 131	130.5
30 31	0 8 8 8 4 8 8 8	36 37 38	33 4 4 1 4 0	4 4 4 2 8 4	45

		de-enoxidase
-		axanthin
3	20	×

violaxanthin de-epoxidase precursor - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000

C. Accession: T03750
R. Bugos, R. C.; Hieber, A.D.; Yamamoto, H.Y.
S. Bugos, R. C.; Hieber, A.D.; Yamamoto, H.Y.
J. Biol. Chem. 273, 15321-1534, 1988
A; Title: Xanthophyll cycle enzymes are members of the lipocalin family, the first ide A; Reference number: 215054; MUID: 98288256
A; Stetus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-478 < BUGO>
A; Crossreferences: EMBL: U34817; NID: 91463122; PIDN: AAC50031.1; PID: 91463123
A; Crossreferences: EMBL: U34817; NID: 91463122; PIDN: AAC50031.1; PID: 91463123
C; Genetics:

A; Gene: TVDE1

C; Function:

A; Description: violaxanthin de-epoxidase and zeaxanthin epoxidase catalyze the additi A; Notesting the photosynthetic apparatus from excessive light A; Note: established as member of the lipocalin family F;1-134/Domain: transit peptide (plastid) *status predicted <TNP>F;1-134/Domain: transit peptide (plastid) *status predicted <MAT>

Gaps ; 0 Length 478; Indels Query Match 34.1%; Score 2557; DB 2; I Best Local Similarity 100.0%; Pred. No. 4.4e-142; Matches 477; Conservative 0; Mismatches 0;

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474 MALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSP 533 ŏ g

534 RICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAI 593 á

g

594 VAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETEC 653 ò

g

δ q

RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773 714 ŏ

241 RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 300 d

HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 774 ŏ

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Best Local Similarity 21.1% Matches 122; Conservative
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-522 <STO>
                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                     A; Gene: At2g21860
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                      C; Genetics:
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                                                                                                                                                                                                                                    violaxanthin de-epoxidase homolog F22013.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C;Accession: T00708
R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Consubnited to the EMBL Data Library, April 1998
A;Bescription: Genomic sequence for Arabidopsis thaliana BAC F22013.
A;Reference number: 214200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: EMBL:AC003981; NID:93063438; PID:93063441; GSPDB:GN00059; ATSP:F2201
A.Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1011 RPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1071 ACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 DNKLYGNISWRIKTLDSGFFTRSAVQKFYQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1251 NKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDN 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1311 TCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELK 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 360
                                      834 LQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDK 893
                                                        1 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 60
                                                                                                                 894 EVTLFSKLFEGFKELORDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 950
                                                                                                                                 421 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 QDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.4%; Score 2430; DB 2; L
100.0%; Pred. No. 1.1e-134;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T00708
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
A; Introns: 72/3; 128/2; 160/3; 292/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-462 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: ATSP: F22013.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: A84606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE002093; NID:g4417279; PIDN:AAD20404.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T28677; C45521
R;Keen, J.; Sinha, K.; Brown, K.; Holder, A.
Mol. Biochem. Parasitol. 65, 171-177, 1994
hypothetical protein At2g21860 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: A84606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      741 LSWRIRTPDGGFFTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVE 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 PEPPV--KLIALVGKGEVSPLK-STSWEEVMLHTARRLKWVD------EGYEMLVFDD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 E----IVSSNDQRAMN-LTQELNQTDILVVVA--------VNNSESV----- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 TDVGSVNKD------KEVTEVVKTVGDAWERRNSDDIRFCLLVIINAYIRPVPVL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 ---ASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 ONLRSK-----GFSTLSCMVKNCGPQILNCLLDPNCRKALQCLNQCS--PVDQVCSYRCI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 659 DLFENSVYDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK----- 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 ASYEGPYFEAFSLCVLQKHNCLELDAKIPEKPYVPP-----MTSFRGKELCHDTAED 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------WFITRGINPTFDAFDCQLHEFH-------TEENKLVGN 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 LFVGWLGELEWSWRVVAGQNPAYDQFPCQYQLFYRGKGKSSFWYEPVFQVRTLEEKLV-- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 --WRRR------WINGVYSNEF----GKIPATFRFSVLDNGVVSNEF------WILVD--VS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 DDLSWGLFHYHGAARVAGQSYTGAVLVTPDGSYPAEKDKERLQSALEKCGIKEWELF-AV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 PEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 ENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKIRMALAPHSNFLANHETIKYVG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 SKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNL 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 SPAHSINQNVPKGNSGCKFPKDVALMV-----WEKWG----QFAKTAIVAIFILSV--- 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.1%; Pred. No. 8.3e-U5;
tive 77; Mismatches 186; Indels 194; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 -----NWIQTNSKNVKNMIC-----FESSPNLMNRLGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 210; DB 2; Length 522; Pred. No. 8.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          852 DNTCGPEPPLVERLEKKVEEGER-----TIIKEVEEIEE 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 DNCSCENPPL----GIPQGSRLHSRISIIEEPDSEEK 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%; Score 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rhoptry protein - Plasmodium yoelii
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A;Tit A;Ref	.le: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii. erence number: Z20508; MUID:95021522	902 FEGFKELORDEENFLRELSKEEMDV	DVLDGLKMEATEVEKLFGRALPIRKLMAVAT 955
A; ACC	ession: T28677	1	
A; Mol	coule type: DNA		76/
A; Res A; Crc R; Kee	A; Residues: 1-2269 <kee> A;Cross-references: EMBL:L27838; NID:g457145; PID:g457146; PIDN:AAA21304.1 R; Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.</kee>	QY 956 HCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTF	HCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSA 1015
MOL. A;Tit	Blockem. Parasitol. 42, 241-246, 1990 Le: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple of Serone sumbor. 346531, MITIPLE of	1016 FRSGFSKGIFDIVPLPSKNELKEL-	ELKELTAP 1042
A; Acc	ession: C4551 first ore impary	Db 843 SQNHNSDINQCLNEVANIYNILKLNK	SQNHNSDINQCLNEVANIYNILKLNKIKKIIDKVKEYTSEIEKNKKNINDELNNSEK 899
A; Mol A; Res A; Crc	A;Molecule type: DNA A;Residues: 2131-2269 <ke2> A;Cross-references: GB:M34283</ke2>	QY 1043 LLLKLVGVLACAFLIVPSADAVDALKTCA :: : : Db 900 VIKKIEGDLS	LLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQT 1099 :: :
Que	ore 194.5; DB 2; Length 2269;	1100 CNNRPDETECQIKCGDLFENSVVDEFNEC- :	CNNRPDETECQIKCGDLFENSVVDEFNEC
Mat 0v	cnes 255; Conservative 213; Mismatches 436; Indels 483; Gaps 65; 304 YII.SOTERKPHDYTEVYVERNDAWDCYGGGVIYWRGDWIDEGTIDNIOKA 366	1129AVSRKKCVPRKSDLGE	-AVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPT 1175
7 점	TELETITETARE STATES OF THE STA	998 KSHKDKSNGYKTEADQNKKAIQKNKELFEQYKEEVTVLLNKYYAVELKNK	
yo d	356 AKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEI 401	1176 FDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFT	FDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLY 1229
λο i	EEEVEKEVEKVRDTEMTLEQRLLEGEKELQO-DEENFVRELSKEEK 44	1230 NHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLP	FVYYRGRNDAWDGYGGAVVYTRSSVLP 1284 : AITSIKVSVEPFKTKI 1118
a ko t	136 AKELEKNNATIDELANQSPYKVIGTIENKNTIYNTIKSYFDOIYEGDIDFFYNELSSIVK 195 447 E-ILNELQMEATEVEKLEGRALPIRKLEMALAPHSNFLANHETIKYYV 493	Qy 1285NSIIPELEKAAKSIGR	NSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGER 1331
a ko t	190 EDFIDDIE-DKTKLENLEKSKIDNVYDKIQKMEIETVKSHLANNIETNNKLPNTILEIKKYI 254 494 GSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSH 549 1:	Qy 1332 IIVKEVEEIEEEVEKEVEKUGRTEMTLFQ Db 1176KNIEDQKKELDEVNSKIKNIENTVNQ	IIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELS 1381 : : :: :: : : : - - - - - - - - - - - -
3 6 E	533 IDEL SKELNKMILELFRUNEKELSNILSDIDKRKEQL-SEIRSKMILEIRNHINSQ 30/ 550GKHNLSPAHSINQNVPKGNSGKFPKDV 577 10 mannamerepsakoanananananananananananananananananana	1382 KEEMEFL 1388 :: : 1233 KPTIQHI 1239	
75 75	578 ALMVWEKWQQFAKTAIVAIPILSSVASKADAVDALKTCTCLLKECRLELAKCISNPACAAN 637	RESULT 5 128676	
g &	PENECAVEDERCH.	rhoptry protein - Plasmodium yoelii (fr C;Species: Plasmodium yoelii	(fragment)
g G	CEQSFNDNKSLINETKNSIEKEYONINTLKKVDEYIKVCKSTKESITKFSSKQTIL	Date: 15-Oct-1999 #Sequence_revision Accession: T28676; A45521 Sinha, K.A.; Keen, J.K.; Ogun, S.A.;	<pre>15 -Oct 1999 #text_change UI-bec-2000 Holder, A.A.</pre>
y g	686VGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEE- 734	1. Biochem. Parasitol. 76, 329-332, 1 Title: Comparison of two members of a Reference numbber: Z20507; MUID:970774	1996 a multigene family coding for high-molecular ma 455
3 6	ALMANDATALINETURE LINE E. QILICK QIRLENK TEFELAMNHEANNNELNKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSS	Accession: 1286/6 Status: preliminary; translated from Molecule type: DNA	GB/EMBL/DDBJ
q	508 IKYFSDLKANLGINEENMLYNQFTEKEKTFNDIKEKNIHINEEIS 552	Residues: 1-2401 <sin> Cross-references: EMBL:U36927; NID:91</sin>	1041784; PID:91041785; PIDN:AAB41263.1
Qy Db	791 KVENSPEDYIFGY 814	keen, J.; Holder, A.; Flaylair, J.; L. 1. Biochem. Parasitol. 42, 241-246, 1 litle: Identification of the gene for Reference number: A45521: MITD:911016	N;Neel, J.; Holder, A.; Flaylalr, J.; LOCKYer, M.; Lewis, A. Mol. Biochem. Parasitol. 42, 241-246, 1990 A;Title: Identification of the gene for a Plasmodium yoelli rhoptry protein. Multiple A:Reference number: A45521: MITD:91101660
Qy	84	A;Accession: A45521 A;Status: preliminary	
QΩ	613 EGNIKYTDKIKKINDDIMAVSQQIDQHINGLDDIQKKSESYVSEMKEQINKLEKVSNTEI 672	A; Residues: 126: 240: A; REE> A; Cross-references: GB: M34281	
oy D	850 KTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKL 901	2.2%;	Score 167.5; DB 2; Length 2401;

Be	f)	ari	da .	1227	ILDIQLSVE KRINGTFLI
Qy Dp	23 PCNERFHRSGQPPTNIIMMK - IRSNNGYF 1 1 1 1 1 1 1 1 1	PCNERFHRSGQPPTNIIMMKIRSNNGYFNSFRLFTSYKTSSFSDSSHCKDKSQICSID 80 : : :	qa -		KNIT-LE
Qy	81 TSFEEIQRFDLKRGWTLILEKOWRQFIQLAIVLVCTFVIVPRVDAVDALKTCACLLKECR	IVLVCTFVIVPRVDAVDALKTCACLLKECR 140	qq .		
QZ	141 IELAKCIANPSCAANVACLQTCNNRPDETECQIKC :	QTCNNRPDETECQIKCGDLFENSVVD 185 : :	ර් <u>අ</u>		
QY Db	186 QFNECAVSRKCVPRKSDYGEF : : : : : : : : : : : :	FNECAVSKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWY 229 : : : : : SLNNHESNNKELLTYFYDLKANLGKNKENMLYKQFNEKEKAVE 658	y d		
Qy	230 ITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKT) :::::: :::::: 659DIKKKNVDINKIVSNIEITIYT	ITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPGAL 289 :: ::::	OV QD		
Qy	290 YNHDNEFLHYQDDWYILSSQIENKPDDYIEVYY: :	SQIENKPDDYIEVYRGRNDAWD 330 :	^୪ ପ୍ର		
Qy	331 GYGGSVIYTRSPTLPESIIPNLOKAAKSVG 	GYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEG 390 :: :: :	. — . — .		
Qy	391 EKLLIKEAVEIEEEVEKUVEKUPTEMTLFQRLLEGFKELQODEEN- : : :	EKLLIKEAVEIEEEVEKEVEKVROTEMTLFQRLLEGFKELQQDEEN 436 : : : :: : : : : : : : KTWENEDFKEIEKKIENIVEX 847		1348	VEKVGRTEN : : LNLIFEN
Qy	437FVRELSKEEKEI	LNELQMEATEVEKLFGRALPIRK 471 : :: :: : : DDLDNIKKKSQEIEKEMNINMDIKMDIHKE 907		RESULT T38077 hypotheti	6 cal coiled
Qy	472 LRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAK :WGWEDYFGSIVVAK :	RFSWGWEDYFGSIVVAK 518 :	D O O &	Species Date: 0 Accessi Connor,	C; Species: Schizose C; Date: 03-Dec-1995 C; Accession: T38077 R; Connor, R; Churc
Qy Db	519 ICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINONVPKGNSGCKFPKDVA :: : : : :	HGKHNLSPAHSINONVPKGNSGCKFPKDVA 578 : : :: YNILKLNKIKKIIDK998	1	Dmitted Referen Accessi Status:	to the ENce number:
Qy	579 IMVWEKWGQPAKTAIVAIFILSVASKADAVDALKTCTCL 	ILSVASKADAVDALKTCTCLLKECRLELARCISN 631 : ::	, ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	Molecul Residue Cross-r Experim	Molecule type: DN Residues: 1-1957 Cross-references: Experimental sour
Qy	632 -PACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSD	KCGDLFENSVVDEFNECAVSRKKCVPRKSD 685 : : : : : -INTYFKNAEEYNQ 1082	. A A	C;Genetics: A;Gene: SPDB:SPN A;Map position:	.cs: SPDB:SPAC1E sition: 1
Qy	686 VGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRI 	LNPTFDAFDCQLHEFHTEENKLYGNLSWRI 745 ::: : : NIKKNNGTNNTDYNI 1117	··········	Query Match Best Local S Matches 265	atch cal Simila 265; Cc
Qy dd	746 RIPDGGFFTRSAVQKFVQDPKYPGILYNHD : 1118 KR	RTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYK 805 		305	YKTSSFSDS: :: :
γο .		TAAQKVGRDENTFIKTDNTCGFEPPLVERL	3 & a		IVPRVDAVI
Qy	866 EKKVEEGERTIIKEVEBIBEEVEKVRDKEVTL ::: ::: ::::::::::::::::::::::::::::	EKKVEGGERTIIKEVEEIEBEVEKVRDKEVTLFSKLFEGFKELQRDENFLRELSKEEMD 925 :::: :::: ::::::::::::::::::::::::::	. У д	176	GDLFENSV:
λό		THCFTSPCHDRIRFFSSDDGIGRLGITR 982			

qq	1227 IL	ILDIQLSVEPFKIKFLKIKDLRTKSDDCLKETKDIETKISNLSIDTQETKL-IEN 1280
OY	983 KR	RINGTFLLKILPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAP 1042
qq	1281 KN	KNILNT-LEKLLESLKNQ
Qy .		LIVPSADAVDALKTCACLLKGCRIELAKCI 1 : : :
qq	1315 IK	IKNIESNVNOHKKNYEIGIVEKINEIAKANKDQIESTOKLIIPTIKNL 1362
oy a		ANDACAANVACLQTCNNRPD-ETECQIKCGDLFENSV 1121
g ò	1363 15 1122 VD	ITSGLNPTF 117
qq		: : : : : : : : :
Οy	1177 DA	DPNQPGVLYNHDNEYL 1
qq	1481 DN	DNISNSINNVKKSTDENLLLNILNQTKEMYANIVSKKYYSYK 1522
Qy	1237 HY	HYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAK 1296
qq	1523 YE	NIFINIPK
QY	1297 SI	TDNTCGPEPALVE
qq	1569	DILTEIPSPEKTSETYTKISDSYNTLLDILKRSQELQKKEQQA 1611
Qγ	1348 VE	VEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEKL 1401
Ор	1612 LN	LNLIFENRLLHDKVQATNELKDTLSDLKNKKEQILNKVKLLLHKSNELNKL 1662
RES 1338 1338 C;30 C;D R;C Sub	SULT 6 8077 pothetical Species: S Date: 03-E Accession: Connor, R. Omitted	RESULT 6 T38077 hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38077 R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. Submitted to the EMBL Data Library, April 1996 A;Reference number: Z21767
A A A	Accession: Status: pr Molecule t	: T38077 reliminary; translated from GB/EMBL/DDBJ :ype: DNA
A A A	Residues: Gross-refe	1-1957 <con> zrences: EMBI:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c</con>
4 0 4 4 4 0 6 8	Experiment Senetics: Sene: SPDB Map positi	al source: scrain 9/20,7 COSMILO CIFS 3:SPACIF3.06c ton: 1
O m X	Query Matc Best Local Matches 2	Query Match 2.1%; Score 158.5; DB 2; Length 1957; Best Local Similarity 17.6%; Pred. No. 0.54; Matches 265; Conservative 227; Mismatches 503; Indels 511; Gaps 68;
Οy	59 YK	YKTSSFSDSSHCKDKSQICSIDTSFEELQRFDLKRGMTLILEKQWRQFIQLAIVLVCTFV 118
qq	305 HN	HUVANYSDAIVHKDK-LIEDLSTRISEFDNLKSERDTLSIKNEKLERL 353
Qy	VI 911	IVPRVDAVDALKTCACLLKECRIELARCIANPSCAANVACLQTCNNRPDETECQIKC 175
qq	354	KDSRTSNSOLEEEMVELKESNRTIH
ko t		GDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFN 220
or T		* (
ΟŊ	221 MK : I	MKDFSGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDG-GFFTRSAV 2/6

qq	457	IKDFEKIEQDLRACLNSSSNELKEKSALIDKKDQELNNLREQIKEQKKVSESTQSSL 513	
ογ	277	QTFVQDPDL.PGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSV 336 : :	
qq	514	QSLQRDILNEKKKHEVYESQLNELKGELQTE544	
70 4	337	GPEPPLVERLEKTAEEGEKLLIK :	
9	0.40	AAEKEAAVATNNELSESKNSLQT	
oy Og	397	EAVEIEEEVRKEVEKYRDTEMTIFORLLEGFKELQODEENFVRELSKEEKEILN 450 1 1 1 1 1 1 1 1 1	
ó	451		
o qo	641	TLSDENNDLRTKLLKLEESNKSLIKKQEDVDSLEKNIQTLK69	
οχ	496	KLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKH 552	
qq	969		
οy	553		
g	727	ETLEAQRNDLHSSLSDAKNTNAILSSELTKSSEDVKRLTANVETLTQD 774	
Oy Dp	603	SKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIK 656	
Οy	657	CGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDP 694	
QQ	822	: : ::: ; ::: ; : ;	
Οy	695	SVLVQKFDM-KDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIR 746	
qq	882	: IRLDKLTGKLK	
ΟŊ	747	TPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKG 806	
q	938	::: :: :: :: :: :: ::	
δy	807	RNDAMDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLE 866	
qq	977	KLDETLSKSSKL-EADIEHLKNKVSEVEVERNALLASNERLM 1017	
ΟŊ	867	KKVE-EGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELORD 911	
qq	1018	DDLKNNGENIASLQTEIEKKRAENDDLQSKLSVVSSEYENLLLISSQTNKSLE-D 1071	
δς d	912	υ	
3	7	NINGENTIERNWYNALDERDZKWYELEELISNIGNEERNAUINDELLALKKK 1124	
oy Oy	958	FTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIGSAD 1001	
ŏ	1002		
qq	1184		
οy	1062	DAVDALKTCACLLKGCRIELAKCIANPACAANVACLOTCNNRPDETECOIKCGDLFFNSV 1121	
q	1207		
οy	1122	VDEFNECAVS-RKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYIT-SGLNPTFD 1177 : : : : :	
g		EESFNKYAVSLRELCTKSEIDVPVSEILDDNFVFNAGNFSELSRLTVLSLENYLD 1295	
žo d		AFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLH	
G G	1296	AFN-QVNFKKMELDN	

QY	1238	YQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKS 1297
QQ	1331	
QY	1298	IGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVE 1345
qq	1349	SEKNFLRKEAEMTENIH-SLEEGKEETKKEIAELSSRLEDNQLATNKLKNQ 1398
QY	1346	KEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEA 1395
qq	1399	LDHLNQEIRLKEDVLKEKESLIISLEESLSNQRQKGKESSLLDAKNELEHMLDDTSRKNS 1456
Qy	1396	SEVEKL 1401
qq	1457	SLMEKI 1462
RES	RESULT 7	
130 1mp C;S	ozz 1 prote pecies:	ein – Mycoplasma hominis Mycoplasma hominis
Q;O	ate: 22 ccessic	xt_cha
R;U Inf	ensen, ect. Im	L.T.; Ladertoged, S.; Birkelund, S.; Christiansen, G. mun. 63, 3336-3347, 1995 pallortion of Movoplasma hominis DG21 deletion mutants by cultivation in the
A; R	eferenc	
A, A	tatus:	preliminary; translated from GB/EMBL/DDBJ type: DNA
# # C C # #	A;Residues: 1-13 A;Cross-referenc C;Genetics: A;Gene: lmp1 A;Genetic code:	A, Residues: 1-1365 <jen> A, Residues: 1-1365 <jen> A, Cross-references: EMBL:U21962; NID:g790243; PID:g790244; PIDN:AAA81013.1 C, Genetics: A, Gene: Impl A, Genetic code: SGC3</jen></jen>
OM	uery Ma est Loc	Query Match 2.1%; Score 156; DB 2; Length 1365; Best Local Similarity 16.8%; Pred. No. 0.46;
×	atches	vative 18
QY	272	SAVOTFVODPDLPG
qa	282	TRNQLQEFINTNKNNPNYSELISQLTSKRDSKNSVTDS 319
QY	332	YGGSVIYTRSPTLPESII-PNLOKAAKSVGRDFNNFITTDNSCGPEPPLVERLEK 385
ΟD	320	SNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVSNANTLSA 369
QY	386	TAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVREL 441
QQ	370	KLTDKDNTIQQAKTELEKEVQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETF 425
Οy	442	SILNELOMEATE
QQ	426	NKDKEAKFNELKQTRNQIQEF446
Qy	502	RIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPA
QΩ	447	
Qy	561	NONVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKE 620
QQ	490	KQALAKANDNLAKS 509
Qy	621	CRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCV 680
qq	510	IKEQLNNSVSNTIQQAKTE 541
λō	681	PRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENK 736
qq	542	LEKEVQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETFNKDKEA 588

C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Qy	737	LVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSP 796	
οg	589	KFNELKQTRNQIQEFINTNKNNPNYSELISQLTSKRDS 626	
ΟŽ	797	-	
qq	627	KNSVTDSSNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVS 676	
δλ	851	TDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLF 898	
QQ	219	NANTLSAKLTDKDNTIQQAKTELEKEIQKANQAIKSNNTASMQSAKSSLD 726	
δy	899	SKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVAT 955	
g	727		
δý	926		
QQ	992	NNPNYSELISQLTSKRDSKNSVTDSSNKSDIESANTELKQALNTAKAKK 814	
οy	1010	SPPLSAFRSGFSKGIFDIVPLPSKNEL-KELTAPLLLKLVG 1049	
qq	815	SSIDNELRPLKNDLQSKIEEFGPIRNTNFSWISSKLETTKNKLAEELT 862	
δy	1050	1050 VLACAFLIVPSADAVDALKTCACLKGCRIELAKCIANPACAANVACLQTCN 1101	
qq	863		
ΟŊ	1102	1102 NRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQ 1155	
QQ	806	SIIGYRLFKLAQAEQFUNSDVDKLKNAWEEKQTLLSKKQKLGNQSTKDYLTQLSTEMSTQ 967	
٥y	1156	1156 NFNISDFNGKMYITSGLNPTFDAFDCQLHEFHTBGDNKLVGNISWRIKTLDSGFFTR- 1212	
Op	896	ESTIKKVIVNIQAHIRNNLNSQYRLEAD-KLIANMKRGYGDKV 1009	
δy	1213	SAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRN 1265	
QQ	1010	GIESLOKW-QDLMDDSVLSVDDSLKDDFNKALRVLVGDYTKNPPVSSWFINKRNRS 1064	
δ	1266	-DAWDGYGGAVVYTRSSVLPNSI1300	
qq	1065	1065 IENYQNLRNLILVRENEILLIDKRAKDLDKRAEKTIKFVDENINSLDQRAKRLKQEILNAKN 1124	
δy	1301	DESTFIRTDNTCGPEPALVEREKTVEEGERIIVKEVEEIEEEVEKEV 1348	
g	1125	1125 DLSNFTLNHQKNQFTAKDITPKISLLENKLNEINQYLLPIIKEKAVSKISBIEKN-KKEL 1183	
οy	1349	1349 EKVGRTEMTLFQRLAEGFNELKQDESNFVRELSKEEMEFLDEIKME 1394	
qq	1184	1184 EDIIRSNFYLWEKVEINKYISELTNKQVELRSNINFE 1220	
RESULT	17.		

C) Species: Archaeoglobus fulgidus
C; Species: Oce-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C; Accession: H63378
R; Klenk, H.P.; Clayton, R.A.; Toub, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woses, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech A; Recession: H63378
A; Reference number: A69250; MUID:98049343
A; Status: Preliminary; nucleic acid sequence not shown; translation not shown

A; Cross-references: GB: AE001032; GB: AE000782; NID: 92689355; PIDN: AAB90211.1; PID: 9264956 A; Molecule type: DNA A; Residues: 1-886 <KLE>

27; 1289 PELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEV 1348 1349 EKVGRTEMTLFQRLAEGFN---ELKQDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKA 1405 968 FFSSDDGIGRLGITRKRINGTFLLKILPPIQSA - DLRTTGGRSSRPLSAFRSGFSKGIF 1025 1026 DIVPLPSKNELKELTAPL-------LUKLVGVLACAFLIVPSADAVDALKTC 1070 1071 ACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130 1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190 -----DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYN-- 1230 1231 --HDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSII 1288 594 ------QSLRPFYNKWLELKDAESRLESELKRRE-KLEDEISEAIAKLEEANGKA 641 405 KLKKLIAKKSSLKTRGAQLKKAVEE------LKSAERTCPVCGRELDEEHRKN 451 452 IMAEYTREMKRIAEELAKADEIEKKLKERLEKVEKALEKOETVLKYROWVDELKALENEL 511 512 SSHDAE------KLSAESEE----YRKVKERLDGLRGQOKILLSSA---SRI 550 198 RISBEIKSIESLREKLSEEVRNLESRIKELEEHKSRLESLRKQESSVLQEV-----R 249 330 D-----TLKPKMDRMQGIK-- 372 -----KMYDLLSKAKEEE-KEITE 404 797 EDYIFVYYKGRNDAWDGYGGSV--LYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTD-N 853 854 TCGPEPPLVERLEKKVEEGERTI---IKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQR 910 911 DEENFLRELSKEEMDV---LDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIR 967 152 EDY-----ENAWKNLGAVIRMLEREKERLKEFLSQEEQIKROKEEK-----KAEIE 197 Gaps 85; Mismatches 221; Indels 221; Length 886; Query Match 2.1%; Score 155.5; DB 2; Best Local Similarity 20.6%; Pred. No. 0.27; ... Matches 137; Conservative 85; Mismatches 221; 1406 LPIR 1409 290 1191 Dp g Óλ δ a g δλ δ q δ ద à qq ŏ qq δy g ŏ δ g

reticulocyte-binding protein 1 - Plasmodium vivax A4277

642 EEIR 645

RESULT

C.Species: Plasmodium vivax
C.Species: Plasmodium vivax
C.Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C.Accession: A42771
R.Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.
Cell 69, 1213-1226, 1992
A.Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites.
A;Reference number: A42771; MUID:92315338
A;Accession: A42771
A;Status: preliminary
A;Status: preliminary
A;Status: Belem strain, merozoites
A;Residues: 1-2829 <GAL>
A;Residues: 1-2829 <GAL>
A;Residues: sequence extracted from NCBI backbone (NCBIN:108114, NCBIP:108115)

Om;	Query Matc Best Local	h 2.1%; Score 155.5; DB 2; Length 2829; Similarity 17.4%; Pred. No. 1.4;	
		ches 573; Indels 529; Gaps	76;
δ		WRQFIQLA 11	
Q C	0111	TSNKNEILKSVKEVEDKLNLVEQNEDYKKVKNPENEKQLEAIRGSMSKLKE 1160	0
δý	111	IVLVCTFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETE 170	
QQ	1161	VINKHVSEMTQLESTANTIKSNAKGKENEHDLEELNKTK 1199	6
ò	171	CQIKCGDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNM-KDF 224	
р	1200	DIYEKLKKIAEELKEGTVNELKDANEKANKVE-PEPERNIIGHVLERITVEKDK 125	9
δλ	225	SGKWYITSGLNPTFDAFDCQLHEF HMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQD 282	
QQ	1257	AGKVVEEMNSLKTKIEKLIQETSDDSQNELVTTSITKHLENAKG 1300	0
δλ	283	PDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRN-DAWDGYGGSVIYTRS 341	
QQ	1301		80
δy	342	PTLPESIIPNLOKAAKSVGRDFNNFITTDNS 372	
QQ	1329		8
Οy	373	CGPEPPLVERLEKTAEEVEKLLIKEAVEIBEEVEKEVEKVROT 415	
qq	1389		9
ò	416	EMTLFQRLLEGFKELQODEENFVRELSKEEKEILNELQME455	
qq	1447	ALTFWEE-SEKFKQMCSSHMENAKEGKKKIEYLKNNGDGGKANITDSQMEEVGNYVSKAE 150	2
δ	456	ATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYY 492	
QQ	1506	:::	æ
Οy	493	VGSKLPGHKRRSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKH 552	
qq	1559	: : : : -SAKL	3
δy	553	NLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALK 612	
qq	1604	: :	o.
δ	613	TCTCLLKECRLELAKCISNPACAANV ACLQTCNNRPDETECQ-IKCGDLFENSVVDEF 669	
QQ	1660	: : : : 3ARESYEKNLETVQNEMSRINVEEGSLTDIDKKITDIENDLLKMKKQYEEGLLQKI 1719	ı,
οy	670	FIT	
QQ	1716	: : : : :	vo.
οy	729	BEHTEENKLVGNLSWRIRTPDGGFFTRSAVQK 760	
QQ	1767		ıo
δŽ	761	FVQDPKYPGILYNHDNEYLLYQDDWYILS789	
Op	1827	VESLKLLKEMMKKVSAEYEGMKRDHTSVSQLVQDMKTIVDELKTLNDISECSSVLNNVVS 1886	9
οy	190	SKVENSPE-DYIEVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN 846	
Dp	1887	IVKKVKESKHADYGREDANSMYESMYTLANYFLSDEAKISSGMEFN 1933	_
οy	847	TFIXTDTICGPEPPLVERLEKKVEEGERTILKEV 880	
Op	1932	AEMKSNFKTDLELEIFSVISNSNELLKKIEQDSNDVIQKERESEQLAKDATDIYNVIKLK 1991	

```
hypothetical protein ORF64 - saimiriine herpesvirus 1 (strain 11)

C.Species: saimiriine herpesvirus 1

C.Species: saimiriine herpesvirus 1092

C.Species: sequence_revision 16-Oct-1992 #text_change 08-Oct-1999

R.Abbrecht, J.

S.Babrited to the EMBL Data Library, January 1892

A.Description: Primary structure of the herpesvirus saimiri genome.

A.Reference number: A36806

A.Residues: 1-2469 (ALBA)

A.Residues: 1-2469 (ALBA)

A.Residues: 1-2469 (ALBA)

A.Residues: 1-2469 (ALBA)

A.Conserreferences: 1-34846; NID:960320; PIDN:CAA45687.1; PID:960385

R.Albrecht, J.C.: Nicholas, J.; Biller, D.; Cameron, K.R.; Blesinger, B.; Newman, C.; J. Virol. 66, 5047-5058, 1992

A.Tille: Primary structure of the herpesvirus saimiri genome.

A.Contents: annotation; protein-coding frames

A.Contents: annotation; protein-coding frames

C.Genetics:

A.Gene: 64
                                                                 995 PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNE----LKELTAPLLLKLVGV 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2078 --TQLEGIVVSAGESKE------DIEKLERSNEEMRNISEKISTIDSK---- 2117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1051 LACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2118 -----VIEMNSTIDELYK---LGKNCOAHWISLISYTANMKTSKKLIMINKEKENTE-- 2166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 | : : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2313 SVNDHMHSMEAEMIKNGLKYTPESVQNINNIYSVIEAEVKTLEEIDRDYGDNYQIVEEHK 2372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1354 TE-----EFLDE 1390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1268 ------WDGYGGAVVYTRSSV--LPN--SIIPELEKAAKSIGRD------- 1301
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881 EEIEEEVEKVRDKEVTLFSKLFEGFKELQRDE-----ENFLRELSKEEMDVLDGLKMEA 934
                                                                                                                                                                                                                      935 TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2041 -ELENL-----KKMVTIY-----RDKKSERESGLQEM---ENEMN-TYSNSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1228 LYNHDNEYLHYQDDWYILSSKIENKPEDY-----IFVYYRGRNDA----
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58; Ouery Match 2.1%; Score 155; DB 2; Length 2469; Best Local Similarity 17.3%; Pred. No. 1.2; Matches 230; Conservative 208; Mismatches 497; Indels 396; Gaps

Wed Nov 7 09:23:54 2001

Ö E	QY 1207 SGFFTRSAVQKFVQDPNQPGVLY :	SGEFTRSAVQKEVQDPNQPGVLXNHDNEYLHYQDDWYLLSSKIENKPEDYIFVYY 1261
0	1262 RGRNDAWDGYGGAVVYTRSSVL	12 JERUSTINI TOTAL
Ω	1125	:: FTPPKFDWIHYYESNVNFHLKTINLPKVSTVAH
Ø Å	OY 1297 SIGRDFSTFIRTDNT-CGPEPALVERIE- Db 1185 NIGHELSLLSQALNSKTLPEAVVGTSLEQ	SIGRDESTFIRTDNT-CGPEPALVERIE
ð A	OY 1338 EEIEEEVEKEVEKVGR ::	EEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFL 1388 :: :
о 	QY 1389 DEIKMEASEVE 1399	
Ω	Db 1305 -ENTVKAAELQ 1314	
ME HO	RESULT 11 118372 repeat organellar protein - Plasm C;Species: Plasmodium chabaudi	
	C; Date: 1.5-OCT-1999 #Sequence_revision is-OCCT-1999 C; Accession: T18372 R; Werner, E.B.; Taylor, W.R.; Holder, A.A. Mol. Biochem. Parasitol. 94, 185-196, 1998 A:fitle: A Plasmodium chabaudi protein contains a	*text_change is out iss repetitive region with a
	A, Reference number: 218922; MUID: A, Accession: T18372 A, Status: preliminary; translated	,
444	A; Molecule type: DNA A; Residues: 1-1939 <wer> A;Cross-references: EMBL:U43145;</wer>	NID:91151157; PID:91151158; PIDN:AAC63403.1
	Query Match 2.0%; Best Local Similarity 17.5%; Matches 189; Conservative 16	2.0%; Score 151; DB 2; Length 1939; Llarity 17.5%; Pred. No. 1.5; Conservative 167; Mismatches 299; Indels 422; Gaps 50;
Ο Δ	QY 380 VERLEKTAEEGEKLLIKEAVEIE	VERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLEQRLLEGFKELQQDEEN 436 :
ο д	Qy 437 FVRELSKEEKELLNELQN : :	FVRELSKEEKEILNELQMEATEVEKLFGRALPIFKLRMALAPHSNFLANHE 487 :
о <u>о</u>	QY 488 TIKYYVGSKLPGHKRFSWGWEDY : :: : Db 197 KLTCEVQEKKDNLEKIN	TIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLF 547 :
0 4	548	SHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKMGQFAKTAIVAIFILSVASKADA 607
	809	ACAANVACLQICNNRPDETECQIKCGDLFENSVVD
a 0	QY 668 EFNECAVSRKKCVPRKSDVGDFF	DKFDMKDFSGKWFITRGLNPTFDAFDCQL
Ω	DD 288 KENEILIEKLKDIESRE	
о п	QY 728 HEFHTEENKLVGNLS-WRIRTPDGGFFTRSAVQKFVQI : :: :: :: :: : Db 322 NTLKSDLSKNACQMEVYKLEIKDLSQSLVEKERE	HEFHTEENKLYGNLS-WRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWY 786
о 	QY 787 ILSSKVENSPEDYIFVYYKGRNI	ILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN 846
<u>п</u>	Db 366KINNMKEKLSSINF	KINNMKEKLSSINDKGIDNTVLHSEEEKI-NKLLKEKETELNEIHKKYN 413

O A	о <u>п</u>	о <u>п</u>	О О	о <u>п</u>	σ Δ	о <u>о</u>	о <u>о</u>	о д	α <u>α</u>		
OY 847 TFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVT 896	QY 897 LFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMA 952	QY 953 VATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRP 1012	OY 1013 LSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCAC 1072	QY 1073 LLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVD 1123 1	QY 1124 EFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTF 1176 I <td< td=""><td>Δ .</td><td>QY 1234 EYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEK 1293 1</td><td>QY 1294 AAKSIGRDFST-FIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEEVEKEVEK 1350 </td><td>OY 1351 VGRTEWTLAGGIAAEGENELKQDEENFVRELSKEEMEFLDEIKMEASEVEKLEG 1403 :</td><td>Sulr 12 Sals heavy chain beta chain, cardiac - pig Species: Sus scrofa domestica (domestic pig) Species: Sus scrofa domestica (domestic pig) Species: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep- Accession: A59286 Reference number: A59286 Accession: A59286 Reference number: A59286 Reference number: A59286 Reference number: A59286 Residues: 1-1935 KGO) Residues: 1-1935 KGO) Experimental source: Strain domestica Superfamily: myosin heavy chain; myosin motor domain homology Residues: cardiac muscle; heart Residued: 2.0%; Score 148.5; DB 2; Length 1935; Best Local Similarity 16.7%; Pred. No. 2; Matches 248; Conservative 220; Mismatches 555; Indels 459; Ga 166 PDETECQIKCGDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRN</td><td>QY 21/ ONFINMATESSGRWITSGLMFTFDAFDCQLHEFHWENDKL 255 1 </td></td<>	Δ .	QY 1234 EYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEK 1293 1	QY 1294 AAKSIGRDFST-FIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEEVEKEVEK 1350 	OY 1351 VGRTEWTLAGGIAAEGENELKQDEENFVRELSKEEMEFLDEIKMEASEVEKLEG 1403 :	Sulr 12 Sals heavy chain beta chain, cardiac - pig Species: Sus scrofa domestica (domestic pig) Species: Sus scrofa domestica (domestic pig) Species: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep- Accession: A59286 Reference number: A59286 Accession: A59286 Reference number: A59286 Reference number: A59286 Reference number: A59286 Residues: 1-1935 KGO) Residues: 1-1935 KGO) Experimental source: Strain domestica Superfamily: myosin heavy chain; myosin motor domain homology Residues: cardiac muscle; heart Residued: 2.0%; Score 148.5; DB 2; Length 1935; Best Local Similarity 16.7%; Pred. No. 2; Matches 248; Conservative 220; Mismatches 555; Indels 459; Ga 166 PDETECQIKCGDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRN	QY 21/ ONFINMATESSGRWITSGLMFTFDAFDCQLHEFHWENDKL 255 1
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δy d		-VGNLTWRIKTLDGGFFTRSAVQTFV	
a a	480	HMFVLEQEETKKEGLEWEF1DFGMDLQACIDLIEKFMGIMSILEEECMFPKA	
Oy Dp	281	QDPDLPGALY-NHDNEFLHYQDDWYILSSQIENKPD-DYIFVYYRGRNDAWDGYGG 3	334 593
Q 4	335	LVERLEKTABEGEKL	393
3 8		FKELOODEENFVRELSKEEKE	447
r qq	645	SPGVID	685
Οy	448		492
Dp	989	NPLVMHQLRCNGVLEGIRICRKGFPNRILYGDFRQRYRILNPAAIPEGGFIDSRKGAEKL 7	745
Qy	493	CCGLDSRGLQLFSHGKH	552
QQ	746	LGSLDIDHNQYKFGHTKVFFKAGLLGLLEEMRDERLSRIITRIQAQSRGVLSRMEFKK 8	803
Οy	553	NLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVD 6	609
QQ	804	LERRDSLLIIQWNIRAFMSVKNW-PWMKLYFKIKPLLESAETEKEMA 8	850
Qy	610	ALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFE 6	662
QQ	851	THE	910
Qy	663	NSVVDEFNECANSRKKCVPRKSDVGDFPVPDPSVLVQKFD 7	702
QQ	911	NKIQLEAKVKEMTERLEDEEEMNAELTAKKRNVEDECSELKRDIDDLELTLAKVEKEK 9	896
Qy	703	MKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFV 7	162
Dp	696	-VKNLTEEMAGLDEIIAKLT	993
Oy	763	FVYYKGRNDAWDGYGGSVLYTR	822
QQ	994	KEKKALQEAHQQALDDLQAEEDKVNTLTKAKVKLEQHVDDLAGSLEQEK 1	1042
QY	823	SARDFRDFRDF	357
οp	1043	KVRMDLERAKRKLEGDLKLTQESIMDLENDKQQLDERLKKKDFELNALNARIEDEQALGS 1	1102
Οy	858	1 1	889
qq	1103	. : : : : :	1161
Qy	890	VRDKEVILFSKLFEGFKELQRDEENFLREL 9	919
QQ	1162	EMNKKREAEFQKMRRDLEEATLQHEATAAALRKKHADSVAELGEGIDNLQRVKQKLEKEK 1	1221
Qy	920	MAVATHCFTSPCHDRIRFFSSDDGIGRLG	979
qq	1222	SEFKLELDDVISNMEQIIKAKANLEKMCRTLEDQMNEHRSKAE 1	1264
QY	980	IFDIVPLPSKNEL	1036
qq	1265	ETQRSVNDLKLTYTQQTENGELSRQLDEKEALISQLTRGKLTYTQQL 1	312
δλ	1037	KELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC 1	1096
qq	1313	DIKRQLEEEVKAKNALAHALQSARHAADLLREQYEEETETKAELQRVLSKANSEVAQ 1	370
ογ	1097	FPAPDPSVLVQN 1	156
QQ	1371	WRTKYETDAIQRIEELEEAKKKLAQRLQDAEE1	402

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A Accession: 812-105. F. 1. 123-123. A', 1125-1702, DE', 1705-1935 <-BOB>
A Molecule type: MRNA
A Accession: 812-105. F. 1. 124. De A RESENTION OF THE ACCESS TORESTON OF THE ACCESS TO
                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1854-1865, A, 1867-1935 <SAE>
A; Cross-references: GB:X05631; GB:Y00362; NID:934643; PIDN:CAA29119.1; PID:934644
A; Cross-references: GB:X05631; GB:Y00362; NID:934643; PIDN:CAA29119.1; PID:934644
R; Diederich, K.W.; Eisele, I.; Ried, T.; Jaenicke, T.; Lichter, P.; Vosberg, H.P.
Hum. Genet. 81, 214-220, 1989
A; Title: Isolation and characterization of the complete human beta-myosin heavy chain
A; Reference number: 154254; MUID:89154425
R;Saez, L.J.; Gianola, K.M.; McNally, E.M.; Feghali, R.; Eddy, R.; Shows, T.B.; Leinw Nucleic Acids Res. 15, 5443-5459, 1987
A;Title: Human cardiac myosin heavy chain genes and their linkage in the genome. A;Reference number: A93669; MUID:87260010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 653-720 <RES>
A;Cross-references: GB:M27636; NID:g179511; PIDN:AAA79019.1; PID:g601916
R;Bober, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1280-1935/Region: light meromyosin
F;1280-1935/Region: light meromyosin
F;184/Binding site: Ar.P (Lys) #status predicted
F;184/Binding site: Ar.P (Lys) #status predicted
F;595,705/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.9%; Score 146; DB 1; Length 1935; Best Local Similarity 16.9%; Pred. No. 2.9; Matches 238; Conservative 207; Mismatches 529; Indels 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, January 1989
A,Reference number: $12458
A,Accession: $12458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: 154254
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                       A; Accession: A27858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A92770; MUID: 88299163
A; Accession: B28908
A; Molecule type: mRA
A; Rolecule type: mRA
A; Residues: 1412-1518, R',1520-1574,'NV',1577-1935 <KUR>
A; Rosidues: 1412-1518
A; Cross-references: GB: M21665
A; Note: the authors translated the codon AGC for residue 108 as Arg
A; Note: the authors translated the codon AGC for residue 108 as Arg
B; Lichter, P.; Umeda, P.K.; Levin, J.E.; Vosberg, H.P.
Eur. J. Biochem. 160, 419-426, 1986
A; Title: Partial characterization of the human beta-myosin heavy-chain gene which is exp
A; Reference number: A24997; MUID: 87030293
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A.Residues: 1-106, E'.108-671, TLYH', 675-857, A', 859-941, NNV', 944-1123, A', 1125-1158, 'C',
A.Residues: 1-106, E'.108-671, TLYH', 675-857, 'A', 859-941, NNV', 944-1123, 'A', 1125-1158, 'C',
A.Cross-references: EMBL:X52889; NID:g29726; PIDN:CAA37068.1; PID:g29727
R;Yamauchi-Takihara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989
A.Title: Characterization of human cardiac myosin heavy chain genes.
A.Reference number: A94224; MUID:89264452
A.Reference number: A94224
A.Molecule type: DNA
A.Residues: 1-87, 'Q', 89-106, 'E', 108-177;1325-1702, 'DR', 1705-1786,1788-1803, 'E', 1804-1935
B.Yamauchi-Takihara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A37102
myosin beta heavy chain, cardiac and skeletal muscle - human
myosin beta heavy chain, cardiac and skeletal muscle - human
M.Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: A37102; S12733; A94224; B28908; A24997; A27858; I54254; S12458; S09331; S02
R;Jaenicke, T.; Diederich, K.W.; Haas, W.; Schleich, J.; Lichter, P.; Pfordt, M.; Bach,
A;Jaenicke, T.; Diederich, K.W.; Haas, W.; Schleich, J.; Lichter, P.; Pfordt, M.; Bach,
A;Reference number: A37102; MUD:91065634
A;Accession: A37102
A;Molecule type: DN
A;Residues: 1-1935 cJARA
A;Residues: 1-1935 cJARA
A;Residues: 1-1935 cJARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M57965; GB:M30603; NID:9179507; PIDN:AAA51837.1; PID:9179508; GB:R;Liew, C.C.; Sole, M.J.; Yamauchi-Takthara, K.; Kellam, B.; Anderson, D.H.; Lin, L.; Li kucleic Acids Res. 18, 3647-3651, 1990
A;Title: Complete sequence and organization of the human cardiac beta-myosin heavy chain A;Reference number: S12733; MUID:90301496
                   1157 FNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQ 1216
                                                                                                                  --- VERSNAA 1438
                                                                                                                                                                                                            1217 KFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVV 1276
                                                                                                                                                                                                                                                                                                                                                                                                     1277 YTRSSVLPNSIIPELE-----KAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1478 STELFKLKNAYEESLEHLETSKRENKNLQEEISDLTEQLGSSGKTIHELEKVRKQLEAEK 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1331 RIIVKEVEEIEEEVEKEVEKVGRTEMTLFQ-----RLAEGFNELKQDEENFVRELS-- 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1538 LELQSALEESEASLEHEEGKILRAQLEFNQIKAEMERKLAEKDEEMEQAKRNHLRVVDSL 1597
                                                                                                                                                                                                                                                                                                      -----ARSL 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KEEME-FLDEIKMEASEVEKLFGKA 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1598 QTSLDAETRSRNEALRVKKKMEGDLNEMEIQLSHANRMAAEA 1639
                                                                                                                                                                                                                                                                                                      1439 AAALDKKQ----RNFDKILAEWKQKYEESQSELESSOKE----
                                                                                                                  1403 ------AVEAVNAKCSSLEKTKHRLONEIEDLMVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 682-721; 975-1112; 1854-1935 <LIC>
A, CTOSS-references: GB: X04627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S12733
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51;

Gaps

oy Bb	203	DVGEFPVPDRNAVVQNFINMKDFSGKMYITSGLNPTFDAFDCQLHEF 248 :
δδ	249	HMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPGALYNHD 293
q	521	IDLIEKPMGIMSILEEECMFPKATDMTFKAKLFDNHL 557
ΟŸ	294	DWY I
qq	558	EAHFSLIHYAGIVDYNIIGWLQKNKDPLNE
οy	349	IPNLQKAA-KSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEK 407
q	909	VGLYQKSSLKLLSTLFANYAGADAP-IEKGKGKAKKGSSFQTVSALH-RENLNK 657
οy	408	EVEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILNELQMEAT- 457
đ	658	LMTNLRSTHPHFVRCIIPNETKSPGVMDNPLVMHQLRCNGVL 699
οy	458	EVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWG 506
qq	700	EGIRICRKGFPURILYGDFRQRYRILNPAAIPEGQFIDSRKGAEKLLSSLDIDHNQYKFG 759
Qy	507	WEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQN 563
q	760	HTKVFFKAGLLGLLEEMRDERLSRIITRIQAQSRGVLARMEYKKLLERRDSLLVIQWN 817
ογ	564	VPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKEC 621
QQ	818	IRAFMGVKNW-PWWKLYFKIKPLKKSAEREKEMASMKEEFTRLKEALE 864
Qy	622	RLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNE 671
qq	865	KSEARRKELEEKMVSLLQEKNDLQLQVQAEQDNLADAEERCDQLIKNXIQLEAKVKEMNE 924
δλ	672	CAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGL 716
ф	925	RLEDEEEMNAELTAKKKKLEDECSELKRDIDDLELTLAKVEKEK 968
δλ	717	NPTEDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDN 776
qq	696	HATENK-VKNLTEEMAGLDEIIAKLTKEKKALQEAHQQAL 1007
Qy	117	EYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSA 824
qq	1008	DDLQAEEDKVNTLTRAKVKLEQQVDDLEGSLEQEKKVRMDLERAKRKLE 1056
Oy	825	VLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVE 863
q	1057	GDLKLTOESIMDLENDKQQLDERLKKKDFELNALNARIEDEQALGSQLQKKLKELQARIE 1116
οy	864	RLEKKVEEGERT
Ωp	1117	
δŏ	890	VRDKEVTLFSKLFGFKELQRDEENFLRELSKEEMDVLDGLKME 933
qq	1176	RDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKLELDDV 1231
ογ	934	MAVATHCFTSPCHD
qq	1232	TSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAEETQRSVNDL 1273
ογ	994	LPPIQSADLRTIGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGV 1050
Q	1274	ENGELSROLDEKEALISOLT
οy	1051	LACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ 1110
qq	1327	NALAHALQSARHDCDLLREQYEEETEAKAELQRVLSKANSEVAQWRT 1373
οy	1111	IKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKMYITS 1170

qq	: :
Qy	1171 GLNPTFDAFDCOLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYN 1230
qq	1406 AVNAKCSSLEKTKHRLQNEIEDLMVDVERSNAAAAALDKKQRN 1448
Qy Db	1231 HDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPE 1290
Qy	NTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEV 13 : : :
Oy Oy	1302 DEFINITION OF THE PROPERTY OF THE PROPERT
QQ	LRAQLEFNQIKAEIER
Qy Dp	1382KEEME-FLDEIKMEASEVEKLFGKA
RES	RESULT 14
nuc N;A	nuclear migration protein NUM1 - yeast (Saccharomyces cerevisiae) N:Alternate names: protein YD8358.06; protein YDR150w
	C;Species; Saccharomyces cerevisiae C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000 C;Accession: S57976; S19052: S17018
R; M Sub	R;Murphy, L.; Richards, C.; Harris, D. submitted to the EMBL Data Library, July 1995 A:Reference number : S7971
A A	Accession Style Ave. DNA.
A A A	<pre>desidues: 1-2748 <mur> Lross-references: BMBL:Z50046; NID:g899393; PID:g899399; MIPS:YDR150w</mur></pre>
 	formation of the control of the cont
A; T	Title: Nuclear migration in Saccharomyces cerevisiae is controlled by the highly re- Reference number: \$19052; MUID:92079907
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A (A)	A; Restudes: I-loby, VV, 10/1-1821, KV, 1823-1959, RHL, 1963-1970, RNV, 1973-2048, NV, 205 A; Cross-references: EMBL:X61236; NID:94071; PIDN:CAA43554.1; PID:94072 C; Genetics:
A A A	A;Gene: SGD:NUM1 A;Cross-references: SGD:S0002557; MIPS:YDR150w A;Map position: 4R
α	ery Match 1.9%; Sco
MΣ	No.
Qy	62 SSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQFIQLAIVLVC 115
QQ	YEDLVKCKENPDVEFLKEKSAKLGH
Qy	116 TFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDET 169
QQ	801 LAYLVEHAKATDHHLLSDSAYEELVKCKENPDMEFLKEKSAKLGHTVVSNEAYSEL 856
Qy	170 ECQIKGGDLFENSVVDQFNECAVSRKKCVFRKSDVGEFPVPDRNAV 215
qq	SAYEDLV
δλ	216 VQNFNMKDESGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSA 275
qq	900LKEKSAKLGHTVVSNEAYSELEKKLEQPSLAYLVEHAKATDHHLLSDSA 948

DD 332 INISKDAPVPRLYDNMCGHNWGDIYHDNKYTWLAYYRDSINDQIKKTFLS 381 807 RNDAMDGYGGSLYTRRAVLPESIIPELQTAAQKVGRDFNFFIKTDNTGGPEPPLW 862 808 BELEKKVEGGKGLMKYENAR							•					
332 INISKDAPVPRLYDNMCGHNWGDIYHDNKVTWLAYYKDSINDQIKYTFLS 807 RNDAMDGGGSVLYTRSAVLPESIIPELQTAAQKYGNDFNTFIKTDNTCGFEPPLY 382 AQSKFKGYKDLMKYENAR	381	862 433	922	979	1038 559	1096 607	1152 666	1212 703	1271 738	1331 758	1390 802	
	INISKDAPVPRLYDNMCGHNWGDIYHDNKVTWLAYYKD		ERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKE : . : : : : DFLALRV-GGEKDIDEEADTVGCCSLRVEHISFAHDIPFK		ITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNE-LKE : : : :	LTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC :		LVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTR	SAVQKFVQDPNQPGVLYNHD-NEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGY ::	GGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGER :: :: : : : : :	IIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLABGFNELKQDEENFVRELSKEEMEFLDE- 	
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

November 6, 2001, 05:04:21; Search time 67.97 Seconds (without alignments) 711.619 Million cell updates/sec Run on:

US-09-075-375A-2 7495 1 MALSLHTVFLCKEEALNLYA......MEASEVEKLFGKALPIRKVR 1412 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	a	010411 schizosacch	00	9		3 ношо	sacch	_	Q12176 saccharomyc	Q02455 saccharomyc	P11533 gallus gail		a			P15917 bacillus an	P40457 saccharomyc	_		Q13439 homo sapien	•••	Q39565 chlamydomon	P20103 lactococcus		074712 candida alb	_	P57235 buchnera ap	aquifex a	_	Q58445 methanococc	Q58357 methanococc	Q28178 bos taurus	Q03640 saccharomyc	P53804 homo sapien
SUMMARIES	ID	D86_;	RBP1_PLAVB	TEGU_HSVSA	MYSB_PIG	MYSB_HUMAN	NUM1_YEAST	MYSB_RAT	MK21_YEAST	MLP1_YEAST	DMD_CHICK	MYSP_HUMAN	MSP1_PLAFK	MSP1_PLAFW	MYSB_MESAU	LEF_BACAN	YIO9_YEAST	HMW2_MYCGE	YM68_CAEEL	GOG4_HUMAN	USO1_YEAST	DYHB_CHLRE	NISB_LACLA	TANA_XENLA	HIS2_CANAL	POL1_GFLV	SYGB_BUCAI	METE_AQUAE	DMD_MOUSE	RPA1_METJA	SYI_METJA	TSP1_BOVIN	YMH2_YEAST	TTC3_HUMAN
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	Score	158.5	155.5	155	148.5	146	7		139.5	137.5	135	134.5	134	13	133.5	132	130	129.5	129	128	127.5	126.5	126	126	125.5	124		123.5	\sim			121.5	121.5	121
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			Q12386 saccharomyc Q58698 nyrococciis	Q03660 saccharomyc P05661 drosophila	002224 homo sapien P07271 saccharomyc
SPCA_HUMAN	TERT_OXYTR CUT3_SCHPO	DYHC_DICDI	ARP8_YEAST SYL PYRHO	YM66_YEAST MYSA_DROME	CENE_HUMAN PIF1_YEAST
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120.5	120 120	120	119	119 119	118 117.5
34 35	36	38 30 80	40	4 2	44

ALIGNMENTS

RESULT 1 YD86_SCHPO ID YD86_SCHPO STANDARD; PRT; 1957 AA.	O1-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) HYPOTHETICAL 222.8 KDA PROTEIN CIF3.06C IN CHROMOSOME I.	Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.	A. her C.M., Barrell B.G., Rajandream M.A., Walsh S.V 996) to the EMBL/GenBank/DDbJ databases.	gh a collaborat EMBL outstatio strictions on t is in no and for commerc b-sib.ch/announ	90; CAA94624.1; al protein. 1957 AA; 222785	Query Match 2.1%; Score 158.5; DB 1; Length 1957; Best Local Similarity 17.6%; Pred. No. 0.35; Matches 265; Conservative 227; Mismatches 503; Indels 511; Gaps 68;	59 YKTSSFSDSSHCKDKKQICSIDTSFEELQRFDLKRGMTLILEKQWRQFIQLAIVLVCTFV 118 : :: :: :: :: :: :: :: :: :: :: :: ::	119 IVPRVDAUALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIKC 175 :::	176 GDLFENSVVDQFNECAVSRKKCVPRKSDVGEFFVPDRNAVVQNFN 220	221 MKDFSGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDG-GFFTRSAV 276 :	277 QTFVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSV 336 : : : : : : : : : : : : : : : : : : : : : : :
RESULT YD86_S ID Y	GN	00000 00000	RR RC RL	388888888	SQ SQ	ÖÄÏ	Oy Db	Qy Db	Qy	Qy Db	Qy Dp

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Οÿ		GPEPPLVERLEKTAEEGEKLLIK
g	545	AAEKEAAVATNNE
Qy Dh	397	EAVEIEEEVEKEVEKVROTEMTLEQRILLEGFKELQQDEENFYRELSKEEKEILN 450 :
δy		ELQMEATEVEKLFCRALPIRKLRNALAPHSNFLANHETIKYYVGS 495
Ωp	641	
δλ	496	IVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKH :
QQ	969	EDED
Qy		LMVWEKWGQFAKTAIVAIFILSVA
рр	727	
yo da	603	SKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECOIK 656 SKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECOIK 656 SKA
, o	657	KKCVPRK
o Q	822	HKHVNQESKVSELKEVNGKLSLDLKNL
οy	695	SVLVQKFDM-KDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIR 746
ор	882	
δy	747	TPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKG 806
qq	938	
οy	807	RNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLE 866
qq	716	KLDETLSKSSKL-EADIEHLKNKVSEVEVERNALLASNERLM 1017
QY	867	KKVE-EGERTIIKEVEEIEEEEVEKVRDKEVTLFSKLFEGFKELQRD 911
qq	1018	DDLKNNGENIASLQTEIEKKRAENDDLQSKLSVVSSEYENLLLISSQTNKSLE-D 1071
δλ	912	EENFIRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHC 957
qq	1072	KTNQLKYIEKNVQKLLDEKDQRNVELEELTSKYGKLGEENAQIKDELLALKKK 1124
QY	958	FTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD 1001
Dp	1125	SKRQHDLCANFVDDLKEKSDALEQLTNEKNELIVSLEQSNSNNEALVEERSDLANRLSD 1183
Qy	1002	LRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKKUGVLACAFLIVPSA 1061
QQ	1184	MKKSLSDSDNVISVIRSDLVRVN 1206
ΟŊ	1062	DAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSV 1121
qq	1207	DELDTIK1240
ΟŊ	1122	VDEFNECAVS-RKKCVPRKSDLGEFFAAPDFSVLVQNFNISDFNGKWYIT-SGLNPTFD 1177
<u>අ</u>	1241	EESFNKYAVSLRELCTKSEID
δλ	1178	APDCOLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLH
g	1296	AFN-QVNFKKMELDN *EKLTTDAEFTKVVADLEKLQH
Ϋ́ς d	1238	1238 YQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKS 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1150 TSNKNEILKSVKEVEDKLNLVEQNEDYKKVKNPENEKQLEAIRGSMSKLKE----- 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1201 -----VINKHVSEMTQLESTANTLK-----SNAKGKENEHDLEELN----KTK 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS.
1298 IGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVE------ 1345
                                1349 SEKNF-----LRKEAEMTENIH-SLEEGKEETKKEIAELSSRLEDNQLATNKLKNQ 1398
                                                                  1346 ----KEV---EKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFL--DEIKMEA 1395
                                                                                       1399 LDHLNQEIRLKEDVLKEKESLIISLEESLSNQRQKGKESSLLD--AKNELEHMLDDTSRKNS 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 IVLVCTFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 TSYKTSSFSDSSHCKDKSQICSIDTSFEEI-----QRFDLKRGMTLILEKQWRQFIQLA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 CQIKCGDLFE--NSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNA----VVQNFNM-KDF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 2.1%; Score 155.5; DB 1; Length 2869; Local Similarity 17.4%; Pred. No. 0.86; nes 283; Conservative 242; Mismatches 573; Indels 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
W; B9DBE442205EBCFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETICULOCYTE BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                             Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDIJINE-92315338; Pubmed-1617731;
MEDIJINE-92315338; Pubmed-1617731;
MEDIJINE-92315338; Pubmed-1617731;
MEDIJINE-92315338; Pubmed-1617731;
"A reticulocyte-binding protein complex of Plasmodium vivax merozoites.";
                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last Sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
RETICULOCYTE BINDING PROTEIN 1 PRECURSOR.
                                                                                                                                                                                                                                                                        2869 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMODIMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malaria; Receptor; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC.
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                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium vivax (strain Belem).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M88097; AAA29743.1; -. HSSP; P36956; 1AM9.
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 69:1213-1226(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2808
2827
1030
2599
2869
                                                                                                                                              1396 SEVEKL 1401
                                                                                                                                                                                1457 SLMEKI 1462
                                                                                                                                                                                                                                                                        RBP1_PLAVB
Q00798;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
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RBP1_PLAVB
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ž	225	SGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQD 282	
q	1297	AGK VVEEMNSLKTKIEKLIQETSDDSQNELVTTS	
ζ	283	PDLPGALYNHDNEFLHYQDDMYILSSQIENKPDDYIFVYYRGRN-DAMDGYGGSVIYTRS 341	
α .	1341	X	
. <u>X</u>	342		
ą	1369	KKLVOQVNMNLQSAIQGNAGISKELNELKGVIELLISTNYSSILEYVKKNSSESVRFSQL 1428	
ζ.	373		
ą	1429	ANGEFTKAEGEEKNASARLAEAEKLKEQIVKDLDYSDIDDKVKKIEGIKREILKMKES 1486	
⋩	416		
ą	1487	ALTEWEE-SEKFKÇMCSSHMENAKEGKKKIEYLKNNGDGGKANITDSÇMEEVGNYVSKAE 1545	
ζ	456		
a	1546	HAFHTVEAQVDKTKAFCESIVA	
λ	493	VGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKH 552	
Q	1599	SAKLKPYDGRI-K	
۲	553	NLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALK 612	
ą	1644	SILQIDNCRQQLDSVLSNIGRVKQNALQYFDSADKSMKSVLPISELGAEKSLDKVK 1699	
λ	613	TCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQ-IKCGDLFENSVVDEF 669	
Q	1700	AAKESYEKNLETVQNEMSRINVEEGSLTDIDKKITDIENDLLKMKKQYEEGLLQKI 1755	
λi	670	NECAVSRKKCVPR-KSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLH 728	
ą	1756	KENADKRKSNFELVGSEINALLDPSTSIFI-KLKEKDMTGDLKNYGVKMN 1806	
<u>≻</u>	729		
ą	1807	EIHGEFTKSYNLIETHLSNATDYSVTFEKAQSLRELAEKEEEHLRRREEEAIFLLNDIKK 1866	
<u>≻</u> ,	761	Ľ	
ā	1867	VESLKLIKEMMKKVSAEYEGMKRDHTSVSQLVQDMKTIVDELKTLNDISECSSVLNNVVS 1926	
<u>≯</u> ,	790	SKVENSPE-DYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKV	
ą	1927	IVKKVKESKHADYRRDANSMYESMYTLANYFLSDEAKISSGMEFN 1971	
<u>≯</u> .	847	TFIKTDTIIKEV 880	
ð	1972	AEMKSNFKTDLELEIFSVISNSNELLKKIEQDSNDVIQKERESEQLAKDATDIYNVIKLK 2031	
Ϋ́	881	BEIEBEVEKVRDKEVTLFSKLFBGFKELQRDEENFLRELSKEEMDVLDGLKMEA 934	
ā	2032	NEFNEKLEBAKNKEBYVSEKVREALKRLSQVEGIRCHFENFHRLIDNTE 2080	
Þι	935	TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL 994	
۾	2081	- ELENLKKWYTYRDKKSERESGLQEMENEWN-TYSNSI- 2117	
>-	995	PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGV 1050	
q	2118	TQLEGIVVSAGESKE 2157	
^	1051	LACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLOTCNNRPDETECQ 1110	
д	2158	VIEMNSTIDELYKLGKNCQAHWISLISYTANMKTSKKLIMINKEKENTE 2206	

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                            2207 -KCVDYIKDNSSSTDGYVETL------KGFYGSKLTFSSASEIVQNADTYSVNFAKH 2256
                                                                                                                     -----EGGVQNML-----A 2292
                                                                                                                                                                                1354 TE-----EFLDE 1390
                                                                                                                                                                                                                                                                                                                                                                                                                  1168 ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGV 1227
                                                                                                                                                         1228 LYNHDNEYLHYQDDWYILSSKIENKPEDY-----IFVYYRGRNDA------ 1267
                                                                                                                                                                                                                                        1301
                                                                                                                                                                                                                                                                                                               --FSTFIRTDNTCGPEPALVERIEKTVEEGE----RIIVKEVEEIEEEVEKEVEKV--GR 1353
1111 IKCGDLFE--NSVVDEFNECAVSRKKCVPRKSDLG-EFPAPDPSVLVQNFNISDFNGKWY 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-92333688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                                                                                                                                                                                                          2413 KQFSILIDRIN-----ALMDDIEIFKKENNYNLMEVNTETIHRVNDYIEKITNKLVQAK
                                                                                                                                                                                                                                                            2353 SVNDHMHSMEAEMIKNGLKYTPESVQNINNIYSVIEAEVKTLEEIDRDYGDNYQIVEEHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organization between (W.Y.) and Epstein-Barr Virus.";
Virology 188:296-310(1992).
-!- FUNCTION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=92330228; PubMed=1314457; Micholas J., Comeron K.R., Coleman H., Newman C., Honess R.W.; Nicholas J., Comeron K.R., Coleman H., Newman C., Honess R.W.; "Analysis of nucleotide sequence of the rightmost 43 kbp of herpesvirus saimiri (HVS) L-DNA: general conservation of geneti
                                                                                                                                                                                                                                     1268 ------WDGYGGAVVYTRSSV--LPN--SIIPELEKAAKSIGRD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary structure of the herpesvirus saimiri genome."; J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 25, Last annotation update)
                                                                                                                2257 EKESLNAIRD-IKKELYLFHONSDISIV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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64 OR EERF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X64346; CAA45687.1; -. EMBL; M86409; AAA46140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; H36812; H36812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1391 IKMEASE 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEGU_HSVSA
Q01056;
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TEGU_HSVSA
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ø	SEQUENCE 2469 AA; 280165 MW; D2B4B8DC08644CDB CRC64;	qa
ÖMŽ	Query Match 2.1%; Score 155; DB 1; Length 2469; Best Local Similarity 17.3%; Pred. No. 0.75; Matches 230; Conservative 208; Mismatches 497; Indels 396; Gaps 58;	y do
<u>≽</u> 9	271 FTRSAVQTFVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYR 323	6 6 6 6
<u>≽</u> .α	324 -GRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDFNNFI 367 1	À 6 €
ž ā	368 TIDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTL 419 1	AA GG ,
გ დ	420 FQRLEGFKELQQDEENFVRELSKEEKEILNELQMEATEVEKL 462	ර් සි ර්
λ Q	463 FGRALPIRKLRMALAPHSNFLANHETIKYYVGSKL,PGHKRFSWGWEDYFGSIVVA 517	da da
<u>⊁</u> 9	518 -KICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKG 567	RESU MYSB ID
<u>ک</u> و	568 NSGCKFPKDVALMVWEKWGGFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAK 627 : : :	DT DT
≿ q	628 CISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVG 687 ::	OS UN
≱ g	688 DFPVPDPSVLVQKFDM	RRY
Z q	721 DAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPG 769 : :	S & B S
λ q	770 ILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVL 826	3888
λ Q	827 PESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTI-IKEVEE 882 1	2888
≿ વ	883 IEEEVEKVRDKEVTLFSKLFBGFKELQRDEBNFLRELSKEEMDVLDGLKMEATEVEKLFG 942 	8888
≿ g	943	8888
73 q	999 S-ADLRTTGGRSSRPLSAF : : : : : 879 EISDILQSNQYIHQSETIK	8888
≵ q	1046KLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC 1096 :: :: :: :: 939 KFRESNTICETISTLVSLGSLLSKSTTVBALKSIDTLKEKL 983	8888
χ.	1097	DR BG

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                                                                                    1150 PSVLVQNF--NISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDN-KLVGNISWRIKTLD 1206
                                                                                                                                                                    1028 PSRDVKTFIQNAPSMKAKQYAKKALKDQIQAMEIDVDPESVIEDNIKANGQKAWQ----- 1082
                                                                                                                                                                                                                                                                                                                               1083 -----KIQSAFQDLNFSILI------PDDWLSL-AKEYTRPKSTLFTVIGPILL 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1185 NIGHELSLLSQALNSKTLPEAVVGTSLEQHAAKFSCMFKTLEATWHDHQVDTRTKIDEYI 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1338 EEIEEEVEK----EVEKVGR----TEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFL 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNIT: MUSCLE MYOSIN IS A HEXAMIL LIGHT CHAIN SUBUNITS (MLC) A BALKALI LIGHT CHAIN SUBUNITS (MLC) SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPET PATENR COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR WYOSIN ATPASE ACTIVITY.

MISCELLANGOUS: BACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SELLY INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
----KMEVDSF-VPT 1027
                                                                                                                                                                                                                                                        1207 SGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIF-----VYY 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1125 KFVEEVLESVKNLKEAKLKSLLPNGPVFTPPKFDWIHYYESNVNFHLKTINLPKVSTVAH 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1297 SIGRDFSTFIRTDNT-CGPEPALVERIE------KTVE-----EGERIIVKEV 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANDOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
-!- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.
    984 ---TAVDRPLKRELYNVIRKLQKQLKTLLEQQEFDNW----
                                                                                                                                                                                                                                                                                                                                                                                                                            1262 RGRNDAWDGYGGAVVYTRSSVLPNSII-------
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                  186 QQFFNHHMFVLEQEEYKKEGIEWEF -- IDFGMDLQACIDLIEKPMGIMSILEEECMFPKA
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METHYLATION (TRI-) (POTENTIAL).
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W; 149CDBFD910DBB08 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              980 ITRKRINGTFLLKILPPIQSADLRTTGGRSSRPL---SAFRSGFSKGIFDIVPLPSKNEL 1036
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                                                                                                                             1043 KVRMDLERAKRKLEGDLKLTQESIMDLENDKQQLDERLKKKDFELNALNARIEDEQALGS 1102
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QDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTR 822
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Pfordt M., Bach A., Vosberg H.P.;
"The complete sequence of the human beta-myosin heavy chain gene and
                                                                                                                                                                           E-----PPLVERLEKKVEEGERT-----IIKEVEEIEEEVEK-----
                                                                                                                                                                                                                                                                   ----VRDKEVTLFSKLFEGFKELQRDEENFLREL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-0CT-1989 (Rel. 12, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.
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VARIANT CMH1 GLN-403.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Missense mutation of the beta-cardiac myosin heavy-chain gene in
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                                                                                                                             SEQUENCE OF 1-115 FROM N.A.
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comparative analysis of its product.";
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                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88299163; PubMed-2969919;
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            Genomics 8:194-206(1990).
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ò	ISAG.THGSGTVTVRGSVTVRG	ΟY	1231	HDNE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQF-----IQLAIVLVC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748 SAYEDLVKCKENPDV-----EFLKEKSAKLGHTVVSSEEYSELQRKYSELEKEVEQPS 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 TFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSC-----AANVACLQTCNNRPDET 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 ECQI-------KGGD--LFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: ADDITIONAL REGIONS OF LOWER HOMOLOGY TO THE REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283; Conservative 231; Mismatches 582; Indels 486; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Nuclear migration in Saccharomyces cerevisiae is controlled by the highly repetitive 313 kDa NUM1 protein."; Mol. Gen. Genet. 230:277-287 (1991).
-!- FUNCTION: CONTROLS NUCLEAR MIGRATION. NUM1 SPECIFICALLY CONTROLS THE INTERACTION OF THE BUD NECK CYTOSKELETON WITH THE PREDIVISIONAL G2 NUCLEUS PERHAPS BY RECOGNIZING G2-SPECIFIC
                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC MICROTUBULI OR OTHER COMPONENTS OF THE NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONSENSUS (ALWAYS STARTING WITH PROLINE) ARE FOUND IN BOTH FLANKING DOMAINS OF THE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 PH DOMAIN.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 143; DB 1; Length 2748; 17.9%; Pred. No. 4.1;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 28383 / FL100;
MEDLINE-92079907; PubMed=1745235;
KOTMBADEC J., Schaaff-Gerstenschlaeger I., Zimmermann F.K.,
Perecko D., Kuentzel H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW; B2FBD67C9F6211AE CRC64;
                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.5 X TANDEM REPEATS.
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                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --
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NUCLEAR MIGRATION PROTEIN NUM1.
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2573 2683
2748 AA; 313202 M
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                                                                                                                                                                 NCBI_TaxID=4932;
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1771 GMNKILVDQIEYDET-----IRKC-------NHPTRMELEESCH 1802
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                                                                                                                                                                                                                                                                                                                                                                                                                    1063 HAKATNHHLLSDSAYEELVKCKENPDVEFLKEKSAKLGHTVVSNEAYSELEKKLEOPSLE 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1123 YLVEHAKATNHHLLSD--SAYEELVKCKENPDVEFLKEKSAKLGHTVVSNEAYSELEK-- 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1218 EFLKEKSAKLGHTVVSNEAYSELEKK-----LEQPSLAYLVEHAK--ATDHHLLSDSA 1268
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                                                                                                                                                                                                                                                                                                                 1003 TNHHILSDSAYEDLVKCKENPDMEFLKEKSAKLGHTVVSNEAYSELEKKLEQPSLEYLVE 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518
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                                                                                                                                                                                                                                                               325 RND---AWDGYGGSV-----IYTRSPTLPESIIPN----LQKAAKSVGRDF--- 363
                                                                                                                                                                                                                                                                                                                                                                     ----NNFITTDNS-----CGPEPPLVERLEKTAEEGEKLLIKEAV-EIEEEVEKE--- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --VEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILNE--LQMEA-TEVEKLF 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ICSSRRIPRYFRKSPRICCGLDSRGL-QLFSHGKHNLSPAHSINQNV 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          565 PKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKAD-----AVDALKTCTCL 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECAVSRKKCVPRK-SDVGDF-----PVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAF 723
857 EKKLEQPSLAYLVEHAKATDHHLLSDSAYEDLVKC-----KENSDV-EF----- 899
                                                 216 VQNFNMKDFSGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSA 275
                                                                                                   900 ----LKEKSAKLGHTVVSNEAYSELEKKLEQ-----PSLAYLVEHAKATDHHLLSDSA
                                                                                                                                                           276 VQTFVQDPDLPGALYNHDNEFLHYQ------DDWYILSSQIENKPDDYIFVYYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 GRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAK----
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1115 DLFENSVVDEFNECAVSRKKCVPRK-SDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLN 1173
                                                                                                                                                                                                                 1856 PNFDYLKDSLNK--------MDYVAISRQDYELMVAKYEKPQLDYLKIS 1896
                                                                                                                                                                                                                                                                                        -----NHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDG 1270
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Mahdavi V., Periasamy M., Nadal-Ginard B.;
"Molecular characterization of two myosin heavy chain genes expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matter Maryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WISTAR; TISSUE-Heart; MEDLINE-85179510; PubMed-6241892; Mandadvi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.; "Cardiac myosin heavy chain isozymic transitions during development and under pathological conditions are regulated at the level of mRNA availability.";
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-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
"Complete nucleotide sequence of full length cDNA for rat beta
                                                                                                                                             PTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1935 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 297:659-664(1982).
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P02564;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56;
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28 RESIDUE REPERT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARRACTERISTIC FOR ALPHA-HELLCAL COILED COILS.
                                                                                                                                                                                                                                                          SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES, WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
                                                                         PIW: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LAM) AND 1 HEAVY MEROWYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                          THE RAT, TWO OF WHICH ARE SPECIFIC FOR ADULT CARDIAC MYOSIN HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 PDETECQIKCGDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRN-----AVV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 PDGTE-----EADKSAYLMGLNSADLLKGLCHPRVKVGNEYVTKGQNVQQVAYAIGALA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FDAFDCQLHE---FHMENDKL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459; Gaps
                                                                                                                                                                           -!- MISCELLANBOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
-!- MISCELLANBOUS: THERE ARE 10 OR MORE MYOSIN HEAVY CHAIN GENES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Methylation; Alkylation; Multigene family.

DOMAIN 1 839 GLOBULAR HEAD (S1).

DOMAIN 840 1935 RODLIKE TAIL (S2 AND LAM DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1935;
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METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRK -> VRR (IN REF. 3).
D -> H (IN REF. 3).
N -> K (IN REF. 3).
T -> N (IN REF. 3).
T -> N (IN REF. 3).
R -> K (IN REF. 3).
MW; C8376C324A7BDB2B CRC64;
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Best Local Similarity 16.7%; Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 QNFNMKDFSGKWYITSGLNPT------
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PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X15939; CAA34065.1; -. EMBL; J00752; AAA41654.1; -. EMBL; M32698; AAA41659.1; -.
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                                                                                                                                                             SUBFRAGMENT (S2).
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A02989; A02989.
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Db

7	256		282
ð	486	QQFFNHHMFVLEQEEYKKEGIEWTFIDFGMDLQACIDLIEKPMGIMSILEEECMFPKATD	545
Δ·	283	PDLPGALY-NHDNEFLHYQDDWYILSSQIENKPDDYIEVYYRGRNDAWDGYGGSVI	337
ð	546	MTFKAKLYDNHLGKSNNFQKPRNIKGKQEAHFSLIHYAGTVDYNILGWL	594
λ	338	YTRSPTLPESIIPNLQKAA-KSVGRDFNNFITTD	396
Q	595	QKNKDPLNETVVGLYQKSSLKLLSNLFANYAGADAP-VDKGKGKAKKGSSFQTV	647
ΔŢ	397	EAVEIEEEVEKEVEKVEDTEMTLFQRLLEGFKELQQDEENFVRELSKEEFE	447
ą	648	SALH-RENINKLMINLRSTHPHFVRCIIPNETKSPGVMDNPL	688
<u>≯</u> .	448	ILNELQMEAT-EVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGS	495
ą	689	VMHQLRCNGVLEGIRICRKGFPNRILYGDFRQRYRILNPAAIPEGQFIDSRKGAEKLLGS	748
⊼	496	KLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLS	555
ō	749	LDIDHNQYKFGHTKVFFKAGLLGLLEEMRDERLSRIITRIQAQSRGVLSRMEFKKLLE	806
<u>≯</u> ;	556	PAHSINONVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAV	608
ą	807	RRDSLLIIQWNIRAFMGVKNWPWMKLYFKIKPLIKSAETEKEMANMKE	854
Δī	609		662
ð	855	EFGRVKD	910
Δī	663	NSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFD	702
ą	911	NKIQLEAKVKEMTERLEDEEEMNAELTAKKRKLEDECSELKRDIDDLELTLAKVEKEK	896
Σ	703	MKDFSGKWFITRGLNPTFDAFDCQLH	762
ą	696		863
Δi	763	QDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTR	822
ð	994	KEKKALQEAHQQALDDLQAEEDKVNTLTKAKVKLEQQVDDLEGSLDQDK	1042
λ	823		857
ą	1043	KVRMDLERAKRKLEGDLKLTQESIMDLENDKQQLDERLKKKDFELNALNARIEDEGALGS	1102
λi	858		688
ð	1103		1161
λi	890		919
ð	1162	EMNKKREAEFQKMRRDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLEKEK	1221
λį	920	SKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHGFTSPCHDRIRFFSSDDGIGRLG	616
ð	1222	SEFKLELDDVTSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAE	1264
λį	980	ITRKRINGTFLLKIL	1036
ð	1265	ETQRSVNDLTRQRAKLQTENGELSRQLDEKEALISQLTRGKLTYTQQL	1312
ξį	1037	KELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC :: :: :: ::	1096
>	1097	LOTCINNRPDETECOIKCGDI-PENSVVDEFNECAVSRKKCVPRKSDI-GEFPAPDPSVLVON	1156
. Q	1371		1402

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1157 FNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQ 1216
                                  --VERSNAA 1438
                                                                       1217 KFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVV 1276
                                                                                                1277 YTRSSVLPNSIIPELE-----KAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE 1330
                                                                                                                                                                         1331 RIIVKEVEEIEEEVEKEVEKVGRTEMTLFQ-----RLAEGFNELKQDEENFVRELS-- 1381
                                                                                                                                                                                                                                            MEDILINE=9900321; PubMed=9786894;

Edskes H.K., Ohtake Y., Wickner R.B.;

Mak2lp of Saccharomyces cerevisiae, a homolog of human CAATT-binding protein, is essential for 60 sribosomal subunit biogenesis.";

J. Biol. Chem. 273:28912-28920(1998).

-!- FUNCTION: REQUIRED FOR 60S RIBOSOMAL SUBUNIT SYNTHESIS.

-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS (PROBABLE).

-! SIMILARITY: BELONGS TO THE CBF / MAK21 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96381256; PubMed=8789263; Brandt P., Ramlow S., Otto B., Bloecker H.; Brandt P., Ramlow S., Otto B., Bloecker H.; "Nucleotide sequence analysis of a 32,500 bp region of the right arm Yeast 12:85-90(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBOSOME BIOGENESIS PROTEIN MAK21.
MAK21 OR YDROGOW OR D4237 OR YD9609.14.
SACCHAROMYCES CEREVISIAE (BAKEY'S YEAST).
EUKAIYOta; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STANDAN-SEQUENCE FROM N.A. STRANS-SZABAN-SZABAN HOLD S. BOWMEN S., Harris D., Barrell B.G., Rajandream M.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                              1382 -------KEEME-FLDEIKMEASEVEKLFGKA 1405
                                                                                                                                                                                                                                                                                                                   1403 -----AVEAVNAKCSSLEKTKHRLQNEIEDLMVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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POLY-ASP.
POLY-GLU.
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SGD; S0002467; MAK21.
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986
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Q12176;
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DOMAIN

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41;
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                                                                                                                                                                                                      ----EEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEEN-- 436
                                                                                                                                                                                                                                       460 PNADYHTTYYSVITLNQTILKRSEDSVANKLVK ---TYFTLFEKFL-----INTDKDNTN 511
                                                                                                                                                                                                                                                                              -FVRELSK--EEKEILN------ELQMEATEVE-----KLF-----GRALPIR 470
                                                                                                                                                                                                                                                                                                                 512 GVVKSNSKSYEEKRKKNFKKGKHGGKSVKIEKTENEVLDEKNSKLFSALLTGINRAFPFA 571
                                                                                                                                                                                                                                                                                                                                                                                       572 QIPASVYEVHMETLFKITHSSNFNTSIQALVLINQVTVK----AKLNSDRYYRTLYESLF 627
                                                                                                                                                                                                                                                                                                                                                                                                                          512 GSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGC 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 PACAANVACLQTCNNRPDETECQIKCGDLFENSVYDEFNECAVSRKKCVPRKSDVGDFPV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    692 PDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH----TEENKLVGNLSWRIRT 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PKFANAEKSSLWEINNFIN------HFHPTVKTYANAYVTGETEQIAK 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748 PDGGFFT-------RSAVQ-----KFVQDPKYPGILYN---------HDNEYLL 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDLGLFTLSHFLDRFVYRSAKQTNTARGTSIMQPLFSGSRVNDSVLVKASDIMHD-QGPV 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  781 YQDDWYILSSKVEN-SPEDYIFVYY-----KGR------NDAWDGY 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKM 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         939 QES--DOEEGLDEDIFYSFDGEQDNSDKK-RSFAESSEEDESSEEEKEEEENKEVSAKRA 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 KPPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISN
                                                                                                                                                                                                                                                                                                                                                    471 KLRMA------LAPHSNF-----LANHETIKYYVGSKLPGHKRFSWGWEDYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 693 ----PQIKNLLT--NTPVDYE-----YESDAEEEQGDKDIKRKEYDGRKRD-----
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Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                          Length 1025;
1025 AA; 116676 MW; FB80378727ED71D8 CRC64;
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                                                    1.9%; Score 139.5; DB 1;
20.9%; Pred. No. 1.8;
ive 94; Mismatches 225;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                       Matches 159; Conservative
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MLP1 OR YKR095W OR YKR415.
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996 KKKQRKNML-KSLPV----
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                                                                      Similarity
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Q02455;
SEQUENCE
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCQLHEFHM---END-----KLVGNLTWRIKTLDGGFFT-----RSAVQTFVQDPDLPG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 DERLKEIELVRVENNRSNSECKKLRSTIMDLETKQQGYITNDLNSRTELERKTQELTL-- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 ALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPES 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 IIPNLQKAAKSVGRDF-----NNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 VILDIRNELNRIRNDFOMERTNNDVLKOKN-----NELSKSLO--EKLL--EIKGLS 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 17.5%; Pred. No. 5.1;
Matches 252; Conservative 240; Mismatches 525; Indels 421; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 DLLKELQLTKEKLAQCEKECLRLSSITDEADEDNENLSAKSSSDFIFLKKQLIKERRTKE 401
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                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-94205265; PubMed-8154186; Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G., Bou G., Esteban P.F., Baladron Y., Gonzalez G.A., Revuelta J.L.; Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.; "The complete sequence of a 15,820 bp segment of Saccharomyces cerevisiae chromosome XI contains the UBI2 and MPLI genes and three
                                                                                                                                                                                                                                                                                                                      ·! - FUNCTION: MYOSIN-LIKE PROTEIN THAT IS PROBABLY INVOLVED IN DNA
                                                                         Koelling R., Nguyen T., Chen E.Y., Botstein D.; "A new yeast gene with a myosin-like heptad repeat structure."; Mol. Gen. Genet. 237:359-369(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 137.5; DB 1; Length 1875; 17.5%; Pred. No. 5.1;
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1875 AA; 218455 MW; 683A0D34C9066867 CRC64;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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-!- CAUTION: REF. 2 MISQUOTES THE GENE NAME AS "MPL1".
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                                                      MEDLINE=93247549; PubMed=8483450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L01992; AAA34783.1; -. EMBL; X73541; CAA51948.1; -. EMBL; Z28320; CAA82174.1; -. PIR; S38173; S38173. SGD; S0001803; MLP1.
                                                                                                                                                                                                                                                                              new open reading frames.";
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1866
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                    SEQUENCE FROM N.A.
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1242 WYILSSKIENKPE-----DYIFVYYRGRNDAWDGYGG-----AVVYTRSSVLPNSIIP 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1015 KSEY-----ESKLSKIQNDL-----DQQTIYANTAQNNYEQELQKHADVSKTISELRE 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           955 THCFTSPCHDRIRFFS-----SDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTG 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 MKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFV 762
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                                               402 HLQNQIETFIVELEHKVPIINSFKERTDMLENELNNAALLLEHTSNEKNAKVKELN---A 458
                                                                                                  -----GOFAKTAIVAIFILSVASKA 605
                                                                                                                                                 459 KNOKLVECENDLQTLTKQRLDLCRQIQYLLITNSVSNDSKGPLRKEEIQ--FIQNIMQED 516
                                                                                                                                                                                                    606 DAV----DALKTCTCLLKECR--LELAKCISNPACAANVACLQTCNNRPDETECQIKCG- 658
                                                                                                                                                                                                                                                                                                      659 ---DLFENSVVDEFNECAVSRKKCVPRKSDVGD------FPVPDPSVLVQKFD 702
                                                                                                                                                                                                                                                                                                                                        666 QD-----LYDSKSDISIKLGKEKSSRILAEERFKLLSNTLDLTKAENDQLRKRFDYLQN 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          807 -----RNDAWDGYGG----SVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTD- 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         720 TILKQDSKTHETLNEYVSCKSKLSIVETELLNLKEE------QKLRVHLEKNLKQEL 770
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506 GWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVP 565
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                                                                                               566 KGNSGCKFPKDVALMVWEKW--------
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STANDARD;

DMD_CHICK

RESULT 10 DMD_CHICK

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              Lemaire C., Heilig R., Mandel J.L.; "The chicken dystrophin cDNA: striking conservation of the C-terminal coding and 3' untranslated regions between man and chicken."; EMBO J 7:4157-4162(1988).
                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODRIN).
SIMILARITY: CONTAINS I WW DOMAIN.
                                                                                                                                                                                                                                                                                                                                                            -! - FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
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K -> R.
MW; 85493DAF6D5B6D4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 SPECTRIN-LIKE REPEATS.
                                                                                                                                                                                                  Lemaire C., Heilig R., Mandel J.L.;
"Nucleotide sequence of chicken dystrophin cDNA.";
Nucleic Acids Res. 16:11815-11815(1988).
          01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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Pred. No. 17;
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                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=89098331; Pubmed=3062582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50021; CH; 2.

PROSITE; PS01159; WW_DOMAIN_1; 1.

PROSITE; PS50020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                      MEDLINE=89210800; PubMed=3072195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0403; WWDOMAIN.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
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PF00435; spectrin; 22.
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InterPro; IPR000433; -..
InterPro; IPR001202; -..
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InterPro; IPR002017; ...
InterPro; IPR002349; -..
Pfam; PF00307; CH; 2.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              PLASMA MEMBRANE
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                          NCBI_TaxID=9031;
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                                                        DYSTROPHIN.
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VARIANT
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PRT; 3660 AA.
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ž.	Matches	245; Conservative 196; Mismatches 482; Indels 472; Gaps 64;	ŧ	
οy	71 1	KDKSQICSIDTSFEEIQRFDLKRGM-TLI-LEKQWRQFIQLAIVLVC 115	Š	
qa •	1923 F	KKKEDLNAVNRQAERLSKDGAAKAVEPTLVQLSKRWRDFESKFAQFRRLNYAQIQTVLED 1982	QC ·	
οy	116 1	TFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIKC 175	Oy.	
qq	1983 1	TTFVMTESMTVETTYVPSTYLAEI-LQLLQALSEVEERLNSPVLQAKDC 2030	g .	
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q	2031 E	EDLLKQEECLKNIKDCLGRLQGHIDIIHSKKTPALQSATPRETÄNIQD-KLTQL 2083	l 8	
δo 7			qa Qa	
Q C		NSQMEKVNKMYRDRQARFDKSKEKWRLFHCEMKSFNEWLTETEEKLSRAQIEAGDVGHVK 2143	ΔO	1164 GKW
οy	261 W	WRIKTLDGGFFTRSAVQTFVQDPDLPG	7 8	
qq	2144 T	TKQFLQELQDGIGRQQTVVVKTLNVTGEEIIEQSSAADANVLKEQLGNLNTRWQEICR 2200	3 6	
Qγ	- 388	ALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAMDGYGGSVIYTR 340	Š i	400 0221
Q C	2201	QLVEKRRRIEEEKNILSEFGEDLNKLILWLEETENVIAIPLEPGNEDQLRDCLGKVKLRV 2260	an	3062 ISP
δλ	341 8	SPTLPESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVE 400	RESU	RESULT 11
qq	2261 E	EELLPHKGILKRLNETGGTTLGSASLNPERKHKLESTLKEASRLLKVSRD 2311	MYSP ID	_HUMAN MYSP_HUM
Οy	401 I	KVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILN	AC DT	P13535; 01-JAN-1
đ	; 2312 L		TO TO	15-JUL-1 01-OCT-2
οy	461 -	KLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFG 512	DE GN	MYOSIN H
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qq	2408 A		RA RT	Karsch-M
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ž 2		AVSKKKCVPKKS	RL RN	Gene 89:
3		MFSSVLLEVPALADFNKAWAELTDWLSRLDREIKAQRV 2495	RP RC	SEQUENCE TISSUE=S]
oy i			RX RA	MEDLINE=
g G		TVGDLDDINDMIIKQKANMQDLEQRRPQLDELITAAQNLKNK 2537	RA	Stedman
ογ		IRTPDGGFFTRSAVQKF-VQDPKYPGILYNHDNE-YLLYQDDWYILSSKVENSPEDYIFV 802 ::	RT RI	transcrip
අු	2538 T	TSNQEARTIITDRIEKIQSQWDDVHGYLQNRRQQLHEMQKDSTQWLEAKQEAEQVLE 2594	R. E	[3]
Qy	803 Y	YYKGRNDAMDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN- 846	R R	TISSUE-SI
qq	2595 0	QAKAKLESWKEISYTVEALKKQNSELKQFSKEIRQWQMNIEGVNDVALKPVRDYSA 2650	RX RA	MEDLINE Bober E.
QY	847 -	TFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVE 881	RA RT	Arnold H "Identif:
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φ	882 E	EIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKE 922	RP RP	[4] SEQUENCE
qq	2707 T	TTANVLÓDATHKEKTLEDPQMVRELMKGWQDLQAEIDAHTDIFHNLDENGQKILRSLEGS 2766	RA K	MEDLINE Feghali
Óλ	923 E	EMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGR 977	R F	Molecula human per
qq	2767 E	EDAVLLQRRLDNMNFRWSELRKKSLNIRSHLEASTDQWKR 2806	RL	J. Cell F [5]

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ALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIK------ 1112
                            ITRKRINGTFLLK------ILPPIQ-:----SADLRTTGGRSSRPLSAF 1016
                                                                                                 GFS----KGIFDIVPLP---SKNELKELTAPLLLKLVGVLACAF--LIVPSAD----A 1063
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3-95324556; PubMed=7601129;

1E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S.,

1H.H., Rubinstein N.A.;

1H.H., Rubinstein N.A.;

1H.H., Rubinstein perinatal myosin heavy-chain

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5-89234168; PubMed=2715179;
1. L. Lainwand L.A.;
1lar genetic characterization of a developmentally regulated perinatal myosin heavy chain.";
1 Biol. 108:1791-1797(1989).
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tai Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Eutheria; Primates; Catarrhini; Hominidae; Homo.
xID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -Skeletal muscle;
3=90323631; PubMed=2373371;
Mizrachi I., Fedhali R., Shows T.B. Jr., Leinwand L.A.;
ttion of a full-length human perinatal myosin
hain-encoding DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1990 (Rel. 13, Created)
1998 (Rel. 36, Last sequence update)
1000 (Rel. 40, Last annotation update)
HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1937 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. 230:1001-1006(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -90235862; PubMed=1691980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. 189:55-65(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNQPGVLYNHDNE 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNKVPYYINHETQ 3076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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67;

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ESSET K., Tidhar A., Myszkowski M.;

ESSET K., Tidhar A., Myszkowski M.;

"Isolation and characterization of the human perinatal MHC promoter.";

"Isolation and characterization of the human perinatal MHC promoter.";

"Isolation and characterization of the human perinatal MHC promoter.";

"Isolation and characterization of the Bub./Genbank/DDBJ databases.

"Isolation will conver the EMBL/Genbank/DDBJ databases."

"Isolation: MWSCLE CONTRACTION TO A LEKALD ILIGHT CHAIN SUBUNITS (MLC.)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC.2).

"ISOLATORY LIGHT CHAIN THE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CHARACTERISTIC FOR ALCHA-HELICAL COLLED COLLES.

CHARACTERISTIC FOR ALCHA-HELICAL COLLED COLLES.

CHARACTERISTIC FOR ALCHA-HELICAL COLLED COLLES.

"INSCELLAMEOUS: EACH WYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

"ENTITE FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   SUBFRAGMENT (S2).
SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RODLIKE TAIL ($2 AND LAM DOMAINS).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE, ARE
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METHYLATION (TRL-) (POTENTIAL).

MIXTLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

A -> R (IN REF. 2).

A -> R (IN REF. 2).

A -> H (IN REF. 3).

A -> H (IN REF. 1 AND 4).

A -> H (IN REF. 1 AND 4).

B -> G (IN REF. 1 AND 4).

C -> DGG (IN REF. 1 AND 4).

C -> C (IN REF. 1 AND 4).

E -> G (IN REF. 1 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Methylation; Alkylation; Heptad repeat pattern;
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EN -> AH (IN REF. 1 AND 4).
E -> D (IN REF. 1 AND 4).
D -> H (IN REF. 2).
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EMBL, X51592; CAA35941.1; --
EMBL, M35250; AAA36346.1; --
EMBL; AF067143; AAC21557.1; --
PIR; A30220; A30220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00193; MYOSINHEAVY.
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SEQUENCE OF 1-46 FROM N.A.
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1.8%; Score 134.5; DB 1; Length 1937;

Query Match

A3EE2D151792E9E8 CRC64;

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AA;

SEQUENCE

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------HATENK-VKNLTEEMAGLDETIAKLSKEKKALQE-----THQQTLD 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1055 KRKLEGDLK--LAQESTMDMENDKQQLDEKLEKKEFEISNLISKIEDEQAVEIQLQKKIK 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838 AQKVGRDFNTFIKTDNTCGPE---PPLVERLEKK------VE----VE------ 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  778 YLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTA 837
                                                                                                                                                                                                                                                                                                                               342 LGFTPEEKVSIYKLTGAVMHYGNMKFKQKQREEQAEPDGTEVADKA-----AYLQSLNS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 VQ-DPDL-----PGALYN-----HDNEFLHYQDDWYILSSQIENKFDDYI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428 KELQQDEENFVREL------SKEEKEILNELQMEAT-EVEKLFGRALPIR----- 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663 TNLRSTHPHEVRCIIPNETKTPGAMEHELVLHQLRCNGVLEGIRICRKGFPSRILYGDFK 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 ----KLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYF---GSIVVAKICSSR 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  723 ORYKVLNASAIPEGOFIDSKKASEKLLASIDIDHTOYKFGHTKVFFKAGLLGLLEEMRDE 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         783 KLAQIITRTQAVCRGFLMRVEYQKMLQRREALFCIQYNVRAFMNVKH--WPWMKLFFKIK 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   718 PTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNE 777
                                                                                                                                                                                 99 LEKQWRQFIQLA------IVLVCT------FVIVPRVD-----AVDALKTC 132
                                                                                                                                                                                                                                    282 AERSYHIFYQITSNKKPDLIEMLLITTNPYDYAFVSQGEITVPSIDDQEELMATDSAIDI 341
                                                                                                                                                                                                                                                                                      133 ACLLKECRIELAKCIANPSCAANVACLQTCNN---RPDETECQIKCGDLFENSVVDQFNE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 ADLLKALCYPRVK-VGNEYVTKGQTVQQVYNAVGALAKAVYEKMFLWMVTR-INQQLDTK 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 FVYYRGRNDAWDG---YGGSVIYT-----RSPTLPESIIPNLQKAA-KSVGRDFNNFI 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 TIDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGF 427
                                                                                                                             239 VRNDNSSRFGKFIRIHFGTTGKLASADIETYLLEKSRV------TFQLK----- 281
                         280; Conservative 243; Mismatches 597; Indels 529; Gaps
                                                                        43 IRSNN----GYFNSFRLFTSYKTSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLI 98
                                                                                                                                                                                                                                                                                                                                                                                                  190 CAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGK------WYITSGLNPT---
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ELQAR I EELGEE I EAERASRAKA EKQRSDLSRELEE I SERLEE EAGGATSAQVELNKKREA		DGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRING	TFLLKILPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIV :	LKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRP	: : : : EETKAKNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSK-	DETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNG : : : : : : : :	KWYITSGLNPTFDAEDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQPPNQ	KCASLEKTKQRLQNEVEDLMLDVE	PGVLYNHDNEY LHYQDDWYILSSKIENKPEDYIFVYYRGRNDAMDGYGGAVVYTRSSVLP	NSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEE	- : : : : :	EKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELS	-FLDE	LRVKKKMEGDLNEMEIQLNHANRLAAESL 1643	LAFK STANDARD; PRT; 1630 AA. 1996 (Rel. 05, Created) 1996 (Rel. 33, Last sequence update) 1996 (Rel. 34, Last annotation update) 1990). EFROM N.A. E-86136024; PubMed=3004972; M., Goman M., Bone N., Hyde J.E., Scaife J Angoral H., Bujard H.; 1996 (All 1985). A 4:3823-3829(1985). TOLIE R., Bujard H.; TOLIER., Bujard H.; TOLIER
	890 1173	928	988	1045	1324	1105	1165	1413	1225	1285	1496	1345	1382	1615	LT 1 MPDAF M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 VDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWYITSGLNPTFDAFDC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 QLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTF--VQDP-----DLPGALYNHDNE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 FLHYQDDWYILSSQIENKPDDY-----IFVYYRGRNDAWDGYGGSVIYTRSPTLPESII 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 PNGVTYPLSY-NDINNALNELNSFG---DLINPFDYTKEPSKNIYTDNERKKFINEIKEK 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8%; Score 134; DB 1; Length 1630;
Best Local Similarity 18.0%; Pred. No. 6.7;
Matches 246; Conservative 207; Mismatches 473; Indels 444; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 IENINELIEESKKTIDK-----INKNATKEEEKKKLYQAQYDLS-----IYNK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 QLEEAH----NLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 IEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNID--ISAKVETKESTEPNE-Y 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLI-----KEAVEIEEE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 VEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILNEL-----QMEAT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 VVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGC--- 571
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Interpro; IPR000561; -.
Pfam: PF00008; EGF: 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                            PROTEIN 1.
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                                                                                                                                                                                                                                        POTENTIAL.

MEROZOITE SURFACE PI
TRIPEPTIDE SG(TP) RI
MEMBRANE ANCHOR.

N-LINKED (GLCNAC.)

N-LINKED (GLCNAC.)
                                                                                                                                             EMBL; X03371; CAA27070.1; -.
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SEQUENCE
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992 KILPPIQSADLRTTGGRSSRP---LSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLV 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 981 LE-EDINKL-----KKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLT---LL 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1030 K-----EQLESKLNSLNNPKHVLQNFSVFFNK------KKEAE----- 1061
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                                                                                                                                                                                     748 TPPAPVNNKTENVSKLDYLE-------KLYEFL------NISYIC 779
                                                                                                                                                                                                                                                                                                                                                             799 YIF-----VYYKGRNDAWDGYGGSV-----LYTRSAVL-----PESIIPELQTAAQ 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                              840 KVGRDFNTFIKTDNTCGPEP-PLVERLEKKVEEGERT-----IIKEVEEI----- 883
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637 NIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPST 696
                                                   652 ECQ1------KGGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQ-- 699
                                                                                                    697 EGEITGQATTKPGQQAGSALEG---DSVQAQAQEQKQAQP-----PVPVPVPEAKAQVP 747
                                                                                                                                                    700 ------KFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRI 745
                                                                                                                                                                                                                                                        746 RTPDGGFFTRSAVQKFVQDPKYPGILYNHD--NEYLLYQDDWYILSSKVEN----SPED 798
                                                                                                                                                                                                                                                                                                         780 H-----YKITKEEESKLSSCOPLD 815
                                                                                                                                                                                                                                                                                                                                                                                                           816 LLFNIQNNIPVMY----SMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAK 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         872 KV----STSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNK 927
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19-AUG-1999 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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P04933;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@libs.sib.ch).
SEQUENCE FROM N.A.
MEDLINE=8601435; PubMed=2995820;
MADLINE=8601435; PubMed=2995820;
MICHOLIS S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                    -!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246; Conservative 207; Mismatches 473; Indels 444; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 VDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWYITSGLNPTFDAFDC 243
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                                                                                                                                                                                                                                                                      KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                Holder A.A.; Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
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                                                                                      "Primary structure of the precursor to the three major surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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N-LINKED (GLCNAC. . .) (POTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED GLCNAC...)
                                                                                                     antigens of Plasmodium falciparum merozoites.";
Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 134;
18.0%; Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X02919; CAA26676.1; -.
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                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                        Freeman R.R.;
                                                                                                                                                                REVISIONS
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SEQUENCE
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990 LE-EDINKL-----KKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLT---LL 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1167 YITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQD---- 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1167 ---TGNSPS-----ENNTDVNNALE---SYK-KFLPEGTDVATVVSESGSDTLEQS 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1211 QPKKPA----STHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVV--rG 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEE 1339
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                                                                                                                                                                                                             596 KITKDENKPDEKILEV----SDIVKVQVQKVLLM-----NKIDELKKTQLILKNVELKH 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  757 IPPAPVNNKIENVSKLDYLE-----NTSYIC 788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             746 RTPDGGFFTRSAVQKFVQDPKYPGILYNHD--NEYLLYQDDWYILSSKVEN----SPED 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 EVEKLFGR--ALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDY-FGSI
                        700 ------KFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     515 VVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGC---
                                                                                                                          559 VVEKEL-----KYYK------NLISKIENEI---ETLVENIKKDEEQLFEK
                                                                                                                                                                  572 -----KFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLE-
                                                                                                                                                                                                                                                     625 -----NVACLQTCNNRPDET
                                                                                                                                                                                                                                                                                             646 NIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPST
                                                                                                                                                                                                                                                                                                                                        652 ECQI------KCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQ--
                                                                                                                                                                                                                                                                                                                                                                                706 EGEITGOATTKPGQQAGSALEG---DSVQAQAQEQKQAQP-----PVPVPVPEAKAQVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLD 1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBBNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBBNITS (MHC-2). 2 ALKALI LIGHT CHAIN SUBBNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBBNITS (MLC-2).
-!- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALHA-HELICAL COLLED COILS.
-!- MISCELLARBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
                                                                                                                                                                                                                                                    STRAIN=FIB; TISSUE-Liver;
MEDLINE-95115033; PubMed=7815459;
Wang R., Sole M.J., Cukerman E., Liew C.-C.;
"Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain gene from Syrian hamster.";
J. Mol. Cell. Cardiol. 26:1155-1165(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINBAVY.
PROSITE; PS50096; IQ; II.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                           Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                      Jandreski M.A., Sole M.J., Liew C.-C.; "Sequence of cDNA encoding the Syrian hamster cardiac beta-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RODLIKE TAIL (S2 AND LMM DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFRACMENT (S2).
SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Methylation; Alkylation; Multigene family.
DOMAIN 1 838 GLOBULAR HEAD (S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
                                                                                           MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM
MYSB_MESAU STANDARD; PRT; 1934 AA. p13540; Q60540; Q60540; Q1-JAN-1990 (Rel. 13, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy chain.";
Nucleic Acids Res. 16:4737-4737(1988).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 962-1935 FROM N.A. MEDLINE-88247788; PubMed-3380703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L12104; AAA62313.1; -. EMBL; X07273; CAA30256.1; -. PIR; A28298; A28298 HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000048; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001609; -. InterPro; IPR002928; -.
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1934
184
676
770
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=10036;
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839
177
654
756
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DOMAIN
DOMAIN
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ACTIN-BINDING

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63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       865 SEARRKELEEKMVSLLQE----KNDLQLQVQAEQDNLADAEERCDQLIKNKIQLEAKVKE 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNE------CAVSRK---KCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            774 HDNEYLLYQDDWY--ILSSKVE----NSPEDYIFVYYKGRND---AWDGYGGSVLYTRS 823
                                                                                                                                                                                                                                                                                                                                                                                                                                390 NSADLLKGMCHPRVKVGNEYVTKGQNVQQVSYALGALAKSVYEKMFN--WMVTR-INATL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 ETKQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKLQOFFNHHMFVLEQEEYKKEGIE 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 -TFVQ-------DPDLPGALY-NHDNEFLHYQDDW 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 YILSSQIENKPDDYIFVYYRGRND----AWDGYGGSVIYTRSPTLPESIIPNLQKAA-KS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567 NVKGKQEAH----FSLVHYAGTVDYNILGW-----LQKNKDPLNETVVGLYQKSSLKL 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 LP------IRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIV 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 VAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHS---INQNVPKGNSGCK 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   768 LLGLLEEMRDERLSRIITRI--QAQSRGLLSRMEFKKLLERRDSLLVIQWNI-RAFMGVK 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FP------KDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKT 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 -------FDAFDCQLHE---FHMENDKLVGNLTWRIKTLDGGFFTRSAVQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507 WTFIDFGMDLQACIDLIEKPMRIMSILEEECMFPKATDMTFKAKLYDNHLGKSNNFQKPR 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 VGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEI--EEEVEKEVEKRTDTE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 MILFQRLLEGFKELQQDEENFVRELSKEEKE-----ILNELQMEAT-EVEKLFGRA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 708 FPNRILYGDFRQRYRILNPAAIPEGQFIDSRKGAEKLLSSLDIDHNQYKFGHTKVFFKAG 767
                                                                                                                                                                                                                                                                                                                                                                                                       188 NECAVSRKKCVPRKSDVGEFPVPDRN-----AVVQNFNMKDFSGKWYITSGLNPT- 237
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 17.0%; Pred. No. 8.9;
Matches 251; Conservative 211; Mismatches 525; Indels 493; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             616 LSNLFANY-----AGADAP-VDKGKGKAKKGSSF---OTVSVLHRENLNKLMTNLRST-
                                                                                                                                                                                                                                                                                                                                    1.8%; Score 133.5; DB 1; Length 1934; 17.0%; Pred. No. 8.9;
                                            D -> E (IN REF. 2).

T -> TE (IN REF. 2).

E -> Q (IN REF. 2).

DLOAEED -> ALEART (IN REF. 2).

L -> Y (IN REF. 2).

L -> Y (IN REF. 2).

D -> Y (IN REF. 2).

E -> D (IN REF. 2).

C -> N (IN REF. 2).

T -> A (IN REF. 2).

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METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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1004 QALDDLQAEEDKVNTLTKSKVKLEQQVDDLGSSLEQEKKVRMDLERAKRKLEGDLKLTQE 1063
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MEDLINE=90034185; PubMed=2509294;
Bragg T.S., Robertson D.L.;
"Nucleotide sequence and analysis of the lethal factor gene (lef)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1356 LQCVLSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEE------
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NCBI_TaxID=1392;
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
LETHAL FACTOR PRECURSOR (EC 3.4.24.-) (LF).
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Gene 81:45-54(1989).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                  ROCALI S.K., Schiavo G., Mock W., Montecucco C.;

In Sinc content of the Bacillus anthracis lethal factor.";

FEMS Microbiol. Lett. 124:343-348 (1994).

In FEMS Microbiol. Lett. 124:343-348 (1994).

AGENT WHICH INFECTS MANY MAMALIAN SPECIES AND THAT MAY CAUSE DEATH. LF IS THOUGHT TO BE A LETHAL FACTOR THAT, WHEN ASSOCIATED WITH PA, CAUSES DEATH. LF IS NOT TOXIC BY ITSELF. PA IS THOUGHT TO BE A SENSITIVE EUKARYOTIC CELLS, THEREBY FACILITATING THE INTERNALIZATION OF LP OR FER.

PROTECTIVE, SECRETED ANTHRAX TOXIN IS COMPOSED OF THREE DISTINCT PROTEINS, A PROTECTIVE ANTHRAX TOXIN IS COMPOSED OF THREE DISTINCT CELLS. THESE IS TOXIC BY ITSELF.

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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Toxin; Signal; Repeat; Plasmid.
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1.8%; Score 132; DB 1; Length 809;
Best Local Similarity 17.2%; Pred. No. 3.4;
Matches 139; Conservative 117; Mismatches 254; Indels 300;
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8C16B4D7277310AE CRC64;
                                                        Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases
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809 AA;
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MEROPS; M34.001; -.
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                                                                                                                                                                                             1050 VLACAFLIVPSADAVDALKTCACILKGCRIELAKCIANPACAANVACLQTCNNRPDETEC 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1223 NQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTR--S 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------EEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRE----- 1379
951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
                                                                                                                                                                                                                                                                                          1110 QIKCGDLFENSVVDE--FNECAVSRKKCVPRK---SDLGEFPAPDPSVLVQNFNISDFNG 1164
                                                                                                                                                                                                                                                                                                                                                                                             1165 KWYITSGLNPTFDAFDCQLHEFHTEGDNKLV--GNISWRIKTLDSGFFTRSAVQKFVQDP 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1281 SVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE-RIIVKEV-- 1337
                            390 L-------NRIQVDSSNP------LSEK--EKEFLKKLDIQPYDINQRLQDTG 429
                                                                                                                                                                                                                                                                                                                            492 -----DNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDNERLKWRIQLSPDTR 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 GLIDSPSINLDVRKQYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATL----
                                                                                                                                                                                                                                                                                                                                                                                                                                            544 AGYLENG--------KLILQRNIGLEIKDVQ----
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                                                                                                                                                                                                                                              484 -----GADLVDST---
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Search completed: November 6, 2001, 05:14:41 Job time: 620 sec

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November 6, 2001, 05:03:46; Search time 119.14 Seconds (without alignments) 1568.027 Million cell updates/sec
                                                                                                                                                                                         1 MALSLHTVFLCKEEALNLYA......MEASEVEKLFGKALPIRKVR 1412
                                                                                                                                                                                                                                                                                                             425026
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_human:*
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Maximum DB seq length: 2000000000
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7495
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sp_bacteria:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_virus:*

Q40593 nicotiana t Q40251 lactuca sat Q93249 arabidopsis Q9sm43 spinacia ol Q9sjd9 arabidopsis Q9sjd3 arabidopsis Q56223 plasmodium Q26213 plasmodium Q49525 mycoplasma Q90337 cyprinus ca Q90337 cyprinus ca Q96722 arabidopsis Q96722 arabidopsis Q96722 arabidopsis Q96722 arabidopsis Q96724 mus musculu Q9d284 mus musculu Q9d276 plasmodium Q9d276 plasmodium Q9d276 plasmodium Q9d276 plasmodium Description SUMMARIES Q40593 Q40251 Q40251 Q40251 Q9SM49 Q9SMD3 Q9FUS5 Q9FUS5 Q96213 Q26216 Q49525 Q99337 Q26216 09S722 Q25662 Q9QZ84 Q9U0P0 Q9G276 Q9H1D5 **09HAW4** a 10 110 110 113 10 Query Match Length DB 244 289 289 222 2226 2271 11365 11335 11339 11339 11786 11387 11387 21.4 17.3 16.3 16.3 2.8 2.2 2.2 2.2 2.1 2.1 Score 2557 2508 2430 1604.5 1319.5 1219.5 161.5 156 155.5 151 151 150 148.5 147.5 146.5 Result Š.

003767 saccharomyc 99vnh4 drosophila 026024 plasmodium 051455 borrelia bu 0996y2 homo sapien 096275 plasmodium 090208 pyrococcus pylay 9 caenorhabdi 09210 helicobacte 061201 caenorhabdi 09210 helicobacte 061201 caenorhabdi 09210 helicobacte 061201 caenorhabdi 09210 mycoplasma 06683 aquifex aeo 049547 mycoplasma 0909054 pomo sapien 099212 homo sapien 09117 arabidopsis 090494 homo sapien 090772 homo sapien 000772 homo sapien	Q00756 oryctolagus O23332 arabidopsis
3 003767 5 09VNH4 4 09Y672 6 051465 5 096024 6 09Y672 5 096275 6 090ZVN 13 09UZC8 13 09UZC8 13 09UZC8 14 09UZC8 1 09Y2L9 1 09Y2L2 1 09Y2L2 1 09Y2L2 1 09Y2L2 1 09Y2L2 1 09Y2L2 1 09Y2L2	6 QUU/56 10 023332
2748 1116 839 839 11558 1958 1159 1109 1109 1103 1103 1103 1105 1105 1105 1105 1105	1676
146 145.5 144.5 144.5 144.5 144.5 142.5 142.5 142.5 142.5 140.5 140.5 139 139 133 137.5	137
22222222222222222222222222222222222222	45

ALIGNMENTS

13 24 24 26 26 26 26 26 26 26 26 26 26	PRELIMINARY; PRT; 478 AA. 1996 (TERMELTel. 01. Created)	(TrEMBLrel. 01, (TrEMBLrel. 13, N DE-EPOXIDASE PR	Nicotiana tabacum (Common tobacco). Nicotiana tabacum (Common tobacco). Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-XANTHI, TISSUE=LEAF; Bugos R.C., Yamamoto H.Y.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases. EMBL, U34817, AAC50031.1, Mendel: 9222: Nicta:Vdei:9222	InterPro; IPR000566; PROSITE; PS00213; LIPOCALIN; UNKNOWN_1. Transit peptide. TRANSIT. 134 POTENTIAL. CHAIN 135 478 POTENTIAL. SEQUENCE 478 AA; 54561 MW; 0967DF4547D7809D CRC64;	Ouery Match 34.1%; Score 2557; DB 10; Length 478; Best Local Similarity 100.0%; Pred. No. 6.9e-138; Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps	WALAPHSNFLANHETIKYYVGSKLPGHKRESWGWEDYFGSIVVAKICSSRRIPRYFRKSP 533 	RICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAI 593 	VAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLOTCNNRPNETEC 653
RESULTATION OF STATE	405 405 1-N	01-NOV-1996 01-MAY-2000 VIOLAXANTHII	icotiana ukaryota agnoliopl olanales CBI_TaxII	L] EQUENCE 1 TRAIN÷XAN UGOS R.C. UDMILLED MBL; U34E	InterPro, PROSITE; F Fransit pe TRANSIT: CHAIN	Query Match Best Local Si Matches 477;		534 RICCG 61 RICCG	594 VAIFI

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462 AA
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114 462 V
462 AA; 52017 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQFIQLAIVLVCTFVIV 120
                                                                                                714 RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773
                                                                                                                                                               101 HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 360
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                     121 VAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETEC 180
                                              QIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MALSLHTVFLCKEEALNLYARSPCNERFHRSGQPPTNIIMMKIRSNNGYFNSFRLFTSYK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MALSLHTVFLCKEEALNLYARSPCNERFHRSGQPPTNIIMMKIRSNNGYFNSFREFTSYK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bugos R.C., Yamamoto H.Y.; ^{\circ} "Molecular cloning of violaxanthin de-epoxidase from romaine lettuce
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca.
                                                                                                                                                                                                                                                    894 EVILFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 950
                                                                                                                                                                                                                                                                   421 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1B22522DC2C62699 CRC64;
                                                                                                                                                                                                                                                                                                                                                      040251;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.5%; Score 2508; DB 10; 100.0%; Pred. No. 4.2e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and expression in Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 93:6320-6325(1996).
EMBL; 91462; Ac49373.1; -.
Mendel, 8691; Lacsa.Vdel:8691.
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                                                                                                                                                                                                                                                                                                                                                                                                          VIOLAXANTHIN DE-EPOXIDASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96270536; PubMed=8692813;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactuca sativa (Garden lettuce).
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InterPro; IPR000566; -.
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473 AA; 54447 MW;
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Matches 47
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Theologis A., Ecker J., Theologis A., Ecker J., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, 444133; AAC5032.1; ---
EMBL, AC003981; AAF99753.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 1010
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                               241 FDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDFDLPGALYNHDNEFLHYQ 300
                                                                                                                                 301 DDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVG 360
                                                                                                                                                                 361 RDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLF 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAVATHCFTSPCHDRIREFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 462;
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) VIOLAXANTHIN DE-EPOXIDASE PRECURSOR.
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100.0%; Pred. No. 1.1e-130;
tive 0; Mismatches 0;
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                                              SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
                                                                                                            DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDL 1142
                                                                                                                                                                        NKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDN 1310
                                                                                                                                                                                                                                     TCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELK 1370
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                                                                                                                          NKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Caryophyllidae,
Caryophyllales, Chenopodiaceae, Spinacia.
                                                             37 FLFQDDARRNIRFNDRKLSCTKFIGASEKLQ------HSKSPKSGLISCGWEVNSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.4%; Score 1604.5; DB 10; Length 472; Best Local Similarity 66.4%; Pred. No. 1.1e-83; Matches 299; Conservative 63; Mismatches 69; Indels 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and sequencing of Spinacia olercea violaxanthin epoxidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIOLAXANTHIN DE-EPOXIDASE
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125 472 VIOLAXANTHIN DE-EPOXIDASE
472 AA; 53658 MW; 12B4C8C69AB61E12 CRC64;
                                                                                                                                                                                                                                                                                                1371 QDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 1412
                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Emanuelsson A.K., Eskling M., Akerlund H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                            472 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spinacia oleracea (Spinach)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3562
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SIGNAL
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1263 GRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERI 1322
                                                                                                                      1323 EKTVEEGERIIVKEVEEIEEEVEKEVEKKGRTEMTLFQRLAEGFNELKQDEENFVRELSK 1382
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                                                                                                                                          Shûne P. Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Com L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLIKLVGVLACAFLIVPSADAVDALKTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Genomic sequence for Arabidopsis thaliana BAC T27G7 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots, Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC006932; AAF22898.1; -. InterPro; IPR000566; -. PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 AA; 26631 MW; 4CD8221F444CF04C CRC64;
                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.3%; Score 1300; DB 10;
100.0%; Pred. No. 9.8e-67;
tive 0; Mismatches 0;
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Arabidopsis thaliana (Mouse-ear cress).
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SEQUENCE
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Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
Nature 402:761-768(1999).
EMBL; AC007019; AADAQU404.1; -
SEQUENCE 522 AA; 59287 MW; 63EF3102F3E96C21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2269.AA; 265158 MW; F3D8CB103FB9A6E1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=YM;
MEDLINE=95021522; PubMed=7935623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium berghei yoelii.
                                                                                                                                                     Matches 122; Conservative
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MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
                                                                                                                                                                                                                                                      STRAIN=CV. ZHENHUI-249;
Lin R.-C., Xu C.-C., Li L.-B., Kuang T.-Y.;
"Molecular cloning and expression of rice violaxanthin de-epoxidase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DEFNECAVSRKKCVPQKSDVGEFPVPDPSALVKNFNMADFNGKHYISSGLNPTFDTFDCQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                   OFFUSS;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VIOLAYANTHIN DE-EPOXIDASE (FRAGMENT).
VIOLAYANTHIN DE-EPOXIDASE (FRAGMENT).
EUKaryote; Viridiplantee; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaeae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.3%; Score 1219.5; DB 10; Length 289; Best Local Similarity 74.8%; Pred. No. 4.7e-62; Matches 217; Conservative 43; Mismatches 29; Indels 1;
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                                                                                                                                                                                                                                                                                                   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF288196; AAF97601.2;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 289 AA; 33496 MW; B91C7BBD4CE1770D CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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                                      289 AA.
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Q9SJ13
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Keen J., Sinha K., Brown K., Holder A.; "A gene coding for a high-molecular mass rhoptry protein of Plasmodium
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                                                                                                                                                                                                       68 PEPPV--KLIALVGKGEVSPLK-STSWEEVMLHTARRLKWVD-----EGYEMLVFDD 116
                                                                                                                                                                                                                                                                                                                                                                                      117 E---IVSSNDQRAMN-LTQELNQTDILVVVA-------VNNSESV---- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ------ NWIQTNSKNVKNMIC-----FESSPNLMNRLGG------ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 ---ASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 ONLRSK-----GFSTLSCMVKNCGPQILNCLLDPNCRKALQCLNQCS--PVDQVCSYRCI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659 DLFENSVYDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK------ 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TEENKLVGN 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 LFVGWLGELEWSWRVVAGQNPAYDQFPCQYQLFYRGKGKSSFWYEPVFQVRTLEEKLV-- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    741 LSWRIRTPDGGFFTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVE 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKT 851
                                                                                                                                                          375 PEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 SKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNL 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          555 SPAHSINQNVPKGNSGCKFPKDVALMV-----WEKWG----QFAKTAIVAIFILSV--- 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 TDVGSVNKD------KEVTEVVKTVGDAWERRNSDDIRFCLLVIINAYIRPVPVL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429 DDLSWGLFHYHGAARVAGQSYTGAVLVTPDGSYPAEKDKERLQSALEKCGIKEWELF-AV 487
                                                                                                                                                                                                                                                                                                             435 ENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYG 494
                                                                             Gaps
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2.8%; Score 210; DB 10; Length 522; 21.1%; Pred. No. 0.0003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                             77; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              852 DNTCGPEPPLVERLEKKVEEGER----TIIKEVEEIEE 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 2269 AA.
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Mol. Biochem. Parasitol. 65:171-177(1994).
EMBL; L27838; AAA21304.1;
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1		Qy
Best Lo	marcii Local Similarity 1843; Pred No. 0.017; Ess 255; Conservative 213; Mismatches 436; Tradels 482.	qa
Oy 3	YILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTI.PRSTITPNIOKA 355	Qy
ପୁ	: : EKTKLETITELTKSNEETVRL	qq
ον	356 AKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEI 401	δ i
Dp	88 EKEIRELFKKYLDEEAERKYLEGLKLELNKKIKDIIAKIEYVKNTVEL 135	gg (
60 40 40 40 40 40 40 40 40 40 40 40 40 40	EEEVEK	Qy Dp
		ô
oy B	447 E-ILMELOMEATEVEKLIFGRALPIRKLRMALAPHSNFIANHETIKYYV 493 196 EDPIDDIE-DKTKLENLRSKIDNYVDKIOKKEIETKSHLNNFFINNKIDNTTIFIKYY 254	qq
0y 4		δy
c qa	a	đ
Oy 5	550GKHNLSPAHSINQNVPKGNSGCKFPKDV 577	Οy
Dp 3	308 INVDNIKEEEAKQNYDKSNEHMTTIPTNEDEISKIISEVKTMKDEILSKVNTYIDFNKKY 367	Q
oy s	578 ALMVWEKWGOPAKTALVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAAN 637	RES
Dp 3	368 KETVNSEHSQFTELTDKIKAEVSDKELKK 396	026 1D
Oy 6	638 VACLOTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSD 685	AC
Dp 3	397CEQSFNDNKSLINETKNSIEKEYQNINTLKKVDEYIKVCKSTKESITKFSSKQTIL 452	566
Oy 6	686VGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEE- 734	SO
Db 4	453 KDMLNQNIKTVKETNSIDKS-YIEKFE-QILTGKQTKLENKFTEFSLNNEBANNNEL 507	88
0y 7	735NKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSS 790	RP
Db 5	508 IKYFSDLKANLGINEENMLYNQFTEKEKTFNDIKEKNIHINEEIS 552	R R
0y 7	791 KVENSPEDYIFGY 814	RA
s qa	: : : : : : : : : : :	R.
Oy 8	815 GGSVLYTRSAV	RP
9 qa	613 EGNIKYTDKIKKINDDIMAVSQQIDQHINGLDDIQKKSESYVSEMKEQINKLEKVSNTEI 672	RC RA
Oy 8		RT
9 qa	KNIYEEINKLLSEISKIEKDNTS	RN
0y 9	902 FEGFKELQNDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVAT 955	주 전 전 전
Dp 1	733 GNLFLE-QIDEEKKKAENTIKSMEAYIDDLDNIKKKSQEIETEMDIKWDINKEMEALKIS 791	RL P.
0у 9	956 HCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSA 1015	SQ
Db 7	792 HDDDKKCHDKSKNHKENISDIYDKSSKIIQDFSRESDINDIKNKLQKNVSE 842	(
0y 10	1016 FRSGFSTAP 1042	z A
B qq	843 SQNHNSDINQCLNEVANIYNILKLNKIKKIIDKVKEYTSEIEKNKKNINDELNNSEK 899	E ¿
Oy 10		S S
	900 VIANTEGDES	

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998 KSHKDKSNGYKTEADQNKKAIQKNKELFEQYKEEVTVLLNKYYAVELKNK------ 1047
                                                                                                                                                                                                                                                                                                       1048 ---FD-----KTKNDSK---QIIKEIKDAHNYCTLESG------KSEKKMNE----- 1082
                                                                                                                                                                                                                                                                                                                                                                                                         1083 -IKNEKIHIEDE---VANNDKSNK-------AITSIKVSVEPFKTKI 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --AVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPT 1175
                                                                                                                                                                                                                                               1176 FDAFDCQLHEFHTEGDNKLVGNISWRIK-----TLDSGFFTRSAVQKFVQDPNQPGVLY 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1230 NHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLP---- 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1285 ---NSI-----IPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGER 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1332 IIVKEVEEIEEEVEKEVEKVGRTEMTLFQR-----LAEGFNELKQDEENFV---RELS 1381
                                | :|| | :|| | 939 -NILNETNITNHFKNAEEYNKIVLSNFNNIEMADNKSQYILEIKKNNGTNDHDYNIKEL 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 YKTSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQFIQLAIVLVCTFV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uery Match 2.2%; Score 161.5; DB 5; Length 2771; est Local Similarity 16.5%; Pred. No. 1.7; atches 250; Conservative 269; Mismatches 481; Indels 519; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-IM;

BIDLINE-97077455; PubMed-8920022;

Sinha K.-A., Keen J.K., Ogun S.A., Holder A.A.;

Sinha K.-A., Keen J.K., Ogun S.A., Holder A.A.;

"Comparison of two members of a multigene family coding for high-molecular mass rhoptry proteins of Plasmodium yoelli.";

Mol. Blochem. Parasitol. 76:329-332(1996).
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Green J.L., Holder A.A.;
Streen J.L., Holder B. gene encoding a high molecular mass rhoptry
protein of Plasmodium yoelii.";
Mol. Biochem. Parasitol. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5861;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U36927; AAB41263.3; ...
SEQUENCE 2771 AA; 325640 MW; COCCB9AB6E7ACF36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
RHOPPER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 2771 AA.
1100 CNNRPDETEC -- QIKCGDLFENSVVDEFNEC ---
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SEQUENCE OF 379-2771 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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<u></u>	915	IVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIK 174 ::	Δ (
¥ q	175 952	CGDLFENSVVDQFPNECAVSRKKCVPRKSDVGEF 207	э д (
⊼ q	208		O A (
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ξ q	455 1256	EATEVEKLFGRALPIRKLRWALAPHSNFLANHETIKYYVGSKLPGHKRFS 504 :: :	дон
λ Q	505 1315	- WGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSP 556	4. 11 11 11
₹ 40	557 1359	AHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTALVAIFILSVASKADAVDALKTCTC 616	1000
λ q	617 1397	LLKECRLELARCISNPACAANVACLQTCNNRPDETECQIKCGDLFEN 663	J O E E I
× 4	664	SVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAF 723 : :	4 14 14 14
≱ q	724	DCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQD 783	дддо
7.7 Q	784	DWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGR 843 :	
7.7 Q	844	DENTFIKTDNTCGPEPPLVERLEKKVVEGGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFE 903	3
7 <u>4</u>	904		п о .
દ્રં લુ	961	PCHDRIRFESSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSAFRSGF 1020	
λζ.	1021	SKGIFDIVPLPSKNELKELTAPLLIKLVGVLACAFLIVPSADA 1063 	- 0
ά	1064	VDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPD-ETECQIKCGDL	н

qq	1718 IESTQKLIIPTIKNLISPFKANDLEGIDINKNLGKYNTEMNNIYEFFIKSYDL 1770	
Οy	1117FENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNF 1157	
Q	1771 ITHYLETVSKEPITYEQIKNKRITAQNELLINIKNVNKAKSYLDDIEANEFDRIVTHFKN 1830	
Qy dq	1158 NISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSA 1214 :	
Qy Qy	5 VQKFVQDPNQPGVLXNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGA 127	
qq	1885 SKKYYSLNIQIKSSSGI 1919	
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qq	- ⊢	
Οy	ODE	
qq	ELO	
Qy Db	1386 EFLDEIXMBASEVEKL 1401 	
RES Q49		
QI K	Q49525 PRELIMINARY; PRT; 1365 AA.	
4 E E E E	01-702-1996 (TTEMBLrel. 01, Created) 01-NOV-1996 (TTEMBLrel. 01, Last sequence update) 01-NOV-1998 (TTEMBLrel. 08, Last annotation update)	
S C	LMP1.	
8008	Mycoplasma hominis. Bacteria: Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmatacea; Mycoplasma. NCBI TaxID=2098;	
RN	[1]	
R R R	SECOLNUL F. NOS N. S STRAIN-MH56; MEDLINE-95369882; PubMed-7543881;	
RA	Jensen L.T., Ladefoged S., Birkelund S., Christiansen G.; "Selection of Mycoplasma hominis PG21 deletion mutants by cultivation	
RI	in the presence of monoclonal antibody 552."; Infect. Immun. 63:3336-3347(1995).	
SQ	EMBL; U21962; AAA81013.1; SEQUENCE 1365 AA; 154982 MW; 847A04992410867F CRC64;	
OМ	atch 2.1%; Score 156; DB 2; Length 1365; cal Similarity 16.8%; Pred. No. 1.3;	
	209; Conservative 187; Mismatches 420; Indels 430; Gaps	
ΟŊ	TRSAVQTEVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAWDG 33	
qq	282 TRNQIQEFINTNKNNPNYSELISQLISKRDSKNSVTDS 319	
QY	332 YGGSVIYTRSPTLPESII-PNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEK 385	
QQ	320 SNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVSNANTLSA 369	
ΟŊ	386 TAEEGEKLLIKEAVEIBEEVEKVEKVROTEMTLFORLLEGFKELOODEENFVREL 441	
QQ	370 KLTDKDNTIQQAKTELEKEVQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETF 425	
QY	442 SKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHK 501	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1213 --SAVQKFVQDPNQPGVLYNHDNEYLHYQDDW-----YILSSKIENKPEDYIFVYYRGRN 1265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1010 S-----RPLSAFRSGFSKGIFDIVPL-------PSKNEL-KELTAPLLLKLVG 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1156 NFNISD--FNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTR- 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKLFEGFKELQ----RDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVAT 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 RFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHS-I 560
                                                    --INTINKNNPNYSELISQLTSKRDSKNSVTDSSNKSDIESANTEL 489
                                                                                                                                                                 -------ADKVQA-----DNLAKS 509
                                                                                                                                                                                                                                                                                                                                                                                                                                              737 LVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSP 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KNSVTDSSNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVS 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 677 NANT-----LSAKLTDKDNTIQQAKTELEKEIQKANQAIKSNNTASMQSAKSSLD 726
                                                                                                      561 NONVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKE
                                                                                                                                                                                                                        CRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCV
                                                                                                                                                                                                                                                                                                                                    581 PRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDA----FDCQLHEFHTEENK
                                                                                                                                                                                                                                                                                                                                                                                            LEKE-------VQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETFNKDKEA
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                                                                                                                                                                                                                                                                             ----ANTLSAKLTDKDN--TIQOAKTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          727 AKVAEITKKLETFNKDKEAKFNELKQTRNQI-----QEFINTNK-
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                                                                                                                                                                 490 KQALAKAN------
                                                                                                                                                                                                                                                                             510 IKEQLNNSVSN-----
                                                    447
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PRT; 1933 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : | : | : | : | HLVTMTQALARGYVMR--KEFVKMMERREAIYSIQYNIRSFMNVKHWP---WMKVYFKIK 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         587 QFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNN 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWG 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSTHPHFVRCLIPNESKTPGLMENFLVIHQLRCNGVVEGIRICTKGFPSRIHYGDFKQRY 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                894 SENLSDAEERCEGLIKSKIQLEGKLKETTERLEDEEEINAELTAKKRKLEDECSELKKDI 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-FAST SKELETAL MUSCLE;
MEDLINE-97176447; PubMed-902393;
Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
"CDMA cloning of myosin heavy chain isoforms from carp fast skeletal muscle and their gene expression associated with temperature
                                                                                                                                   Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.

NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLLKTAESE----KEMASMKENFEKMKEDLTKALAKKKELEEKMVSLVQEKNDLLLQVTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirayama Y., Watabe S.;
"Structural differences in the crossbridge head of temperature-
associated myosin subfragment-1 isoforms from carp fast skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1933;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin.
SEQUENCE 1933 AA; 221092 MW; CDF0CBAA475530F5 CRC64;
01-NOV-1996 (TIEMBLrel. 01, Created)
01-NOV-1998 (TIEMBLrel. 08, Last sequence update)
01-NAR-2001 (TIEMBLrel. 16, Last annotation update)
MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 156; DB 13;
17.0%; Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Biochem. 246:380-387(1997).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-FAST SKELETAL MUSCLE;
MEDLINE-97352533; PubMed-9208928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002928; -.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD0000355; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 17.0%; Pr
Matches 203; Conservative 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acclimation.";
J. Exp. Biol. 200:27-34(1997).
EMBL; D89990; BAA22067.1; -.
EMBL; D50474; BAA09067.1; -.
HSSP; P08799; 1LVK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 738-1933 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000048; -. InterPro; IPR001609; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle.";
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οp	954	DDLELTLAKVEKEKHATENK-VKNLTEEMA	982
Oy Db	747	TPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLXQDDWYILSSKVENSPEDXIFVYYKG E	806 1030
δ. d	807	RNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGR	843
3 8	1031		1003
g 6	1086		1145
Οy	884	BEEVEKVRDKEVILFSKLFEG 9	904
QQ	1146	: - SERLEEAGGATAAQIEMNKKREAEFQKMRRDLEESTLQHEATAAALKKKQADSVAELGEQ	1205
δy	905		964
q	1206	IDNLQRIKQKLEKEKSEYKMEI-DDLSSNMEAVAKAKGNLEKMCRTLED	1253
οy	965	RIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRP	1012
QQ	1254	QLSEIKAKSDENSRQLNDMNAQRARLQTENGEFSRQLEEKEALVSQ	1299
QY Db	1013	LSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCAC :	1072
	1 1		
δŏ.	1073	LLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFE :: :	1118
Q D	1321		1375
οy	1119	NSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDA :	1178
Dp	1376	TDAIQRTEELEESKKKLAQRLQDAEESIEAVNSKCASLEKTKQR	1419
οy	1179	FDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYL	1236
QQ	1420	LQSEVEDIMIDGERANALAANLDKKQRNFDKVLADWKQKYEESQAEL	1466
δλ	1237	H-YQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAA	1295
qq	1467	EAAQKEARSLSTELFKMKNSYEEALDH	1501
ΟŊ	1296	KSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKVEKVGRTE	1355
QQ	1502	KNLQQEISDLSEQLGETGKSIHEIEKAKKTVESEKAEIQTALEEARGTLEHEESKILRVQ	1561
δλ	1356	MILEQEASEGFNELKQDESHFVRELSKEEMEFLDEIKMEASEVEK 1400	
QQ	1562	LELMQVKSEIDRKLAEKDEEMEGIKRNSQRVLDSMQSTLDSEVRSRNDALRVKK 1615	
RESULT 029230	LT 12		

1406 LPIR 1409

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27;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gooayne J.D., Weidman J.F., McDonald L., Utterback T., Gotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       968 FFSSDDGIGRLGITRKRINGTFLLKILPPIQSA--DLRTTGGRSSRPLSAFRSGFSKGIF 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1026 DIVPLPSKNELKELTAPL-------LLKLVGVLACAFLIVPSADAVDALKTC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1191 ------DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYN-- 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1231 --HDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSII 1288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 RISEEIKSIESLREKLSEEVRNLESREKELEEHKSRLESLRKQESVLQEV-----R 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KPKAERY- 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 D-----TLKPKMDRMQGIK-- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 IMAEYTREMKRIAEELAKADEIEKKLKERLEKVEKALEKOETVLKYROMVDELKALENEL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 SSHDAE------KLSAESEE----YRKVKERLDGLRGQQKILLSSA---SRI 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                854 TCGPEPPLVERLEKKVEEGERTI---IKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQR 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       911 DEENFLRELSKEEMDV---LDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIR 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 KLKKLIAKKSSLKTRGAQLKKAVEE------LKSAERTCPVCGRELDEEHRKN 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 155.5; DB 1; Length 886;
20.6%; Pred. No. 0.78;
Live 85; Mismatches 221; Indels 221; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797 EDYIFVYYKGRNDAWDGYGGSV--LYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTD-N 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 EDY------ENAWKNLGAVIRMLEREKERLKEFLSQEEQIKRQKEEK-----KAEIE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 -----KMYDLLSKAKEEE-KEITE 404
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                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:354-370(1997).
EMBL: AE001032; AAB90211.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 886 AA; 103633 MW; D35641D499AA8B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 GLEEKLRELEKQLKEVVERIEDLEKKAKEVKEL------
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001238; -.
InterPro; IPR001238; -.
InterPro; IPR003439; -.
Pfam; PF00470; RecF; 1.
Hypothetical protein.
SEQUENCE 886 AA; 10363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 20.6% Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 KELKSSLREI--
                                                                                                                                                                                                                                                             Venter J.C.;
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279 A-KIDWELGK-VESLRDTLTKKKAQVACLMDESTAMKREIESFHQSAKTAVREKIALQEE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 AILTALCIAFGCRARGTQRAATLKDFIKTGCSYAVVQVEMKNSGEDAFKSEIYGGVIIIE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 SVVDQFNECAVSR----KKCVPRKSDVGEFPVPDRNAVVQNFNM------KDFSGK 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 BEIAORLOOLKKKLAWSWVYDVGRO------LOEOTEKIVKLKERIPTCO 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 ALKTCACLLKECRIE-----LAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFEN 181
                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA;
MEDLINE-99380167; Pubmed-10449416;
Mendiste T., Revenkova E., Bechtold N., Paszkowski J.;
"An SMC-like protein is required for efficient homologous
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                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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EMBO J. 18:4505-4512(1999).
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                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                  SMC-LIKE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   668 EFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQL 727
                                                                                                                                                                                     -----TLRGCANEANYRNLKI-----IIYDFSRPRLNIPRHMVPQTEHPTI
                                                                                                                                                                                                                                                            689 FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTF-----DAFDCQLHEFHTEENKLV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U43145; AAC63403.1; -
SEQUENCE 1939 AA; 229001 MW; B36E462001C6F22F CRC64;
Last sequence update)
Last annotation update)
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(TrEMBLrel. 01, I
(TrEMBLrel. 07, I
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: EL 321	WY 786 365	FN 846 : :YN 413	.VT 896 : :K 449	MA 952	IRP 1012 512	AC 1072	WD 1123 : rID 558	TF 1176	IDN 1233 : IEQ 642	JEK 1293 SEN 687	7EK 1350 AK 745	1403 802	mi; during a
: : : : : : : : : : : : : : : : : : :	LYNHDNEYLLYQDD::: DD	IPELQTAAQKVGRD : : :: .LKEKETELNEIHKK	RDKEVT :	WEKLFGRALPIRKL: : :!	PIQSADLRTTGGRSS : : -ILNKDKQTLG	IVPSADAVDALKTC :: DLINNLKN-	-TECQIKCGDLFENSVVD : : NEEMEGKCVVID	SDFNGKWYITSGLNP : : CEKEFI	SGFFTRSAVQKFVQDPNQPGVLYNHDN :: : : : :: -NLFNKNFEEKKNIYENELNSLRLKYDNEQ	VVYTRSSVLPNSIIPELEK :: : MHWFRSICTKIDMPYSEN	/KEVEEIEEEVEKEV : : :: : \AIVAELEEKHKEEI	SIKMEASEVEKLFG ::: : KLEEEHKDVVTKLG	Euteleosto ; Homo. on of Chkl
 KDFKSK	FFTRSAVQKFVQDPKYPGI :: : -LSQSLVEKERE	WDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN : : : : : : : :	RTIIKEVEEIEEEVEKVRDKEVT 	-ENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMA 	RKRINGTFLLKILPP : VN	PLLLKLVGVLACAFL		-SDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTF 	LDSGFFTRSAVQK :: : NLFNKNFEEKKNI	GGRNDAWDGYGGAVVY	FERIEKTVEEGERIIV : : : 'HKEMVAELEKRHA	-LKQDEBNEVRELSKEEMBFLDEIKWEASEVEKLFG :: :: :: :: : : ILEEKHKDVVTKLGEGHKENIIKLEEBEHKDVVTKLG	PRT; 1332 AA. eated) st sequence update) st annotation update) Craniata; Vertebrata; E Catarrhini; Hominidae; 622; ired for the activation ponse in Xenopus egg ex
: : IESRE	99 :	YYKGRNDA	TFIKTDNTCGPEPPLVERLEKKVEBGERTIIKEVEEIEEEVEKVR : LEIETIKNELNEKEEELEKNK	; E	VATHCETSPCHDRIREFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRP : : : : : :	LSAPRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCAC :: 	LLKGCRIELAKCIANPACAANVACLOTCNNRPDE	EFBECAVSRKKCVPRKSDLGEF : : : : : EIEKKYKNEIFMLEEKLKEKENYADLND-	DAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDN :: : : : : : : : :	EYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEK :	AAKSIGRDFST-F1RTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEVEK 	· H	ARY; PRT el. 16, Creat el. 16, Last el. 16, Last clordata; Cra Chordata; Cra Primates; Cat Primates; Cat cotein require kpoint respon
: : : : : KENEIIIEKLKDIESR		ILS											74 44 47 48 48 48 48 48 48 48 48 48 48
288	728	787	847	897	953	1013	1073	1124	1177	1234	1294	1351	RESULT 1: 11
qq	Qy Db	Qy Db	QY	O.Y.	OY Db	Qy	Q D	QY	QY Db	Qy Db	Q D	Oy Db	RES DT ACO DT ACO DT ACO COC COC COC RAPA RAPA RAPA RAPA RAPA RAPA RAPA RAP

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                                                                                                       136 LQSGNSTDF----TTDRKSSKKH--IHDKEGTA---GKAKVKSKRRLEKE-ERKMEKIRQ 185
                                                                                                                                                                                                                                           ------TEMTLFQRLLEGFKELQ-QDEE-----NFVR 439
                                                                                                                                                                                                                                                                              186 LKKKETKNQEDDVEQPFNDSGCLLVDKDLFETGLEDENNSPLEDEESLESIRAAVKNKVK 245
                                                                                                                                                                                                                                                                                                                                            246 KHKKKEPSLESGVHSFEEGSELSK--GTT---RKERKAARLSKEALKQLHSETQRLIRES 300
                                                                                                                                                                                                                                                                                                                                                                                                   496 --KLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGL----QLFS 548
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                                                                                307 SSQIENKPDDYIFVYYRGRN------DAWDGYGGSVIYTRSPTLPESIIPNLQKA 355
                                                                                                                                                            356 AKS-VGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVERD 414
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Query Match 2.0%; Score 150.5; DB 4; Length 1332; Best Local Similarity 19.3%; Pred. No. 2.6; Matches 255; Conservative 182; Mismatches 405; Indels 477; Gaps
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Search completed: November 6, 2001, 05:13:08 Job time: 562 sec

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Sequence:

Run on:

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6, 2001, 02:54:17 ; Search time 6769.47 Seconds
   (without alignments)
   3630.750 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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98 htg13: **
98 htg13: **
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	U34817 Nicotiana t	U31462 Lactuca sat	U44133 Arabidopsis	AJ250433 Spinacia	AC003981 Genomic s	U39452 Arabidopsis	AF288196 Oryza sat	AC006932 Genomic s
QI	NTU34817	LSU31462	ATU44133	SOL250433	AC003981	ATU39452	AF288196	AC006932
DB	14	14	14	15	12	14	13	12
Query Match Length DB	1589	1760	1555	1686	133843	2884	1173	89479
Query Match	100.0	40.5	39.3	36.9	27.0	26.9	26.4	10.2
Score	1589	643.8	624.2	585.8	428.4	426.8	419	162.4
Result	7	7	e	4	2	ر د	7	ω

75.8 4.8 7218 10 16644	gene 1	peptide ide 500 a	Ouery March Ouery March Dost Local Similarity 100.0%; Score 1589; DB 14; Len Best Local Similarity 100.0%; Pred. No. 0; Matches 1589; Conservative 0; Mismatches 0; Inde Qy 1 tatttcatgagtttgcagttggtgtaatacggttgaagaatggctct	Qy 121 ataaaaggtttagctgggattgggaagattactttggtagtatagtcgt 11	Oy 301 ttaaccagaatgtacctaagggaaattcaggatgcaaatttccaaaga	Oy 481 agtgcaggttagagcttgcgaagtgcattcgaaccctgcatgtgcagc
5.8 4.8 7.218 10 166494 5.4 3.5 194855 90 AL158188 5.4 3.4 194615 61 AC010184 5.4 3.4 194615 61 AC010184 5.4 3.4 194615 61 AC010184 5.4 3.4 178195 64 AC016152 5.2 4 3.3 175152 75 AC0178819 5.2 4 3.3 175152 75 AC013776 5.2 3.3 375152 75 AC013776 5.2 3.3 375152 75 AC013776 5.3 3.3 175152 75 AC013770 6.3 3.2 165425 71 AC034146 1.6 3.2 170396 81 AA289703 1.2 165425 71 AC034146 1.6 3.2 170396 81 AA289703 1.2 3.3 175159 81 AA289103 0.4 3.2 170396 81 AA289104 0.6 3.2 311 97 HS088154 0.6 3.2 170396 87 AC013719 0.6 3.2 311 97 HS088154 0.6 3.1 174989 79 AA35672 0.6 3.1 174989 79 AA35672 0.6 3.1 174989 79 AA35672 0.6 3.1 174989 85 AC004906 0.6 3.2 175588 90 AA35673 0.6 3.1 174989 10 AA38933 0.6 3.1 15299 87 AC013719 0.7 3.1 12240 4 AE010124 0.8 6 3.1 15299 6 AC02134 0.8 8 3.1 15299 6 AC02134 0.9 3.1 12240 4 AE010124 0.9 3.1 123410 76 AC012462 0.9 8 3.1 15299 10 AA38933 0.1 176738 65 AC0041246 0.9 3.1 176739 6 AC012462 0.9 8 3.1 15299 10 AA38933 0.1 176378 65 AC012462 0.9 8 3.1 15299 10 AA35673 0.6 3.1 176379 62 AC012462 0.9 8 3.1 15299 10 AA35673 0.6 3.1 176379 62 AC012462 0.9 8 3.1 15299 10 AA367376 0.0 8 3.1 15299 10 AA3673776 0.0	100494 SQUURINCE 14 AL158158 Human DNA AC025108 Homo sapi AC010184 Homo sapi AC010184 Homo sapi E08995 DNA encodin AC078819 Homo sapi AC078819 Homo sapi AC073776 Homo sapi AC023550 Homo sapi AC023550 Homo sapi AC034146 Homo sapi AL589703 Homo sapi AL589703 Homo sapi AL89703 Homo sapi AL89704 Homo sapien AR077147 Sequence	UBB153 Homo sapien AR077146 Sequence D83006 Saccharomyc 297055 Hunan DNA s AC013719 Homo sapi AL355592 Homo sapi AL355592 Homo sapi AL356824 Human DNA AL390882 Human DNA AC074420 Mus muscu	J03902 Plasmodium AC004906 Homo sapi AC021134 Homo sapi A58933 Sequence 2 AJ07010 Plasmodiu A58932 Sequence 1 AE001424 Plasmodiu AC011632 Homo sapi AC073776 Mus muscu AC073776 Homo sapi AC025752 Homo sapi		heophyta; Spermatophyta s; Asteridae; euasterid e lipocalin family, the	Plant Molecular aile Way, Honolulu,
	010 690 644 645 75 75 71 71 71 70 70 70 70	00 00 00 00 00 00 00 00 00 00 00 00 00	00000000000000000000000000000000000000	rn 1	tabacum. Viridiplantae; Embryophy Viridiplantae; Embryophy Vizi eudicotyledons; core ses; Solanaceae; Nicotiana 1 to 1589) Hieber,A.D. and Yamamot Licycle enzymes are membe tified from plants nem. 273 (25), 15321-1532	Yanamoto, H.Y. Yanamoto, H.Y. Jon AUG-1955) Robert C. Iversity of Hawaii, ion/Qualifiers 589 In="Xanthi" and tabe in="Xanthi" and tabe ref="taxon:4097" ue_type="leaf"

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35KLPGHKRFSWGWEDYFGSTVVA
ALKTGTCLLKEGREGARGERPK
ALKTGTCLLKEGRLELAKCISNPA
BENECAVSRKKCVPRKSDVGDFPV
ALHEFHTERKLVGNLSWRIRTPD
ANTLSSKFWSPDVIFVYYKGR
SRDFNTFIKTUNTGCPEPPLVRKL
KLFGFKELQRDEENFLRELSKEE
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LSU31462 1760 bp mRNA PLN 22-JUL-1996
Lactuca sativa violaxanthin de-epoxidase (VDE1) precursor, mRNA,
Complete cds.
                                                                                      U31462.1 GI:1438874
                                           DEFINITION
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RESULT
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663 TGCAAAATGTATAGCAAACCCATCTTGTGCGGCAAACGTTGCCTGTCTACAGACTTGCAA 722

tgcgaagtgcatttcgaaccctgcatgtgcagctaatgttgcctgtctccagacttgcaa

tgatgcggttgatgctctcaagacttgtacttgcttactgaaagagtgcaggttagagct

603 TGATGCCGTTGATGCTCTTAAAACTTGTGCTTGTTTACTCAAAGAATGCAGGATTGAGCT

543 GAGACAATTCATACAATTGGCTATCGTATTGGTTTGCACATTTGTTATCGTTCCCAGAGT

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Eukaryotta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactucae.

II (bases 1 to 1760)

Bugos, R.C. and Yamamoto, H.Y.
Molecular cloning of violaxanthin de-epoxidase from romaine lettuce and expression in Escherichia coli
Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6320-6325 (1996)
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/gene="VDE1"
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Bugos, R.C.
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Matches

Similarity

Query Match Local

40.5%; Score 643.8; DB 14; Length 1760; 71.8%; Pred. No. 8.2e-128;

317 taagggaaattcaggatgcaaatttccaaaagatgtagctttgatggtttgggaagaatg 376 gggccaatttgccaaaacagcaattgtagctatattcattttgtcagttgcttcaaaagc 436

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U44133.1 GI:1465734

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VERSION KEYWORDS SOURCE

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CAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ
IKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEPPAPDPSVLVQNFNISDFNGKWYI
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                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-JAN-1996) Robert C. Bugos, Plant Molecular
Physiology, University of Hawaii, 3190 Maile Way, Honolulu, HI
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Bugos, R.C. and Yamamoto, H.Y.
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                                    664 TCAACATCTCGGACTTTAACGGGAAGTGGTACATTACAAGTGGCTTGAATCCAACCTTG 723
                                                                                   aattogtgcaagatccaaagtatccggggatactctacaatcatgataatgagtatcttc 960
                                                                        atttatcttggagaatacgtacacctgatggaggattttttactcgatcagcggtgcaaa
                        atgettttgattgecaattgeatgagttecatacagaa---gaaaacaaacttgtgggga
                                                                                                                                    ttgaggagatagaagaagaagtagagaggtgagagataaaggaag-------tca
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1 (bases 1 to 1686)
Emanuelsson,A.K., Eskling,M. and Akerlund,H.E.
Cloning and sequencing of Spinacia olercea violaxanthin
SOL250433 1686 bp mRNA PLN 21-OCT-1999
Spinacia oleracea mRNA for violaxanthin de-epoxidase (svdel gene).
AJ250433
                                                                                          svdel gene; violaxanthin de-epoxidase
                                                                  AJ250433.1 GI:6103242
                                                                                                                                                                                                                                                                                                      (bases 1 to 1686)
                                                                                                                            Spinacia oleracea
                                                                                                                                                                                                                                                                  de-epoxidase
                                                                                                                                                                                                                                                                                  Unpublished
2 (bases 1
                                                                                                          spinach.
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DEFINITION

ACCESSION VERSION KEYWORDS

SOL250433

ORGANISM

SOURCE

REFERENCE

AUTHORS TITLE JOURNAL REFERENCE

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KFAQDPSQPCMLYNHDNAYLHYQDDWYLLSSK I ENQPDDYVFVYYRGRNDAWDGYGGA
FLYTRSATVPENI VPELNRAAQSVGKDFNKF I RTDNTCGPEPPLVERLEKTVEEGERT
I I KEVEQLEGEI EGDLEKVGKTEMTLFQRLLEGFQELQKDEEYFLKELNKEERELLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNNRPDETECQIKCGDLFANKVVDEFNECAVSRKKCVPQKSDVGEFPVPDPSVLVKSF
NMADFNGKWFISSGLNPTFDAFDCQLHEFHLEDGKLVGNLSWRIKTPDGGFFTRTAVQ
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Submitted (20-OCT-1999) Emanuelsson A.K., Dept. of Plant
Biochemistry, Lund University, Chemistry Center, POB 117,
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                                                                                                                                                                                                                                                                                                                                       function="part of the xanthophyll cycle"
                                                                                                                                                                                                                                                                                                                                                                            /product="violaxanthin de-epoxidase"
/protein_id="CAB59211.1"
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296 c 375 g 466 t
                                                                                                                                                       /organism="Spinacia oleracea"
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                                                                                                                                                                        /db_xref="taxon:3562"
/country="Sweden"
                                                                                                                                                                                                                    /tissue_type="leaf"
                                                                                                             Location/Qualifiers
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373. .1416
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  Emanuelsson, A.K.
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Shinn, S., Erooks, S., Buehler, E., Chao, O., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Liam, B., Lee, J., Lee, J., Lee, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Direct Submission
Submitted (05-JAN-2001) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-JUL-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA Ecker, J.R.
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Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
8 (Dases 1 to 133843)
Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, O.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bell, B., Chin, C.,
Chiou, J., Choi, E., Conn, L., Lee, J., Lec, J., Liu, A., Hansen, N.,
Howing, B., Koo, T., Lam, B., Lee, J., Lec, C., Li, J., Liu, A., Liu, A.,
Howing, B., Koo, T., Southwick, A., Thaveni, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
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Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Liu, S., Whixbrarsky, N., Nguyeni, M., Palm, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
Submitted (08-JAN-1998) Arabidopsis thaliana Genome Center, popartment of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 133843)
                                                                                                                                                                                                Submitted (26-JAN-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 133843)
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-APR-1998) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA 6 (bases 1 to 133843)
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/protein_id="AAF99755.1"
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LQALDLSNNAFESSLPKSLSNLTSLKVIDVSVNSFFGTFPYGLGMATGLTHVNASSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSGFLPEDLGNATTLEVLDFRGGYFEGSVPSSFKNLKNLKFLGLSGNNFGGKVPKVIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRKLLRKWRREQKDMVEKGLVTMEDVEMASAQAASEDSKKSPRKFSVKKSLKLNKLNN
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SMCYSLGVHVLPFFRFYRGSQGRVCSFSCTNATIKKFRDALAKHGPDRCSLGPTKGLE
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                                                                                                                  14113. .14274))
/note="unknown protein; similar to EST dbj|AV530752.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // 16782. 19871
/note="similar to receptor protein kinase-like protein emb[cAB66905.1; similar to ESTs db]|AV522839.1, db]|AV528375.1, and db]|AV541093.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    578 atgtcagataaaatgtggtgatttgtttgaaaaacagtgtcgtagacgagttcaatgagtg 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6305 ATATCAGATTAAATGTGGGGATCTGTTTGAGAACAGTGTTGTTGATGAGTTCAACGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6665 CTACAATCATGACAACGAGTACCTTCACTATCAAGATGACTGGTAATAACATCTTGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 tgcagtctcccgaaagaaatgtgtacctcgtaaatctgatgttggtgactttcctgtacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 tgatcccagtgttcttgtccagaagtttgacatgaaagattttagcgggaaatggttcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758 tactcgcggtttgaatcccacttttgatgcttttgattgccaattgcatgagttccatac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6545 AGAAGGTGACAACAAGCTTGTTGGAAACATCTCTTGGAGAATAAAGACCCTAGACAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    875 attttttactogatcagoggtgcaaaaattogtgcaagatccaaagtatccggggatact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6725 CACCCACGAGGAGGAGTCTTGATAGTGCTGCTATTCTTTTTGGCCTAACAAGCTTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 976 -----ggtatattttgtcatccaaagtagaaatagtccagaggattacatat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 818 agaa---gaaaacaaacttgtggggaatttatcttggagaatacgtacacctgatggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctacaatcatqataatqaqtatcttctctaccaagatgact-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6785 ATGATTTTGCAGGTATATCCTGTCATCAAAGATAGAGAATAAACCTGAAGACTATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.0%; Score 428.4; DB 12; Length 133843; 67.6%; Pred. No. 1.3e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 231; Indels 106;
                                                                                                                                                                                                                                                  /evidence=not_experimental/product="F22013.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/product="F22013.7"
                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF99782.1"
/db_xref="G1:9802580"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGKKKKNQKASGEKSADCMLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703; Conservative
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                                                                          /protein_id="AaF99751.1"
/db_xref="G1:9802549"
/tb_xref="G1:9802549"
/tb_xref="G1:9802549"
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/db_xref="GI:9802581"
/translation="MSYVDLKKAAMKDMEAGPDFDLEMASTKADKMDENLSSFLEEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVKAEMGLISETLARIEQYHEESKGVHKAESVKSLRNKISNEIVSGLRKAKSIKSKLE
EMDKANKEIKRLSGTPVYRSRTAVTNGLRKKLKEVMMEFQGLROKMMSEYKETVBRRY
FTVTGEHANDEMIEKIITDNAGGEEFLTRAIQEHGKGKVLETVVEIQDRYDAAKEIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTEVISKTSLFLGACGNHHRVDDFSFSPVSFGGFGLKKSFSCLK
LKSQKPLRSVFYGKQIVFGDSQDESFRRSSAITAQTTLRIGTAQKWWEKGLKDNMREI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
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/translation="MSSCLLPQFKCPPDSFSIHFRTSFCAPKHNKGSVFFQPQCAVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPALLTSMLDVAKLRLPSFDTDSDSLISDRQWTYTRPDGPSTEAKYLEALASĒTLLTS
BARVVVAAAARAVALARAAVKVAKDATLFKNSNTNLLITSSTADKRKSWOFTRERBA
GILGHLAVSDNGIVSDRITJASSNRBSIGDLESERGEVELLĒROPSVSLAVRSTROT
ERKARRAKGLEKTASGIPSVKTGSSPKKRLVAQĒVDHNDPLRYLRWITSSSKLLTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEHELSAGIQDLLKLERLQTELTERSGRQPTFAQWASAAGVDQKSLRQRIHHGTLCKD
KMIKSNIRLVISIAKNYQGAGMNLQDLVQEGGRGLVRGAEKFDATKGFKFSTYAHWWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KQAVRKSLSDQSRMI RLPFHMVEATYRVKEARKQLYSETGKHPKNEE I AEATGLSMKR
LMAVLLSPKPPRSLDQKI GMNQNLKPSEVI ADPEAVTSEDI LIKEFMRQDLDKVLDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTREKQVIRWRFGMEDGRMKTLQEIGEMMGVSRERVRQIESSAFRKLKNKKRNNHLQQ
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PPIQSADLRTTGGRSSRPLSAFRSGFSKG1FDIVPLPSKNELKELTAPLLLKLVGVLA
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IKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYI
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VLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLP
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EVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLLELHQVFLDMAVMVESQANELKTAKSHQRNSRKWMCIGIIVLLLIILIVVIPIITS
                                                                                                                                                                                                                                                                            join(1385. .1463, 2004. .2185, 2419. .3015, 3461. .3691, 3803. .3943, 4030. .4230, 4333. .4620)
/note="similar to sigma factor 2 gb|AAB69385.1; similar to EST dbj|AV557315.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to thioredoxin-like 1
gb|AAD35005.1|AF144387_1; similar to ESTs gb|T46281.1,
dbj|AV442467.1, and dbj|AV549179.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to s-syntaxin-like protein
gb|AAF00648.1|AC009540_25; similar to ESTs
dbj|AV556140.1, dbj|AV566414.1, and dbj|AV555627.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /6798. 7311)
/note="similar to viiolaxanthin de-epoxidase
emb[CAB59211.1; similar to ESTS gb|A1994713.1,
dbj|AV440942.1, and dbj|AV521985.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(5386. .5601,5679. .5845,6111. .6207,6312.
6798. .7311)
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/evidence=not_experimental
    experimental
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/db_xref="G1:9802552"
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/protein_id="AAF99753.1"
/db_xref="G1:9802551"
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CDS

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6484

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 2596)
Lukowitz,W., Mayer,U. and Jurgens,G.
Cytokinesis in the Arabidopsis embryo involves the syntaxin-related KNOLLE gene product
Cell 84 (1), 61-71 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Entwicklungsgenetik, Universitaet Tuebingen, Spemannstrasse 37-39, D-72076 Tuebingen, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATU39452 2884 bp DNA PLN 09-FEB-1996
Arabidopsis thaliana syntaxin-related knolle mRNA, complete cds.
                                                                                                                                              1372 gaqaqctqaqcaaagaaqaaatgatgttttggatggacttaaaatggaagcaactgagg 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                        1432 tagaaaaactttttgggcgtgctttaccaataaggaaattaaggtaagtatttttaaaac 1491
1084 caagaagtgcagttttgcctgaaagcattataccggagttgcaaaccgcagctcaaaaag 1143
                     6905 CGAGAAGTTCTGTATTACCCAATAGCATTATACCAGAAACCGGAAAAAGCA 6964
                                                                        1144 ttgggcgtgatttcaacacattcataaaaacagacaatacatgtggccctgaacctcccc 1203
                                                                                                                                                                                                                                                         7085 AAGAGATAGAAGAAGAGGTAGAGAAGGAGGTGGAAAGGTCGGTAGGATGACCT 7144
                                                                                                                                                                                                                                                                                              1312 tattcagtaaactgtttgaaggttttaaagagctccaacgagatgaagagaacttcttaa 1371
                                                                                                                                                                                                                                                                                                                  7025 TCGTGGAGAAATTGAGAAGACAGTGGAAGAAGGTGAAAGGGTAATCGTAAAAGGGTTG 7084
                                                                                                                                                                                                                                                                                                                                                                                                       7205 GAGAGTTAAGTAAAGAAGAGATGGAGTTTTTGGATGAAATCGAAATGGAAGCAAGTGAGG 7264
                                                                                           1264 aggagatagaagaagtagagaaggtgagagataa-----agaagtcacct
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/translation-"MNDLMTKSFMSYVDLKKAAMKDMEAGPDFDLEMASTKADKMDEN LSSFLEEABYVKAEMGLISETLARIEQYHEESKGVHKAESVKSLRNKISNEIVSGLRK

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AKSIKSKLEEMDKANKEIKRLSGTPVYRSRTAVTNGLRKKLKEVMMEFQGLRQKMMSE
YKETVERRYFTVTGEHANDEMIEKIITDNAGGEEFLTRAIQEHGKGKVLETVVEIQDR
                                       YDAAKEIEKSLLELHOVFLDMAVMVESQGEOMDEIEHHVINASHYVADGANELKTAKS
HORNSRKWMCIGIIVLLIILIVVIPIITSFSSS"
569 c 582 g 900 t
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                                                                                                                                                                                     26.9%; Score 426.8; DB 14; Length 2884; 67.5%; Pred. No. 2.3e-81;
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0; Mismatches 232; Indels 106;
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YISSGLNPPEDTEDCQLHERPVEGBKLJANLTWRIRTPDSGEFTRATORFVQDPAQP
ALIYNHDDRELHYQDDWYIISSKVBWREDDVIFYYRGRNDAWDGYGGALLYTRSKVV
PESIVVBELERAAKSVGRDFSTFITRTDNTCGPBPPLVBRIEKTVBQGERTIIREVOEIE
GEIGGVKELEBEBEVTLFKRLJTDGLMEVKQDLANFFQGLSKEEMELLDQNNMBATEVE
                                                                                                                                                                                                                                                                                                 Oryza sativa subsp. indica.
Oryza sativa subsp. indica.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                             AF288196 1173 bp mRNA PLN 18-SEP-2000
Oryza sativa subsp. indica violaxanthin de-epoxidase mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                          Lin,R.-C., Xu,C.-C., Li,L.-B. and Kuang,T.-Y. Molecular cloning and expression of rice violaxanthin de-epoxidase Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     China
3 (Bases 1 to 1173)
Lin,R.-C., Xu,C.-C., Li,L.-B. and Kuang,T.-Y.
Lin,R.-C., Xu,C.-C., Li,L.-B. and Kuang,T.-Y.
Direct Submission
Submitted (18-SEP-2000) Photosynthesis Research Center, Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin, R.-C., Xu, C.-C., Li, L.-B. and Kuang, T.-Y.
Direct Submission
Submitted (18-JUL-2000) Photosynthesis Research Center, Institute
of Botany, Chinese Academy of Sciences, Xiangshan, Beljing 100093.
                                                          1432 tagaaaaactttttgggcgtgctttaccaataaggaaattaaggtaagtatttttaaaac 1491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa subsp. indica"
/cultivar="Zhenhui-249"
/sub_species="Indica"
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/protein_id="AAF97601.2"
/db_xref="G1:10181228"
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AC006932 89479 bp DNA PLN 11-OCT-2000
Genomic sequence for Arabidopsis thaliana BAC T27G7 from chromosome
I, complete sequence.
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1 (asss 1 to 89479)
Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bei,Q., Chin,C., Chiou,J., Chol,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          981 attttgtcatccaaagtagaaaatagtccagaggattacatatttgtgtactataagggc 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1041 agaaatgatgcatgggatggatatggtggttctgtactttaccacaagaagtgcagttttg 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cctgaaaagcattataccggagttgcaaaccgcagctcaaaaagttgggcgtgatttcaac 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1161 acattcataaaaacagacaatacatgtggccctgaacctccccttgttgagaggttggag 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---gaagaagaagtagagagagagagagataaagaagtcaccttattcagtaaactgttt 1328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aagaaagtggaagaaggagaaggacgatcataaaaagaagttgaggagata----- 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggtgactttcctgtacctgatcccagtgttcttgtccagaagtttgacatgaaagatttt 740
                                                                61 GCCGAGTTCCCAGTCCCTGATCCATCCGCCCTTGTCAAGAACTTCAACATGGCTGATTTC 120
                                                                                                                                                                               801 ttgcatgagttccatacagaagaaaacaaacttgtggggaatttatcttggagaatacgt 860
                                                                                                                                                                                                                                                                                                                            181 CTTCACGAGTTCCGTGTCGAGGAGACAAACTTATATAGCGAACTTGACATGGAGAATTCGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                    acacctgatggaggattttttactcgatcagcggtgcaaaaattcgtgcaagatccaaag 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ACCCCCGACTCTGGCTTCTTCACCAGAACAGCCATACAGCGGTTTGTGCAGGACCCAGCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tatocgggggatactctacaatcatgataatgagtatcttctctaccaagatgactggtat 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CAACCCGCGATCCTCTATAACCATGACAACGAGTTCCTGCACTATCAAGATGACTGGTAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 AAGACCGTCGAGCAAGGAGAGAACCATCATCAGGGAAGTGCAGGAGATAGAGGGCGAG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 ATCGAGGAGAGGTGAAGGAGCTGGAGGAGGAGGAGGACATTGTTCAAGAGGTTGACA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721 GATGGCCTCATGGAGGTGAAACAGGACTTGATGAACTTCTTTCAGGGCCTGAGCAAGGAG 780
                                                                                                                                         741 agcgggaaatggttcattactcgcggtttgaatcccacttttgatgcttttgattgccaa 800
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Arabidopsis thaliana
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SGEDHEWWWRYVFLYCTAFFSIQTCGFD"
join(17065. .17069,17482. .17701,17921. .18116,18380. .18528)
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LOPHHNNMANSSSTSGLPSTSRTLAPPRPSEDKVLIIIIIIIIIIIFF"
join(11373. 11439,11990. 12266,12331. 12619,12691. 12921,
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GEKEKDNEEEEEDEEEEEEEEDEDEDEEEEGGGVIIKEEEASEIIKVVADEHKSGSI
KSEFEGSSATDEKGDNGVVQPPICSSNP"
complement(join(14188 .14733,14829 .14985,15122 .15253,
15357 .15945,16043 .16083,16294 .16439))
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FHPISOKIHPFSFLUSTVVVLLIGIISFLFRRHLKNELRSYSIGBEBERKBGWKLU
HSDVFRCPRNISWLCAILGTGTGLILIIALFALAFTGFLYPYNRGMLITSLVIMYTL
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GTIVIILLIFTLLNIPFLMLGGVLGNRFGLLEFQPPSAVKRNPREIPPQNWYRRKLYQ
VFLGGFVPFSAVVLEWHQLYASLWGFKIYTSPGIMLFTFIVLIFLSSSVGIILTYIQL
                             ERNVFDTLRDDFMVCFGQWDFEPADLSISTKSYIHIWHGKEDKVVPFQLQRCILQKQP
LINYHEIPQGGHLIYHYDGICDTILAKEEQQKLYKIN"
comptement(join(1334. 2261,3126. 3268,4062. 4283,
4505. 4776,4882. 4930,5090. 5167,5499. 5558,5719. 5796
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similar to ESTs gblH76000, gblAa651460"
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Ab_xref="61:6664324"

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CFLVIGEYYGRLRALSSLWLSRPRDSVSEQTRAAALAELRIISKQDFDSRLIIAADGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPYIAETLYSSSHSSQENAAATLLNLSITSREPLMSSRGLLDALSHALRHHDTTTSPA
AVQSSAATIYSLLIAEESYRPIIGSKRDIIFSLIHIIRYPDSHPRSIKDSLKALFAIA
LYPMNRSTMISLGAIPALFSLIVKDSRCGIVEDATAVMAQVAGCEDSEDGMRRVSGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLADLIDPCTGSSLRIKENSVGALLNIARCGGAAARSEVÄAAVASGADEGAMEGIVYV
AENGSIKGRKKAVDLIKLVVSGNGGDSREDVLFNENENBNSRS*
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8179. .8287,8565. .8654,8797. .8890,9113. .9184))
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RGYLDPLPSEQYMQCESDEDFYKVYRLLPQTEASLLNWAINLMADVIQFEHYNKMNSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /traislation="MNRDRPLHLINCQVLASPLTAIKLIEKGGEKERVMNHKGFFTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13105. 13503)
Anote-"putative rac GrPase activatin protein gb|AAD15596; similar to ESTs gb|T20436"
Codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chao, O., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzaler, A., Hansen, N., Hewing, B., Koo, T., Lam, B., Lee, J., Lee, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Trafaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Theologis, A. and Ecker, J.
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                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-MAR-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3 (bases 1 to 89479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-MAY-1999) Arabidopsis thaliana Genome Center, poppartment of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 89479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-NOV-1999) Arabidopsis thaliana Genome Center, bepartment of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 89479)
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/note="unknown protein gb|AAD21437.1; similar to EST
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/db_xref="taxon:3702"
/chromosome="1"
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/product="T27G7.1"
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/db_xref="G1:6664302"
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Submitted (05-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk replaced gi:12733508.

On Apr 6, 2001 this sequence version replaced gi:12733508.

During sequence assembly data is compared from overlapping clones. Where differences are found these are amonated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a natio overlapping clone, as we submit sequences with This sequence was finished as follows unless otherwise noted: all
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                               DB 10;
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Matches 23; Conservative 237; Mismatches 149;
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EFNIELSQWSRKDVEGSLFVVKRLLLSIFNYYLLIFNRLLKSDWILFFVSFRSTQPRF
GFNYMRRTDNLVBNLLGDFEXFYGPSTLLFRNASQEVNGTWFTRECEEVATLFN
RILSAYSKVNGKPRASSKSEFEARPTMAVMDGPLEPSSTARDAPDDPAFVNFFS
STMNLGNTASGSASGRYGSAIPHQPHQPHQPTIAPPYAAAAPQJIGSPPPLQSSSPF
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                                                                                                                                                                                           /translation="MSKLQSEAVREAITTITGKSEAKKRNFVETIELQIGLKNYDPQK
DKRFSGSVKLPHIPRPKMKICMLGDAQHVEEAEKMGLENMDVESLKKLNKNKKLVKKL
                                                                                                                                                                                                                                             AKKYHAFLASESVIKQIPRLLGPGLNKAGKFWLQLIFHFGNLSMEEKQIFQNVQMSVN
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LTSNLNHDCSDLNDRLLHLRTDLTKHAVSWISTSLSAKVSLEDLRLNLESLLLCLHIEF
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/note="putative ribosomal protein L10 gi|3860277; similar to ESTS gb|T41543, gb|R86781, gb|AA721952, emb|Z34253, gb|N64989, gb|AA041179, emb|Z26567"
                                                                                                                                                                                                                                                       FINSTLKKNWOWNYCLYLLKSTUMGPPORIF"
join(19189. 19347,19428. 19605,19741. 19885,20087. 2C
20295. 20409,20600. 21079,21145. 21201)
//note="similar to yeast dop1 gl|3169719; similar to ESTs gb|H37036, emb|227040, gb|R90173, gb|A199440.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26545. .26839))
/note="similar to inerleukin-1 beta convertase homolog A
precursor sp|P55865"
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0; Mismatches 56;
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/product="T27G7.8"
/protein_id="AAF22903.1"
/db_xref="G1:6664321"
                                                                                               /evidence=not_experimental
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/product="T27G7.7"
/protein_id="AAF22887.1"
/db_xref="G1:6664305"
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Sequence 14 from patent US 5670367 166494

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DEFINITION ACCESSION

KEYWORDS VERSION

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assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw.; SWISSEROT; Tr., TREMBL; WORNPEP; Information on the WORNPEP database can be found at
                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr9
RPI1-427L11 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707. .2822

Mote-"LlME3A repeat: matches 6017. .6137 of consensus"

1336. .3403

Mote-"34 copies 2 mer cc 66% conserved"

1420. .3725

Mote-"AluSx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1966. .2242
/note="LiME3A repeat: matches 5614. .5894 of consensus"
complement(1992. .2500)
/note="match: GSS: Em:AQ172930"
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596. .5870
note="LIMA9 repeat: matches 6027. .6305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       527. .772
/note="AluSg/x repeat: matches 158. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Alusg/x repeat: matches 150. .302 of consensus"
887. .1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              929. .1168
/note="LlM4 repeat: matches 5149. .5403 of consensus"
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note="AluJ/FLAM repeat: matches 1. .68 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MER5A repeat: matches 61. .106 of consensus"
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1949. .7003
"note="L2 repeat: matches 2090. .2136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="L2 repeat: matches 1284. .2090 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326. .615
/note="AluSg repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: matches 1. .311 of consensus"
(698. .1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1698. .1726
/note="MERSA repeat: matches 16. .44 of consensus"
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/note="MER5B repeat: matches 4. .175 of consensus"
4884. .5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSp repeat: matches 1. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="L1P repeat: matches 3. .226 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the entire insert of clone RP11-427L11.
Location/Qualifiers
1. .194835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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/clone_lib="RPCI-11.2"
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join(8370. .8532,9091. .9156,15133. .15192,15671. .15768)
/note="match: STS: Em:G29920"
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11742. .12929
//note="Tigger3b repeat: matches 2. .1231 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSx repeat: matches 38. .299 of consensus"
10183. .10319
10404. .10492
/note="MER5B repeat: matches 7. .97 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indice="12 repeat: matches 2537. .2703 of consensus" 14394. .14609
/note="MIR repeat: matches 12. .257 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="AluSq repeat: matches 38. .304 of consensus" .7415. .17488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Alusx repeat: matches 1. .312 of consensus"
13678. .13848
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16527. 16558
/note="Alusg repeat: matches 1. .302 of consensus"
16956. 17220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSq repeat: matches 1. .293 of consensus"
19629, .19689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9932. .9967
/note="18 copies 2 mer ta 100% conserved"
9973. .10105
/note="AluJ repeat: matches 1. .133 of consensus"
10133. .10392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12987. .13146
//note="MIR repeat: matches 89. .248 of consensus"
13153. .13468
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complement(23667, .23458)
/note="match: match: 81385"
complement(23074, .23458)
/note="MIR repeat: matches 12. .236 of consensus"
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22591. .22818
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/note="37 copies 2 mer aa 71% conserved"
18552, 18845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8591. .8662
/note="36 copies 2 mer ta 81% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(9897, .10091)
/note="match: STS: Em:HSA108WE1"
complement(9907, .10123)
/note="match: GSS: Em:B17453"
   // Acte="match: STS: Em: G05863" complement(8329. .8495) // Acte="match: STS: Em: G05863" complement(8329. .8495) // Acte="match: GSS: Em: B65750" // Acte="match: GSS: Em: GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(9737. .9894)
/note="match: GSS: Em:AQ281101"
complement(9886. .10119)
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/note="match: GSS: Em:AQ544271"
11354. .11653
                                                                                                                                                                                   complement(8329, .8496)
/note="match: GSS: Em:AQ227987"
complement(8339, .8502)
/note="match: GSS: Em:AQ110861"
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complement(9897. 10091)
                                                                                                                                                                                                                                                                                                                                                  8354. .8529
/note="match: STS: Em:G54088"
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/note="match: GSS: Em:B46502"
15900. .15947
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21481. .21679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8591.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC025108 181636 bp DNA HTG 12-WAY-2000 Homo sapiens chromosome 3 clone RP11-316C10 map 3, WORKING DRAFT SEQUENCE, 18 unordered pieces.
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note="match: GSS: Em:B43132"
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AC025108.3 GI:7770467
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Collympre, A. Coure, F. Destellanu, A. Destellanu, A. Destellanu, A. Dodge, S. Domino, M. Doyle, M., Fereira, P., Fitzhugh, W., Gage, D. Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, M., Grand, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Jahnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoccky, J., Levince, T., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGarthy, M., McBwan, P., McGarthy, M., McBwan, E., Milnova, T., Miranda, C., Mlenga, Y., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, Y., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stanger Thomann, N., Schauer, S., Severy, P., Spencer, B., Schauer, S., Stanger-Thomannin, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirell, A., Travers, M., Trigilio, J., Voussillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Piroch, C., Lander, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-MAR.2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 12, 2000 this sequence version replaced g1:7543769. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Bly Dye, 100% of reads Assembly program: Phrap; version 0.966731 Consensus quality: 171400 bases at least 040 Consensus quality: 176180 bases at least 030 Consensus quality: 176241 bases at least Q20 Insert size: 187000; agarose-fp Insert size: 17936; amn-of-contigs Quality coverage: 4.7 in Q20 bases; sum-of-contigs Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: L6445
Center clone name: 316_C_10
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2080 4451: contig of 2372 bp in length
4452 4551: gap of 100 bp
4552 8942: contig of 4391 bp in length
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of 4391 bp in length
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32392: contig of 4671 bp in length
32492: gap of 100 bp
39294: contig of 6802 bp in length
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27621: cont
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Misc_feature 160408. 181636

MASE COUNT 55146 a 34984 c 34816 g 54978 t 1712 others
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Query Match 3.4%; Score 54; DB 69; Length 181636; Best Local Similarity 52.7%; Pred. No. 0.18; Matches 117; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
T (bases 1 to 194615)

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Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Volo, Wahbah, M.,
Watlington, S., Weinstock, G., Yu, W., Zhou, X., Nelson, D. and
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Sequencing vector: M13; L08821
Sequencing vector: M13; L08821
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 10% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 165259 bases at least Q40
Consensus quality: 179670 bases at least Q30
Consensus quality: 184793 bases at least Q20
Estimated insert size: 188177; sum-of-contigs estimation
Batimated insert size: 204128; agarose-fp estimation
Quality coverage: 3.3 x in Q20 bases; agarose-fp estimation
Quality coverage: 3.6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                   ACULUI84 194615 bp DNA HTG 06-SEP-2000
Homo sapiens chromosome 3 clone RP11-438D8, WORKING DRAFT SEQUENCE,
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Submitted (15-SEP-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 5, 2000 this sequence version replaced gi:8705334.

Center: Baylor College of Medicine
Qy 1337 taaagagctccaacgagatgaagagaacttcttaagagagctgagcaaagaagaatgga 1396
                                                                                                                                                                                                                                                                                        Qy 1397 tgttttggatggacttaaaatggaagcaactgaggtagaaaa 1438
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: RP11-438D8
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Worley, K.C.
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Unpublished
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SEQUENCE, 6 unordered pieces.

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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17-APR-2001

AC016152 178189 bp DNA HTG 17-APR-200 Homo sapiens chromosome 12 clone RP11-1006M13, WORKING DRAFT

DEFINITION

RESULT 13

AC016152

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Mammalia Burnenia; Filmates; Catarrhin; Hominidae; Homo.

I (Dases 1 to 17819)

By Muzny, D. M., Adama, C., Adio-Cduola, B., Ali-Canan, F. R., Allen, C., Aliboroks, S. L., Amaratunge, H. C., Att. J. R., Bands, T., Barbaria, J. Bandsok, J., Bindage, M., Blankenburg, K., Bonin, D., Bouck, J., Burdage, M., Brown, E., Brown, M., Bryati, N. P., Bubhay, C., Burtel, P., Burkett, C., Burrell, K. L., Bytd, N. C., Carron, T. P., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, T., Chowdhy, I., Christopoulos, C., Clevaland, C. D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., Davila, M. L., Davis, C., Dathorne, S. R., Dathorne, R. W. Dotthwaite, K. J., Daraper, H., Dugan-Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C., Esottor, M., Falls, T., Ferraduto, D., Elagor, M., Foster, P., Frantz, P., Cabisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Harnandez, J., Harnandez, J., Hodyson, R., Jolivet, S., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lied, C., Liu, J., Liu, W., Martindale, A., Martinez, R., Massey, E., Mavhiney, E., Moledo, M. P., Mordan, M., Morris, S., Massey, E., Martin, R., Martinez, E., Massey, E., Martin, R., Martinez, E., Massey, E., Martin, R., Wartin, R., Wolleo, R., Martin, R., Wartin, S., Mordan, M., Morgan, M., Morgan, M., Morgan, M., Nguyen, N., Nguyen, R., Potche, R., Pace, A., Tamerisa, R., Tamerisa, R., Tamerisa, M., Tansey, J., Perez, L., Peters, L., Peters, L., Peters, L., Peters, L., Peters, C., Peters,
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                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Chemistry: Dye-terminator Big Dye: 77% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 174861 bases at least Q40
Consensus quality: 176412 bases at least Q30
                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Contact: hgsc-help@bcm.tmc.edu
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                              AC016152.30 GI:13654320
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                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
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0
                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                       Estimated insert size: 177176; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 7.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42121 GGGAGGGAGGGAGGAGGAAGGAAGGAAGGAAGGAAGTAAGTAAGGAAGGAAGGAAGGAA 42180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1329 gaaggttttaaaagagctccaacgagatgaagagaacttcttaagagagctgagcaaagaa 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1389 gaaatggatgttttggatggacttaaaatggaagcaactgaggtagaaaaactttttggg 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1269 atagaagaagaagtagagaagtgagagataaagaagataaagtcaccttattcagtaaactgttt 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1209 gagaggttggagaagaagtggaagaaggagaaaggacgatcataaaagaagttgaggag 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1449 cgtgctttaccaataaggaaattaaggtaagtatttttaaaaactatcaacatata 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.4%; Score 53.4; DB 64; Length 178189; Best Local Similarity 48.8%; Pred. No. 0.24; Matches 144; Conservative 0; Mismatches 151; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     66228: gap of unknown length 102480: contig of 36252 bp in length 102680: gap of unknown length 128603: contig of 26023 bp in length 128703: gap of unknown length 154940: contig of 25237 bp in length 155040: gap of unknown length 176445: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a protein involved in Leucocytozoon phylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 others
                                                                                                                                                                                                                                                                                                                                                                                                                66128: contig of 66128 bp in length
Consensus quality: 177169 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1997 (Rel. 52, Created)
02-SEP-2000 (Rel. 65, Last updated, Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="12"
/clone="RP11-1006M13"
55627 a 36623 c 33812 g 51623 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         be preserved
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128604
128704
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176446
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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1218 gagaagaaagtggaagaaggagaaaggacgatcataaaagaagttgaggagatagaagaa 1277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1338 aaagagetecaacgagatgaagagaaettettaagagagetgageaaagaagaagaat 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 GAAGAAGAAGAAGAGCAAGATGAAGAAGAAGAAGAAGAAGAAGAACAAGATGAAGATGAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAACAAAATGAAGAAGAACAAAAT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                          Kato A., Onaga H., Ueda S.;
POLYPEPTIDE INDUCING IMMUNITY AGAINST LEUCOCYTOZOON PROTOZOAN AND
RECOMBINANT DNA MOLECULE COLOR THE POLYPEPTIDE";
PATENT NUMBER JP199508995-AJ, 04-APR-1995.
DOUBUTSUYOU SEIBUTSUGARUTERI SEIZAI KYORAI, NITSUSEIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1686
/product="a protein involved in Leucocytozoon
phylaxis"
                                                                                                                                                                                                                                                                                                                                                                               04-APR-1995
10-SEP-1993 JP 1993226078
KATO ATSUSHI, ONGCA HIROSUKE, UEDA SUSUMU
CO7K14/44,A61K39/015,C12N1/21,C12N15/09,C12P21/02,G01N33/53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%; Score 52.4; DB 45; Length 1686;
Similarity 52.3%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Leucocytozoon caulleryi" /note="mRNA is derived from 2nd shizont"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 915 A; 129 C; 382 G; 260 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1398 gttttggatggacttaaaatggaagcaactgaggtagaaaaa 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATGAACAAATGAAGATGAACAAAATGAAGAAGAA 447
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (C12N1/21,C12R1:19),(C12P21/02,C12R1:19);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers

    .1686
    /db xref="taxon:32644"

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                                                                                                                                                                                                                                                                                                                                 Leucocytozoon caulleryi
JP 1995089995-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    topology: Linear;
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JP 1995089995-A/1.
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                                                unidentified unclassified.
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EMERIVORIA MELAZONA CHORDARA VALLEDRARA MELAZONAL,
MARMHALLA: BUTCHERAS CATATHINI: HOMINIAGAS: HOME.

I (bases I to 175152)
MULDY, D. M., Adams. C., Adio-Oddolab., All-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,
Burch, P., Burkett, C., Burkelly, K., Bonib, D., Chen, G.,
Carter, M., Burkett, C., Burchly, M., Bryan, N.P., Chang, C.,
Carter, M., Durch, P., Charko, J., Chavez, D., Chen, G., Chen, R.,
Carter, M., Dadvin, S.R., David, R. W., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Deland, C.D., Cox, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delado, O.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delado, O.,
Coyle, M.D. Dathorne, S.R., Davila, M.L., Davis, C.C.,
Elpid, C., Escotto, M., Falls, T., Ferraguto, D., Flagar, D., Edwards, C.C.,
Elpid, C., Escotto, M., Earlbatt, C., Edgar, D., Edwards, C.C.,
Elpid, C., Escotto, M., Earlbatt, M., Haylak, P., Hawes, A.,
Hennandez, J., Hernandez, O., Hodgeon, J., Garrer, M.,
Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunrer, T.,
Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunrer, T.,
Joudah, S., Karlsson, E., Marchis, C., Hart, M., Haylak, P., Hawes, A.,
Hennandez, J., Hernandez, O., Hodgeon, A., Hollows, M., Hollows, J.,
Joudah, S., Karlsson, E., Kally, S., Khan, U., King, L., Korvah, J.,
Martines, E., Massey, E., Manhiney, E., McCed, M.P., Mender, J., Martines, E., Massey, E., Markiney, E., McCed, M.P., Master, M., Mapus, P., Martin, R.,
Martinez, E., Massey, E., Manhiney, E., Wickerson, E., Nocken, M.,
Mayusen, M., Mayusen, W., Martin, R., Mayersh, M., Pearls, M., Mayusen, M., Nguyen, N., Nguyen, N., Nickerson, E., Nacher, J., Nacher, J., Perez, L., Peters, M., Pank, M., Peters, M., Rainington, S., Savery, G., Scherer, J., Spacer, M., Pank, M., Tansey, J., Tansey, J., Tang, H., Tang, H., Mayus, S., Williams Submitted (04-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 11, 2001 this sequence version replaced gi:12965249. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Genome Center (bases 1 to 175152) Worley, K.C. Direct Submission Direct Submission and Gibbs, R. Unpublished JOURNAL JOURNAL REFERENCE AUTHORS AUTHORS TITLE TITLE

REFERENCE

COMMENT

Center: Baylor College of Medicine

Center code: BCM

Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 6.9x in Q20 bases; sum-of-contigs estimation Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ------ Project Information Center project name: HBXP

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is s: contig of 41283 bp in length s: gap of unknown length s: contig of 36297 bp in length s: contig of 34138 bp in length s: contig of 34138 bp in length s: gap of unknown length s: contig of 16184 bp in length s: gap of unknown length s: contig of 14239 bp in length s: contig of 4239 bp in length s: contig of 8257 bp in length 811 others gap of unknown length contig of 6447 bp in length contig of 1045 bp in length. gap of unknown length 52170 a 36385 c 35342 g 50444 t /organism="Homo sapiens" /db_xref="taxon:9606" clone="RP11-490H24" Location/Qualifiers gap of /chromosome="12g" 41283: 174107: 67560: 175152: 77680: 12018: 44864: 67460: 111918: 44764: 59103: 175152 74007 111919 128203 174008 174108 41384 144865 59104 source BASE COUNT FEATURES ORIGIN

0; Gaps Score 52.4; DB 75; Length 175152; Pred. No. 0.39; 0; Mismatches 111; Indels 0; 3.3%; Best Local Similarity 51.7 Matches 119; Conservative Query Match

1210 agaggttggagaagaagtggaagaaggagaaggacgatcataaaagaagttgaggaga 1269

1270 tagaagaagaagtagagaaggtgagagataaagaagtcaccttattcagtaaactgtttg 1329

1330 aaggttttaaagagctccaacgagatgaagagaacttcttaagagagctgagcaaagaag 1389 δ

1390 aaatggatgttttggatggacttaaaatggaagcaactgaggtagaaaa 1439

Search completed: November 6, 2001, 03:04:01 Job time: 11820 sec

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November 6, 2001, 02:55:37 ; Search time 313.48 Seconds (without alignments) 3182.773 Million cell updates/sec
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Oligonucleotide DI
Oligonucleotide DI
Oligonucleotide DI
Oligonucleotide D2
Oligonucleotide D2
Oligonucleotide D1
Oligonucleotide D1
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                                                                                                                                                                                                                                                                                 1 tattttcatgagtttgcagt......tcttttcagaagcaaaaa 1589
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2. SIDSI/gcgdata/geneseq_/geneseqn_NA1980_DAT:*

3. SIDSI/gcgdata/geneseq_/geneseqn_NA1981_DAT:*

3. SIDSI/gcgdata/geneseq_/geneseqn_NA1981_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1981_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1986_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1986_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1980_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1980_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1980_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1980_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1980_DAT:*

5. SIDSI/gcgdata/geneseq_/geneseqn_NA1991_DAT:*

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<u>د</u> ا	Toba	Tobacco viol	laxanthin		xode.	de-epoxidase CDNA		
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3 3	KW Viol	Violaxanthin photoprotect	de-e	da sg	., ;	VDE; light; plant; zeax	ht; photosensitivity; zeaxanthin; antheraxanthin	lvity; neraxanthin;
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(VDE) (AAW09875), an enzyme that catalyses the despoxidation of violaxanthin to zeaxanthin and antheraxanthin. VDE nucleic acids (see also AAT66241, AAT66243), in sense or antisense orientation, can be used in genetic constructs, pref. also contg. a plastid translocation sequence, to modify VDE levels in plants. Increased therefore more productive and/or more resistant to disease. Underexpression of VDE increases photosynthetic efficiency under ornamentals can be modified.
                                                                                                                                                                                      cDNA clone (AAT66242) codes for tobacco violaxanthin de-epoxidase
                                                                                                  DNA encoding plant violaxanthin de-epoxidase - used to modify the
              HX;
              Yamamoto
                                                                                                                                                    Disclosure; Fig 2; 41pp; English.
                                                                                                                  sensitivity of a plant to light
              Rockholm DC,
                                            1997-281036/25
                                                                P-PSDB; AAW09875
              Bugos RC,
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Sequence 1589 BP; 500 A; 261 C; 367 G; 461 T; 0 other;

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    24.1 attcaagaggtctgcaactattctcacacgggaaacacaatctctcccgcacatagca 300
    24.1 attcaagaggtgtgcaactattctcacacgggaaacacaatctctcccgcacatagca 300
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Query Match 99.9%; Score 1587.4; DB 18; Length 1589; Best Local Similarity 99.9%; Pred. No. 0; Matches 1588; Conservative 0; Mismatches 1; Indels 0; (
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Romaine lettuce violaxanthin de-epoxidase cDNA.
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Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; lettuce; ss.

Lactuca sativa L. cv. romaine.

/*tag= e /note= "bases 186-189 are illegible in Fig 1" 226..227 /*tag= f /note= "basses 226-227 are illegible in Fig 1" 235..1656 -/*tag= a /note= "bases 26-29 are illegible in Fig 1" /*tag= b /note= "bases 66-72 are illegible in Fig /*tag= c /note= "bases 105-110 are illegible in illegible 147-149 are Location/Qualifiers /*tag= d /note= "bases /*tag= g 235..609 /*tag= h 610..1653 /*tag= i 105..110 147..149 misc_difference 186..189 26..29 /*tag= misc_difference misc_difference misc_difference misc_difference misc_difference transit_peptide mat_peptide

WO9717447-A2.

15-MAY-1997.

07-NOV-1996; 96WO-US18291

06-AUG-1996; 96US-0023502. 07-NOV-1995; 95US-0006315.

(CALJ) CALGENE INC.

WPI; 1997-281036/25. P-PSDB; AAW09874.

Bugos RC, Rockholm DC, Yamamoto HY;

DNA encoding plant violaxanthin de-epoxidase - used to modify the sensitivity of a plant to light

Claim 3; Fig 1; 41pp; English.

C (VDE) (AAW09874) of romaine lettuce. VDE was purified from romaine lettuce chloroplasts and 2 tryptic peptides were used to develop primers (see also AAT66244-45), which amplified a partial VDE sequence. The amplified sequence was then used to screen a lettuce CDNA library, and the 1981 bp DNA sequence was identified. VDE nucleic acids (see also AAT66242-43), in sense or antisense orientation, can be used in genetic constructs, pref. also contg. a plastid translocation sequence, to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.

Sequence 1981 BP; 608 A; 337 C; 433 G; 577 T; 26 other;

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                                                                                                                                                                   437 tgatgcggttgatgctctcaagacttgtacttgcttactgaaagagtgcaggttagagct
                              12;
  Length 1981;
                            Indels
                              0; Mismatches 325;
Score 647; DB 18;
Pred. No. 3.9e-156;
 40.78;
71.98;
                            Matches 864; Conservative
               Best Local Similarity
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                                                                                                         1445 tgggcgtgctttaccaataaggaaattaaggtaagtaatttttaaaaactatcaacatatat 1504
                                                                                                                                  1325 gtttgaaggttttaaagagctccaacgagatgaagagaacttcttaagagagctgagcaa 1384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de-epoxidate (VDE) (AAM)09876), an enzyme that catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. WDE nucleic acids (see also AAT66241-42), in sense or antisense orientation, can be used in genetic constructs, pref. also contg. plastid translocation sequence, to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to efficiency under row inght. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding plant violaxanthin de-epoxidase - used to modify the
                                                                                                                                                                                                                                                                                                                                                                            photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; lettuce; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A cDNA clone (AAT66243) codes for Arabidopsis violaxanthin
                                                                                                                                                                                                                                                                                                                                                                  Violaxanthin de-epoxidase; VDE; light; photosensitivity;
                                                                                                                                                                                                                                                                                                                                       Arabidopsis violaxanthin de-epoxidase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto HY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana cv. columbia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 3; 41pp; English.
                                                                                                                                                                                                                                                          AAT66243 standard; cDNA; 1555 BP
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transit_peptide 45..383
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                                                                                                                                                                                                                                                                                                                                                                                                                                  783
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                                                                                                                                                                   364 ttgttccatctgcagatgcagttgatgcacttaaaacttgtgcatgcttattgaagggat 423
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              other;
                                                            Score 622.6; DB 18;
Pred. No. 6.3e-150;
0; Mismatches 269;
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                                                               39.2%;
74.3%;
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                                                                                 Similarity
              Sequence 1555
                                                               Query Match
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                              Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    799 aattgcatgagttccatacagaagaaaacaaacttgtggggaatttatcttggagaatac 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              859 gtacacctgatggaggattttttactcgatcagcggtgcaaaaattcgtgcaagatccaa 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 125; DB 22; Length 936; 0.6%; Pred. No. 1.5e-22; ttive 489; Mismatches 289; Indels
                                                                                                                                                                                                                              Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                              CLIN-) CLINICAL MICRO SENSORS INC
                                                                     1489 aactatcaacatatatactacat 1511
                                                                                           1444 caccattqttqtacaaactatat 1466
                                                                                                                                   AAF58252/c
ID AAF58252 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                           26-JUL-2000; 2000WO-US20476.
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                           gene expression; ss
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les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single surface
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                                                                                                                                                                                                                                                              Synthetic.
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Best Local S:
Matches 5,
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atattttgtcatccaaagtagaaaatagtccagaggattacatatttgtgtgtactataagg 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                           aagtagagagatgagagataaagaagtcaccttattcagtaaactgtttgaaggtttta 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttttggatggacttaaaatggaagcaactgaggtagaaaaactttttgggcgtgctttac 1458
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                                       gcagaaatgatgcatgggatggatatggtggttctgtactttacacaagaagtgcagttt
                                                                                                                                                                                                                                                        acacattcataaaaaaagacaatacatgtggccctgaacctccccttgttgagaggttgg
                                                                                                                                                                                                                                                                                                                                                                               Electron-transfer group; ETM; mismatch; genotyping;
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AAFS8254/c
LID AAFS8254 standard; DNA; 936 BP.
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                                                                        AAF58257 standard; DNA; 936 BP.
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17-MAR-2000; 2000US-0190259.
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                                Example 6; Page 128; 159pp; English.
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The present invention relates to a composition comprising two nucleic
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Best Local Similarity 0.6%; Pred. No. 1.5e-22;
Matches 5; Conservative 489; Mismatches 289; Indels
                                                                                                                                                                Electron-transfer group; ETM; mismatch; genotyping;
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                               AAF58262 standard; DNA; 936 BP.
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17-MAR-2000; 2000US-0190259.
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Electron-transfer group; ETM; mismatch; genotyping;
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AAF58252 standard; DNA; 936 BP.

RESULT 10

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                    814 atacagaagaaaacaaacttgtggggaatttatcttggagaatacgtacacctgatggag 873
                                                                                                                                                                                                                                                        874 gattttttactcgatcagcggtgcaaaaattcgtgcaagatccaaagtatccggggatac 933
                                                                                                                                                                                  Gaps
                                                                                                          1534 tgcctggaatagattgcttatacatcatgtattgcttcttttcagaagcaaaaaa 1589
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                                     288;
                    Pred. No. 1.4e-21.
                                    3; Conservative 485; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF58257 standard; DNA; 936 BP.
   7.68;
                 0.48;
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                    Best Local Similarity
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                                                                                                                                                                                                                                                   AAF58259;
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                                                                                                                                                                                                                                                                         The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                Example 6; Page 127; 159pp; English
                                                                                                 (CLIN-) CLINICAL MICRO SENSORS INC
                           26-JUL-2000; 2000WO-US20476.
                                                      26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                         WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                    single surface
                                                        26-JUL-1999;
01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
                                                                                                                              Umek RM;
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1414 aaatggaagcaactgaggtagaaaaactttttgggcgtgctttaccaataaggaaattaa 1473
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                                                             814 atacagaagaaaacaaacttgtggggaatttatcttggagaatacgtaccctgatggag 873
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                                                                                                                                                                                                                                                                                                                                              7.6%; Score 121.2; DB 22; Length 936; 0.4%; Pred. No. 1.4e-21; ve 485; Mismatches 288; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF58259 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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994 aagtagaaaatagtccagaggattacatatttgtgtactataagggcagaaatgatgcat 1053
                                                                           .054 gggatggatatggtggttctgtactttacacaagaagtgcagttttgcctgaaagcatta 1113
                                                                                                                       1114 taccggagttgcaaaccgcagctcaaaaagttgggcgtgatttcaacacattcataaaaa 1173
                                                                                                                                                                   1174 cagacaatacatgtggccctgaacctccccttgttgagaggttggagagaagaagtggaag 1233
                                                                                                                                                                                                              1234 aaggaagaaaggacgatcataaaagaagttgaggagatagaagaagaagtagagaggtga 1293
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1534 tgcctggaatagattgcttatacatcatgtattgcttcttttcagaagcaaaaa 1589
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             Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                          acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nuclectide polymorphisms, e.g. for genotyping,
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Matches 3; Conservative 485; Mismatches 288; Indels
                                                                                                                                                                                                                                                         Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                       Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                      monitoring gene expression.
                                                  a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taccggagttgcaaaccgcagctcaaaaagttgggcgtgatttcaacacattcataaaaa 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              994 aagtagaaaatagtccagaggattacatatttgtgtactataagggcagaaatgatgcat 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1054 gggatggatatggtggttctgtacttacacaagaagtgcagttttgcctgaaagcatta 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to a composition comprising two nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  874 gattttttactcgatcagcggtgcaaaaattcgtgcaagatccaaagtatccggggatac 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                                                                                       Electron-transfer group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 127; 159pp; English
                                                                                                                                                                                                                                                                                                                                      (CLIN-) CLINICAL MICRO SENSORS INC
                          AAF58255 standard; DNA; 938 BP
                                                                                                                                                                                                                                                                                            26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                  26-JUL-2000; 2000WO-US20476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monitoring gene expression.
                                                                                24-APR-2001 (first entry)
                                                                                                            Oligonucleotide D1876
                                                                                                                                                      gene expression; ss
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                                                                                                                                                                                                          WO200107665-A2.
                                                                                                                                                                                                                                      01-FEB-2001
                                                                                                                                                                                  Synthetic
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                                                      AAF58255
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RESULT 15
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1534 tgcctggaatagattgcttatacatcatgtattgcttctttttcagaagcaaaaa 1589
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Search completed: November 6, 2001, 02:55:53 Job time: 11212 sec

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6, 2001, 02:51:13; Search time 166.68 Seconds (without alignments) 2159.069 Million cell updates/sec
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Sequence 1, Appli
Sequence 3, Appli
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Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 193, A
Sequence 191, A
Sequence 189, A
Sequence 187, A
Sequence 185, A
Sequence 184, A
Sequence 3, App
                                                                                                                                             1 tattttcatgagtttgcagt......tctttttcagaagcaaaaa 1589
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Sequence 1
Sequence 1
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
             Compugen Ltd
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S-09-461-697-193
S-09-461-697-191
S-09-461-697-189
S-09-461-697-187
S-09-461-697-187
S-09-461-697-187
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US-09-244-796-17
US-08-688-376-1
US-09-461-697-193
US-09-461-697-193
                                                                                                                                                                                                                                  Potal number of hits satisfying chosen parameters:
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US-08-232-463-14
US-08-574-959A-8
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-08-676-967-2
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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-08-973-462-1
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                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                       IDENTITY_NUC Gapor 10.0
                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:*
                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                       US-09-075-375A-3
1589
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332111
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                                                                                                                                    Perfect score:
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Sequence 3, Appli
Sequence 139, App
Sequence 3, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 53, Appli
Sequence 54, Appli
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      Sequence
                                                                                                                                                                                                                                                    Sequence
US-09-098-487-2

US-08-742-185-101

US-08-948-139

US-09-073-898-139

US-09-007-005-3

US-09-017-005-3

US-08-314-5034-1

US-08-466-603-1

US-08-466-743-1

US-08-466-743-1

US-08-466-743-1

US-08-466-743-1

US-08-687-080-53

US-08-592-126-54

US-08-592-126-54

US-08-687-080-63

US-08-687-080-63

US-08-687-080-64

US-08-687-080-64
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08747574

Patent No. 6015339
GENERAL INFORMATION:
TITLE OF INVENTION: PLANT VDE GENES AND
TITLE OF INVENTION: METHODS RELATED THERETO
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, 1.40 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,574
FILING DATE: NO. 6015939ember 7, 1996
CLASSIFICATION: 435
PION APPLICATION DATA:
APPLICATION NUMBER: 60/003,502
FILING DATE: August 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,315
FILING DATE: NO. 6015939ember 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 119-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEO ID NO: 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
US-08-747-574-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
   43795
1038
1038
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1154
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3393
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis
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Match 1589; Conssis 1589; Conssis 1589; Conssis 1589; Conssis 1589; Conssis 1589; Conssis 1689; Conssis 1689; Conssis 1689; Conssis 1689; Conssis 1689; Conssis 1784AAAAATTTCTGGATTTCTGGAATTTCAGGAATTTCAGGAATTTCAGGAATTTCAGGAATTTCAGGAATTTCAGGAATTTCAGGAATTTAACCAGAATTTAACCAGAATTTAACCAGAATTTAACCAGAATTTAACCAGAATTTAACCAGAATTTAACCAGAATTTAACCAGAATTTGATTGA	Score 1589; DB 3; Length 1589; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	taatacg	catcaaatattatgttgggtcaaagcttcccggtc 12	CATCAAATATTATGITGGGTCAAAGCTTCCCG tagattactttggtagtagtagtcgtagcaaaa 	cctagaatatgctgtggtttgg 24	aatctctcccgcacatagca 30	gatgcaaatttcc 	ttgccaaaacagcaattgtagctatattcattttgt 420 	ttgatgeteteaagaettgtaettgettaetgaaag 480 	goattegaaccetgcatgtgcagctaatgttgcct 540	ctgacgaaacggaatgtcagataaaatgtggtgatt 600 	agttcaatgagtgtgcagtctcccgaaagaaatgtg 660 	gtgactttoctgtacctgatcocagtgttcttgtccaga 720 	ggaaatggttcattactcgcggtttgaatcccactt 780 	gattgccaattgcatgagttccatacagaagaaacaaacttgtgggga 840 	ctgatggaggatttttactcgatcagcggtgcaaa 900 	cggggatactctacaatcatgataatgagtatcttc 960 	tqtcatccaaaqtaqaaaataqtccaqaqqattaca 1020
	Match 100.0%; Local Similarity 100.0%; es 1589; Conservative 0;	attttcatgagtttgcagttggtgg 	caaattttctggccaaccatgaaa	61 CAAATTTTCTGGCCAACCATG 21 ataaaaggtttagctggggtt 	81 gttccagcagacggataccta 	41 attcaagaggt 	L ttaaccagaatgtacctaagg	61 tggtttgggagaaatggg 	21 cagttgcttcaaaagctgatgcgg 	81 agtgcaggttagagcttgcgaagtg 	41 gtctcca 	01 tgtttgaaaacagt 	61 tacctcgtaaatctgatgttg 	21 agtttgacatgaaagattttagcgg 	81 ttgatgctttt 81 TTGATGCTTTT	41 atttatcttgg 	01 aattcgtgcaagatccaaagtatcc 	961 tctaccaagatgactggtatattttc

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1021 TATTIGIGIACTATAAGGCAGAAAIGAIGATGCAGGGAIGGATAIGGTGGTGTTGTGTACTIT 1080
                                         1081 acacaagaagtgcagttttgcctgaaagcattataccggagttgcaaaccgcagctcaaa 1140
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                                                                                                                                                                       1381 gcaaagaagaaatggatgttttggatggacttaaaatggaagcaactgaggtagaaaaac 1440
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Patent No. 6015939

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/023,502
FILING DATE: August 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,315
FILING DATE: NO. 6015939ember 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,574
FILING DATE: No. 6015939ember 7, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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US-08-747-574-1
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                                                                                                                                                                                                                                                                                                                                                                                                    543 GAGACAATTCATACAATTGGCTATCGTATTGGTTTGCACATTTGTTATCGTTCCCAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1981;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                  Query Match 40.5%; Score 643.8; DB 3; Best Local Similarity 71.8%; Pred. No. 4.1e-167; Matches 862; Conservative 0; Mismatches 327;
       NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 119-7
TELECOMMUNICATION INFORMATION:
TELEFAX: (916) 753-6313
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981
REGISTRATION NUMBER: 34,719
                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                      US-08-747-574-1
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1157 caacacattoataaaaacagacaatacatgtggccctgaacctccccttgttgagaggtt 1216
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                                                                                                                                                                                                                                                                                                                                                                                               1445 tgggcgtgctttaccaataaggaaattaaggtaagtatttttaaaactatcaacatatat 1504
                                                                                                                                                                                                                                                                                                                          1323 TAACAATTTCATAACAACCGACAATAGTTGTGGGCCTGAGCCTCCATTGGTGGAAAGGCT
                                                                                                                                                  1217 ggagaaagaaagtggaagaaggagaaaggacgatcataaaagaagttgaggagatagaaga
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METHODS RELATED THERETO
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FILING DATE: No. 6015939ember 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERRNCE/DOCKET NUMBER: 119-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,574
FILING DATE: No. 6015939ember 7, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,502
FILING DATE: August 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08747574; Patent No. 6015339; GENERAL INFORMATION: APPLICANT: CALGENE, INC. TITLE OF INVENTION: METHODS REL. TITLE OF INVENTION: METHODS REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (916) 753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene,
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                                                                                                                                                                                                                                                                                                                                                                                                544 TTGAGAACAGTGTTGTTGATGAGTTCAACGAGTGTGCTGTGTCGAGAAAAAAGTGTGTTC 603
                                                                                                                                                                      Indels 15; Gaps
                                                                                                                                        Length 1555;
                                                                                                                                        Query Match 39.3%; Score 624.2; DB 3; Best Local Similarity 74.3%; Pred. No. 8.6e-162; Matches 820; Conservative 0; Mismatches 268;
                                                                 TOPOLGGY: linear

MOLECULE TYPE: CDNA to mRNA
US-08-747-574-3
             SEQUENCE CHARACTERISTICS:
LENGTH: 1555
INFORMATION FOR SEQ ID NO:
                                      TYPE: nucleic acid
STRANDEDNESS: single
                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1144
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                                                                             1429 aggtagaaaaactttttgggcgtgctttaccaataaggaaattaaggtaagtatttttaa 1488
                                                                                                                                                                                                  1384 AGGTTGAAAAATTGTTTGGGAAAGCTTTGCCAATCAGGAAGGTCAGGTAGAAACAAGAAC 1443
                                    1264 CCTTGTTCCAGAGATTGGCTGAAGGATTTAATGAACTGAAGCAAGACGAGGAGATTTCG 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINDER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 91 114 300.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               1489 aactatcaacatatatactacat 1511
                                                                                                                                                                                                                                                                                      1444 CACCATTGTTGTACAAACTATAT 1466
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08232463 Patent No. 5670367
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAN: (703)836-9300
TELEFAX: (703)83-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , CLONE: pTZgpt-F1s
US-08-232-463-14
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1059 ggatatggtggttctgtactttacacaagaagtgcagttttgcctgaaagcattataccg 1118
                                                                                            1119 gagttgcaaaccgcagctcaaaaagttgggcgtgatttcaacacattcataaaaacagac 1178
                                                                                                                                                                         1179 aatacatgtggccctgaacctccccttgttgagaggttggagaagaaagtggaagaagga 1238
                                                                                                                                                                                                                                                                                                   1239 gaaaggacgatcataaaagaagttgaggagatagaagaagaagtagagaaggtgagagat 1298
                                                                                                                                                                                                                                                              1299 aaagaagtcaccttattcagtaaactgtttgaaggttttaaagagctccaacgagatgaa 1358
                                                                                                                                                                                                                                                                                                                                                                                                                1107 RYRRKRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRARAGCAAG 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1359 gagaacttcttaagagagctgagcaaagaagaaatggatgttttggatg 1407
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELEPHOME: (617)227-4400
TELEPHOME: (617)227-5941
INPORMATION FOR SEQ 1D NO: 8:
SEQUENCE CHARACTERISTICS:
LEGITH 3211 base pairs
TENEST NUCleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08574959A
Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
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439..3157
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; LOCATION:
US-08-574-959A-8
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Score 50.6; DB 2; Length 3211;
Pred. No. 0.00024;
0; Mismatches 84; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: DFN-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/574,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COUNTRY: USA
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Query Match 3.2%;
Best Local Similarity 54.6%;
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 22
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60 State Street, Suite 510
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REGISTRATION NUMBER: 36,207
REERERCECPOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08574959A
Patent No. 5962224
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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SOFTWARE: Patentl
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US-08-574-959A-6
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1375 agctgagcaaagaagaagtgatgttttggatggacttaaaatggaagcaactgaggtag 1434
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                                                                                                                                                                         APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOF APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                      and Jack L. Strominger
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TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
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MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                          Sequence 6, Application US/09357014 Patent No. 6291645
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                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 22
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Matches 101; Conservative
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ZIP: 02109-1875
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                                                                                                                                                         INFORMATION:
3281 AGGAA 3285
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                                                                  RESULT 8
US-09-357-014-6
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1209 gagaggttggagaagaaagtggaagaaggagaaaggacgatcataaaagaagttgaggag 1268
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APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALBARIAL PERFERENCE
TITLE OF INVENTION: MALBARIAL POET
FILE OF INVENTION: MALBARIAL POET
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT APPLICATION NUMBER: US/08/94
EARLIER PILING DATE: 1996-06-12
EARLIER FILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTI OF VOICE
CONTINUED OF SECTION NUMBER: PROFILE PILING DATE: 1995-06-13
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APPLICANT: DRUBENSIES, PIERRE
TITLE OF INVENTION: MALBARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REPERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FF96/00894
EARLIER FILING DATE: 1996-06-12
1221 aagaaagtggaagaaggagaaaggacgatcataaaagaagttgaggagatagaagaa 1280
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Pred. No. 0.0011;
0; Mismatches 154; Indels 0
                                                                                                                                                                                                Sequence 2, Application US/08973462B Patent No. 6191270
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Best Local Similarity 47.8°
Matches 141; Conservative
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ORGANISM: P. falciparum
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US-08-973-462-2
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US-08-973-462-2
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1281 gtagagaaggtgaggataaagaagtcaccttattcagtaaactgtttgaaggttttaaa 1340
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Fatent No. 625858
GENERAL INFORMATION:
APPLICANT: SCOSTAK, Jack W.
APPLICANT: SCOSTAK, Jack W.
APPLICANT: Liu, Richard W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: UNMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                              Length 6152;
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                                                                                                                                                                                                                                                                                                         Query Match 3.1%; Score 48.6; DB 4; Length 6
Best Local Similarity 47.8%; Pred. No. 0.0011;
Matches 141; Conservative 0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                      DB 4;
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EARLIER APPLICATION NUMBER: FR 95/07007 EARLIER FILING DATE: 1995-06-13 NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
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; LOCATION: (1)...(289)
; CTHER INFORMATION: n = A,T,C or
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: P. falciparum
US-08-973-462-1
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1538 GAAAAAGAAAAGGAACTCTCAGGATGGAAAGGGACC 1573
                       1449 cgtgctttaccaataaggaaattaaggtaa 1478
                                                 IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1996
NN: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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IDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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LOCATION:
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US-08-688-376-1
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                                                                                                                                  RESULT 13
US-08-688-376-1
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                                                                   1269 atagaagaagaagtagagaaggtgagagataaagaagtcaccttattcagtaaactgttt 1328
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                                                                                                                                                                                                                                                                   71 rnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrn 130
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APPLICANT: ROBETS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION: FUSIONS
TITLE APPLICATION NUMBER: 09/9/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER PILING DATE: 1997-01-27
EARLIER PILING DATE: 1997-01-27
EARLIER PILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS 33
SOFTWARE: FastSEQ for Windows Version 4.0
FEARLIER PILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.8%; Score 45.2; DB 4; Length 289; Best Local Similarity 9.3%; Pred. No. 0.0023; Matches 25; Conservative 111; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                  1449 cgtgctttaccaataaggaaattaaggtaa 1478
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; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-244-796-17
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Sequence 1, Application US/08688376
Patent No. 6018039
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: NOVEL PROCESS FOR PRODUCING SUBSTANCES
TITLE OF INVENTION: IN MAMMARY GLAND OF TRANSGENIC ANIMAL BY USING MC26 GENE
TITLE OF INVENTION: EXPRESSION-REGULATORY REGION
NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,376
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DILWORTH & BARRESE
STREET: 4350 LaJolla Village Drive, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1329 gaaggttttaaagagctccaacgagatgaagagaac 1364
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NAME: PEPPEr, Frederick W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 567-TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4410
TELEPHONE: 619-546-4410
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; ORGANISM: Homo sapiens US-09-461-697-191

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APPLICANT: COGENT NEURSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Purnam, Kasturi
APPLICANT: Purnam, Kasturi
APPLICANT: Purnam, Kasturi
APPLICANT: Purnam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COLL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SSOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Rest. Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
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48.5%; Pred. No. 0.063;
tive 0; Mismatches 119; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
; Sequence 193, Application US/09461697; Patent No. 6277974
; GENERAL INFORMATION:
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APPLICANT: COGENT NEUROSCIENCE, Inc.
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Best Local Similarity 48.5%
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-193
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LENGTH: 696
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LENGTH: 699
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Query Match 2.6%; Score 40.6; DB 4; Length 699; Best Local Similarity 48.5%; Pred. No. 0.064; Matches 112; Conservative 0; Mismatches 119; Indels
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November 6, 2001, 00:54:03; Search time 3841.92 Seconds (without alignments) 3909.656 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                      10228115 seqs, 4726426750 residues
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_esthum2:*
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Maximum DB seq length: 200000000
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em_estro9: *
em_estro10: *
em_estro11: *
em_estro13: *
em_estro14: *
em_estro14: *
em_estro16: *
em_estro10: *
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em_esthum24:*
em_esthum25:*
em_esthum26:*
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em_esthum15:*
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118; gb_est49;*
119: gb_est49;*
119: gb_est50;*
120: gb_est50;*
121: gb_est51;*
122: gb_est51;*
123: gb_est52;*
124: gb_est52;*
125: gb_est54;*
126: gb_est54;*
127: gb_est56;*
128: gb_est56;*
139: gb_est60;*
131: gb_est60;*
131: gb_est60;*
132: gb_est60;*
133: gb_est60;*
134: gb_est60;*
135: gb_est60;*
136: gb_est60;*
137: gb_est60;*
138: gb_est100;*
149: gb_est60;*
140: gb_est60;*
150: gb_est100;*
170: gb_est100;
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gb_est110:* gb_est111:* gb_bet1111:* gb_btc:* em_gss_hun:* em_gss_hum2:* em_gss_hum2:* em_gss_hum4:* em_gss_hum6:* em_gss_hum7:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum7:* em_gss_hum6:* em_gss_hum7:* em_gss_hum7:* em_gss_hum6:* em_gss_hum7:* em_gss_hum6:* em_gss_hum7:* em_gss_hum7:* em_gss_hum8:*		
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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B13003 T27G-T7.1
BE343837 EST408999
AV110854 AV410854
AZ12694 OSJNBD007
B12210 T27G-T7 TA
B13009 T27M8-T7 TA
BE395698 PIL_SS_E1
AV521985 AV521985
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BE440946 sp30a05.y
BF623692 HVSMEa000
BG157169 sab23d04.
AL060767 Drosophil
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AL10811 Drosophil
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AL098595 Drosophil
AL098595 Drosophil
AL066537 Drosophil
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Drosophil
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AV440942 AV440942
A1668224 605018D09
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B28051 T27G7FFB TA
B08217 T27M8-T7.1
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                                                            AW398615 EST309115
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AL108415 Drosophil
AL105023 Drosophil
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Lycopersicon pennellii
Enkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                    A1483033 EST242356
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AL052030 Drosophi
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AL065615 I
AZ692361 E
AL074609 I
AL108171 I
                                    Description
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SUMMARIES
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CNS00418
CNS0100X
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BG123331
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AI994713
AV410579
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BE918838
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BF623692
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CNS0155H
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CNS017KX
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BG096454
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4495.4
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AW398615
LOCUS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                       Result
No.
                                                                                               SOURCE
```

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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin
Tanksley, S.D. and Giovannoni, J.
                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cLPT4A14"
/clone_lib="L. pennellii trichome, Cornell University"
/tissue_lip="L. pennellii trichome"
/tissue_ge="mixed stages"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agtgcaggttagagcttgcgaagtgcatttcgaaccctgcatgtgcagctaatgttgcct 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., vencer, c.c., G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gttccagcagacggatacctagatactttcgaaaatctcctagaatatgctgtggtttgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.7%; Score 503.2; DB 115; Length 647; 88.2%; Pred. No. 1.8e-119; ative 0; Mismatches 73; Indels 0;
                                                                                                                                 Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                  Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                        Unpublished (1999)
Contact: David Frisch
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                                                                                                                                                                                                                                                                   prime sequence.
                                                                                                                                                                                                                                                                                                             .647
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Best Local Sim:
Matches 547;
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AI483033
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                                                                                                                                                              BG123331 724 bp mRNA EST 31-JAN-2001
EST468977 tomato shoot/meristem Lycopersicon esculentum cDNA clone
cTOF1J5 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                       Lycopersicon esculentum
Sukaryota, Vitidiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496), Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 724)
van der Hoeven, R. Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Ronning, C. and Tanksley, S.
Generation of ESTS from tomato shoot/meristem tissue
568 GTCTCCAAACATGCAACAATAGACCTGATGAAACGGAATGTCAGATAAAATGTGGTGATT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="shoot/meristem"
/dev.stage="developing shoots from 4-6wks old plants"
/lab_host="SoLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 caaattttctggccaaccatgaaaccatcaaatattatgttgggtcaaagcttcccggtc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
/cultuvar="74496"
/db xref="taxon:4081"
/clone="cTOF1J5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="tomato shoot/meristem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
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100 Jordan Hall, Clemson, SC 29634,
                                                                                                                                                                                                                   BG123331
BG123331.1 GI:12623519
                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                Lycopersicon.
                                                                                                                                                                                                                                                                          tomato.
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A1483033 584 bp mRNA EST 29-JUN-1999 EST242356 tomato shoot, Cornell Lycopersicon esculentum cDNA clone cLEBBK10, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids I, Solanales, Solanaceae, Solanum,
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watern,A.L., Vision,T., Holt,I.E., Liang,F.,
Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L.,
Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Glovannoni,J.J.
                                                                                               480
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                           421 cagttgcttcaaaagctgatgcggttgatgctctcaagacttgtacttgcttactgaaag
                                                                                                                                                                                                                                                                                                                                                              525 AGTGCAGGTAATTTGCAGATGTTACTAAAGTATGCCGGATAGAGCTTGCGAAGTGCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Tanksley,S.D. Generation of ESTs from tomato shoot meristem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon esculentum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="shoot meristem"
/dev_stage="8 week old plants"
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Fax: 864 656 4293
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Clemson University
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/db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dfrisch@CLEMSON.EDU.
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van der Hoeven,R.S., Bezzerides,J.l., Matern,A.L., Holt,I.E., Liang
,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning
,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue
Unpublished (1999)
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Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                  gttccagcagaagatacctagatactttcgaaaatctcctagaatatgctgtggtttgg 240
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                                                                                           61 caaattttctggccaaccatgaaaccatcaaatattatgttgggtcaaagcttcccggtc 120
                                                                                                                                                                                          121 ataaaaagtttagctggggttgggaagattactttggtagtatagtcgtagcaaaaattt 180
                                                                                                                                                                                                                                                                          233 GTTCCAGAAGACAGATACCTACATACTTGCAGAAATCTTCTAGAATATGTTGTGGTTTGG 292
                                                                                                                                                                                                                                                                                                       301 ttaaccagaatgtacctaagggaaattcaggatgcaaatttccaaaagatgtagctttga 360
                                                                                                                                                                                                                                                                                                                                                                                                                 361 tggtttgggagaaatggggccaatttgccaaacagcaattgtagctatattcattttgt 420
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                                                    Gaps
                                                                              1 tattttcatgagtttgcagttggtggtaatacggttgaagaatggctcttgccctcatt 60
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                       Score 423.2; DB 20; Length 584;
Pred. No. 8.6e-99;
0; Mismatches 68; Indels 0;
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100 Jordan Hall, Clemson, SC
Tel: 864 656 4366
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Email: dfrisch@CLEMSON.EDU
5 prime sequence.
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                       26.6%;
87.2%;
                                    Best Local Similarity 87.2
Matches 464; Conservative
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1 (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pG096454 444 bp mRNA EST 29-JAN-2001
EST460973 potato leaves and petioles Solanum tuberosum cDNA clone
cSTB43H21 5' sequence, mRNA sequence.
                                                                                                                                                   /dev_stage="buds 8mm-to-preanthesis"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tggtttgggagaaatggggccaattgccaaacagcaattgtagctatattcatttgt 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caaattttctggccaaccatgaaaccatcaaatattatgttgggtcaaagcttcccggtc 120
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                                                                                      pre-anthesis,
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                                                                                                                                                                                                                                                                                                                                                                                                                        68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 527
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                                                                                      mm to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 agtgcaggttagagcttgcgaagtgcatttcgaaccctgcatgtgca
/organism="Lycopersicon esculentum'
                                   /db_xref="taxon:4081"
/clone="cTOC715"
/clone_lib="tomato flower buds 8 cornell University"
                                                                                                                                                                                                                                                                                                                                                                              26.3%; Score 418.2; DB 1
illarity 87.1%; Pred. No. 1.7e-97;
Conservative 0; Mismatches 68
                                                                                                                              /tissue_type="flower"
                  /cultivar="TA496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG096454.1 GI:12586489
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in light of process.
van der Hoeven,R.S., Bezzerides,J., Holt,I.E., Liang,F., Cho,J., Utterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R., Ronning C.R., Fry,W.E., Tanksley,S.D. and Baker,B. Generation of ESTs from potato leaves and petioles Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 caaattttetggccaaccatgaaaccatcaaatattatgttgggtcaaagettcccggtc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ataaaaagtttagctggggttgggaagattactttggtagtatagtcgtagcaaaaattt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gttccagcagacggatacctagatactttcgaaaatctcctagaatatgctgtggtttgg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 GTTCCAGAAGACGGATACCTACATACTTGCAGAAATCTCCTAGAATAAGATGTGGTTTGG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 attcaagaggtctgcaactattctcacacgggaaacacaatctctcccgcacatagca 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 ttaaccagaatgtacctaagggaaattcaggatgcaaatttccaaaagatgtagctttga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 TATTTACATGAGGTTGGAGTTGGTGGTCATCCAGTTGAATAATGGCGCTTGCCCCTCATT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 CAAACTTTCTGTGCGTTCATGAAACCATCAAATGTCAAGTTGGGTCAAAGCTTCACAGTC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tattttcatgagtttgcagttggtggtaatacggttgaagaatggctcttgccctcatt 60
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                                                                                                     Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 173; Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Indels
                                                                                                                                                                                                                                                                                                                             /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/fistage="8 weeks old plants"
/lab_nost="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%; Score 309.4; DB 1
86.0%; Pred. No. 2.2e-69;
tive 0; Mismatches 56
                                                                                                                                                                                                                                            /organism="Solanum tuberosum"
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/note="Vector: pBluescript II SK+; Site_I: ECORI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from germinating shoots of 3 day old seedling for the
cultivar Williams B2. The seedlings were germinated in
growth chamber using germination paper in a solution
containing 100ppm auxin. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT) sequence
with a XhoI restriction site. EcoRI adapters were ligated
to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). This library was constructed
in the laboratory of Dr. Randy Shoemaker."
                    Spermatophyta; Magnollophyta; audioctyledons; core eudiocts; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine. I (bases 1 to 515)
Shoemaker, K., Kelim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, Public, Soybean, EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Germinating shoot, 3 day old seedling, auxin treatment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available through: Genome Systems, Inc. 4633 World barkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          962 ctaccaagatgactggtatattttgtcatccaaagtagaaaatagtccagaggattacat 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1142 agttgggcgtgatttcaacacattcataaaaacagacaatacatgtggccctgaacctcc 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1202 ccttgttgagaggttggagaagaagtggaagaagaaggagaaaggacgatcataaaagaagt 1261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ATTTGTATACTACCGAGGCAGAATGATGCATGGGATGGTTATGGAGGTGCTGTTATATA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Glycine max"
/db_xref="texon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1067-1991"
/clone="Ib="Gm-c1067"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       info@genomesystems.com web site: www.genomesystems.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%; Score 289; DB 144; Length 515; 72.7%; Pred. No. 4.4e-64;
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                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                         Public Soybean EST Project
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
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/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWL074905_r"
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Lotus japonicus
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//db_xref="taxon:3702"
//clone=lib="A. thaliana, Ohio State clone set"
//note="cDNA library was made from selected clones from the Arabidopsis thaliana Ohio State clone set."
//note="cDNA library was made from selected clones from the liprary was made from the liprary was ma
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                     1382 caaagaaagaaatggatgttttggatggacttaaaatggaagcaactgaggtagaaaaact 1441
                                                                                                      1322 actgitigaaggititaaaagagciccaacgagaigaagaagaactictiaagagagcigag 1381
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 483)
   242 CCTGGTGGAAAGGCTGGAGAAAAGGTAGAGGAAGGAGAAGAAGAACATGTAAGGGAAGT
                                                                                                                                    Confact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
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0; Mismatches 107; Indels
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76.6%;
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Fax: 314-427-3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Lotus.
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/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_l: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
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Asamiau, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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                                                                                                                                                                                                                                              254 AACATCTCGGACTTTAACGGGAAGTGGTACATTACAAGTGGCTTGAATCCAACCTTTGAT 313
                                                                                                                                                                                                                                                                                                                                         786 gcttttgattgccaattgcatgagttccatacagaa---gaaaacaaacttgtggggaat 842
                                                                                                                                                                                                                                                                                                                                                                      194 AGAAAATCTGATCTCGGAGAATTTCCTGCCCCAGACCTTCTGTTCTTGTACAGAACTTC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                843 ttatcttggagaatacgtacacctgatggaggattttttactcgatcagcggtgcaaaaa 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 ATCTCTTGGAGAATAAAGACCCTAGACAGTGGATTCTTTACTAGGTCAGCCGTACAAAA 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV410579 427 bp mRNA EST 23-MAY-2000 AV410579 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWL074905_r 5', mRNA sequence.
                                                                                                                                                                                                                 726 gacatgaaagattttagcgggaaatggttcattactcgcggtttgaatcccacttttgat
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/note—"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light eyrole, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed CDNA.
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large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
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Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N37612 438 bp mRNA EST 05-JAN-1998
18839 Lambda-PRL2 Arabidopsis thaliana cDNA clone 207C23T7, mRNA
                          649 gaaagaaatgtgtacctcgtaaatctgatgttggtgactttcctgtacctgatcccagtg 708
529 ctaatgttgcctgtctccagacttgcaacaatagacctgacgaaacggaatgtcagataa 588
                                                                                                  589 aatgiggigatitgittgaaaaacagigicgiagacgagiicaaigagigigagiciccc 648
                                                                                                                                                                                                                                                  295 GGAAGAAATGTGTACCTAAGAAATCTGACGTGGGAGAGTTTCCTGCTCCAAATCCTGATG 354
                                                                                                                                                                                                                                                                                                                               MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
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                                                                                                                                                  235 AATGCGGGGACCTGTTTGAAAACAGTGTGGTTGATCAATTTAATGAGTGTGCAGTCTCCC
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/strain="var columbia"
/db_xref="taxon:3702"
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/clone_lib="Lambda-PRL2"
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Location/Qualifiers
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Fax: 517-353-9168
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Tel: 517-3
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1 (bases 1 to 400)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Alarige scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                         666 cgtaaatctgatgttggtgactttcctgtacctgatcccagtgttcttgtccagaagttt 725
                                                                                       486 aggittagagcittgcgaagigcatittcgaacccigcaigtgcagciaaigtigccigictc 545
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    Length 438;
                                           79; Indels
12.6%; Score 201; DB 159; 76.3%; Pred. No. 2.5e-41; iive 0; Mismatches 79;
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/dev_stage="two to six-week old"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV440942.1 GI:7611318
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Best Local Similarity 70.6'
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/db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI; Site_2: XhoI; Kernel endosperm cDNA library from Schmidt lab"
           1126 aaaccgcagctcaaaaagttgggcgtgatttcaacacattcataaaaacagacaatacat 1185
                                                                            1246 cgatcataaaagaagttgaggagatagaagaagaagaagtagagagagagataa---- 1300
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                                                                                                                                                                                                                                                                       1414 aaatggaagcaactgaggtagaaaaactttttgggggtgctttaccaataaggaaattaa 1473
                                        216 GTAGGACTGAGATGACCTTGTTCCAGAGATTGGCTGAAGGATTTAATGAACTGAAGCAAG 157
                                                                                                                                                                      276 TAATCGTAAAAGAGGTTGAAGATAGAAGAAGAGGTAGAGAAGGAAGTGGAGAAGGTCG 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \label{eq:main_main} \mbox{Walbot,V.} \\ \mbox{Maize ESTs from various cDNA libraries sequenced at Stanford } \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotéstanford.edu
Plate: 605018 row: D column: 09.
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Stanford University
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Contact: Walbot V
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10.8%; Score 172; DB 23; Length 602;

Query Match

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//Organism="Sorghum propinguum"
//Ob_xref="taxon:132711"
//clone_lib="Floral-Induced Meristem 1 (FM1)"
//note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
DeoRI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 549)
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum propinguum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoldeae, Andropogoneae, Sorghum.
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                                                                                  1106 aagcattataccggagttgcaaaccgcagctcaaaaagttgggcgtgatttcaacacatt 1165
                                                                                                                                                                                            1286 gaaggtgagagataaagaagtcaccttattcagtaaactgtttgaaggttttaaagagct 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1346 ccaacgagatgaagagaacttcttaagagagctgagcaaagaagaaggaatgttttgga 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 TCAGCTCAACATGGAAGCGACTGAAGTTGAGCAAGTCTTCAGCCGTGCACTGACGTTGAG 241
                                                                                                                                       600 AACAATAATACCGGAGCTGGAAAGAGCTGCAAAGAGCGTAGGTCGGGACTTCTCGACGTT 541
                                Gaps
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FM1_2_F01.g1_A003 Floral-Induced Meristem 1 (FM1) Sorghum propinguum cDNA, mRNA seguence.
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Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
                                Indels
Pred. No. 8.5e-34;
0; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 89
High quality sequence stop: 506
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Fax: 706 542 1805
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Page 10

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Unpublished (1997)
Other_GSSs: T27M8-Sp6.1, T27M8-Sp6, T27M8-T7
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                                       /organism="Arabidopsis thaliana"
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                                                                        /db_xref="taxon:3702"
                                                                                                              /clone_lib="TAMU"
/sex="hermaphrodite"
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                                                           /strain="Columbia
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                                                                                            /clone="T27G7
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B08217.1 GI:2089494
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Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Ecker J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T7
Class: BAC ends
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Unpublished (1997)
Cother_GSSS: T27G7TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
induced by short-day conditions); 16 days after being returned to the greenhouse under natural long days during late April/early May, meristems were harvested The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by a 97 c 155 g 132 t
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                  1114 taccggagttgcaaaccgcagctcaaaaagttgggcgtgatttcaacacattcataaaaa 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1414 aaatggaagcaactgaggtagaaaaactttttgggcgtgctttaccaataaggaaattaa 1473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1294 gagataaaagaagtcaccttattcagtaaactgtttgaaggttttaaagggctccaacgag 1353
                                                                                                                                                                                                                                                                                                                                         1174 cagacaatacatgtggccctgaacctccccttgttgagaggttggagagaagtggaag 1233
                                                                                                                                                                                                                                                                                                                                                              121 AAGGAGAAGACCATCGTCAGGGAGGTGAAGGAGATTGAGGAGGAGGTTGAGGAGCTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AGAAGGAGGAGCATCATTGTTTCAAAAGCTGGCAGAAGGTCTCATGGAGGTGAAACAGG 240
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T27G7TFB TAMU Arabidopsis thaliana genomic clone T27G7, DNA
                                                                                                                                                                                                                                                                                                   1 TACCTGAGCTAGAAAGAGCTGCAAAAAGCATAGGTCGGGACTTCTCGACGTTCATCAGGA
                                                                                                                                                                                       Score 168.8; DB 141; Length 549; Pred. No. 5.6e-33;
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Fax: 301 838 0208
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                                                                                                                                                                                     10.6%;
66.5%;
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/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII; Produced by Rod Wing" 130 c 111 g 163 t
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dept. of Biology, University of Pennsylvania, Philadelphia, PA
                                                                                                                                                                                                                                                                                                                                                 578 atgtcagataaaatgtggtgatttgtttgaaaaacagtgtcgtagacgagttcaatgagtg 637
                                                                                                                                                                                                                                                                                                                                                                                 200 IGCIGIGICGAGAAAAAGIGIGITCCIAGAAAAICIGAICICGGAGAAITICCIGCCC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       698 tgatcccagtgttcttgtccagaagtttgacatgaaagattttagcgggaaatggttcat 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               758 tactcgcggtttgaatcccacttttgatgcttttgattgccaattgcatgagttccatac 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  638 tgcagtctcccgaaagaaatgtgtacctcgtaaatctgatgttggtgactttcctgtacc 697
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T27M8-T7.1 TAMU Arabidopsis thaliana genomic clone T27M8, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AGACCCTTCTGTTCTTGTACAGAACTTCAACATCTCGGACTTTAACGGGAAGTGGTACAT
                                                                                                                                                                                                                DB 256; Length 599;
                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                        10.2%; Score 162.4; DB 256; Lengt 77.8%; Pred. No. 2.6e-31; tive 0; Mismatches 56; Indels
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Wed Nov

us-09-075-375a-3.rst

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A2126249 812 bp DNA GSS 02-JUN-2000 OSJNBb0075L17f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone OSJNBb0075L17f, DNA sequence.
                                                                                                                                                                                                                                                                                  tgcagtctcccgaaagaaatgtgtacctcgtaaatctgatgttggtgactttcctgtacc 697
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                                                                                                                                                                                                                                                             578 atgtcagataaaatgtggtgatttgtttgaaaacagtgtcgtagacgagttcaatgagtg 637
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Ming,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                           Length 1147;
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/clone="05ANBb0075117f"
/clone=lib="CUGI Rice BAC Library (EcoRI)"
/tissue_type="Leaf"
                                                                                                                     25 others
                                                                                                                                                                                       Query Match 9.9%; Score 156.6; DB 256; Lengt Best Local Similarity 76.2%; Pred. No. 9.7e-30; Matches 192; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
                                                                                                                     357 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 40
High quality sequence stop: 642.
Location/Qualifiers
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/cultivar="Nipponbare"
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Class: BAC ends
                                                                                                                   195 g
/strain="Columbia"
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/lab_host="E. coli DH10B"
/note="Wector: pBACIndigo; Site_1: ECORI; Site_2: ECORI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 411 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximatley 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
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Job time: 4098 sec
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| SIDSI_/gcgdata_geneseq_geneseqp_AAl980.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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AAG66330
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AAW24790
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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AAR72826 AAB1324 AAB1324 AAB2775 AAW71295 AAW71295 AAW56111 AAR60178 AAX01652 AAX06666 AAX06666 AAX06666 AAX06666 AAX066777 AAX39233 AAG39233 AAG39233 AAG39233 AAG39233 AAG36713 AAG36713 AAG36713	AAR97866 AAX24788 AAW02258 AAW40538 AAX70105 AAX52002 AAX51631 AAX31186 AAW31185 AAW31185 AAW31185 AAW31185 AAW31185 AAW31185
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112 113 114 117 118 118 118 118 118 118 118 118 118	W W W W W W W W A A A A A A A A A A A A

ALIGNMENTS

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Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; tobacco.
                                                                                                                                                                                                                                                               /note= "conserved Cys residue"
Misc-difference 148
                                                                                                                                                                                                                                                                                   /note= "conserved Cys residue"
Misc-difference 155
                                                                                                                                                                                                                                                       'note= "conserved Cys residue"
                                                                                                                                                                                                                                     /label= Highly-charged_domain
                                                                                                                                                                                                          135..206
/label= Cys-rich_domain
385..478
                                                                                                                                                               /label= Transit_peptide
                                                                                                                                                                     135..478
/label=_Mat_protein
                                                                                                                                           Location/Qualifiers
                ¥¥
                                                                     Tobacco violaxanthin de-epoxidase.
                                                                                                                                                                                                 /note= "Claim 8"
               AAW09875 standard; Protein; 478
                                                                                                                          Nicotiana tabacum cv. xanthi.
                                                   (first entry)
                                                                                                                                                                                        135..147
                                                                                                                                                                                                                                                Misc-difference 141
                                                   28-JUL-1997
                                 AAW09875;
                                                                                                                                                     Peptide
                                                                                                                                                                        Protein
                                                                                                                                                                                          Peptide
                                                                                                                                                                                                            Domain
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       AAW09875
                                                                                                                                              Key
RESULT
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The 55 kDa violaxanthin de-epoxidase (VDE) (AAW09875) of tobacco catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. This system, termed energy dependent non-radiative energy dissipation or non-photochemical fluorescence quenching, reduces the quantum efficiency of photosystem II (PSII), helping to prevent PSII over-reduction and photoinhibitory damage. The amino cid sequence of the VDE madeled from an isolated cDNA clone (AAT66242). VDE nucleic acids (see also AAT66241, AAT66243), in sense modify VDE nucleic acids (see also AAT66241, AAT66243), in sense modify VDE levels in plants. Increased levels result in the plant and/or more resistant to disease. Underexpression of VDE increases photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding plant violaxanthin de-epoxidase - used to modify the
/note= "conserved Cys residue"
                               'note= "conserved Cys residue"
                                                            'note= "conserved Cys residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sensitivity of a plant to light
                                                                                                                                                                                                                                                                                                                                                                   96WO-US18291.
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                                                                                                                                                                                                                                                                                                                                                                                                                950S-0006315
                                                                                                       Misc-difference 180
                                                                                                                                                                                                                                                                                                                                                                                                                                           (CALJ ) CALGENE INC.
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                                                                                                                                                                                                Misc-difference 206
                                                                                                                                                                                                                                                           Misc-difference 382
                                            Misc-difference 167
              Misc-difference 161
                                                                          Misc-difference 17.
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                                                                                                                                    Misc-difference
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121 vaifilsvaskadavdalktctcllkecrlelakcisnpacaanvaclqtcnnrpdetec 180
                                                                    714 RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773
                                                                                                                774 HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 833
                                                                                                                              LQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDK 893
                                                                                                                                                                         894 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 950
                                                                                                                                                                                                                    654 QIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT
                                                                                                                                                                                                                                                                                                                                                                               Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; lettuce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "conserved Cys residue"
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Misc-difference 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label = Highly-charged_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218..231
/label= Lipocalin_signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265..272
/label= Tryptic_peptide-11
                                                                                                                                                                                                                                                                                                                                                        Romaine lettuce violaxanthin de-epoxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Tryptic_peptide-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Tryptic_peptide-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= Transit_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label = Cys-rich_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "conserved Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126..473
/label=_Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                      AAW09874 standard; Protein; 473 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Claim 8"
                                                                                                                                                                                                                                                                                                                                                                                                                             Lactuca sativa L. cv. romaine.
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 152
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                                                                                                                                                                                                                                                                                                                                  28-JUL-1997
                                                                                                                                                                                                                                                                                                             AAW09874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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The 55 kDa violaxanthin de-epoxidase (VDE) (AAW09874) of romaine lettuce catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. This system, termed energy dependent con-radiative energy dissipation or non-photochemical fluorescence con-radiative and photosystem II (PSII) chelping to prevent PSII over-reduction and photochinhibitory damage. The amino acid sequence of the VDE was deduced from an isolated con-photosystem of the VDE nucleic acids (see also AAT66242-43), in sense or antisense orientation, can be used in genetic constructs to modify VDE levels in plants. Increased levels result in the photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding plant violaxanthin de-epoxidase - used to modify the
                                                                                                                                                                          /note= "conserved Cys residue"
   'note= "conserved Cys residue"
                                'note= "conserved Cys residue"
                                                                                                     note= "conserved Cys residue"
                                                                                                                                     'note= "conserved Cys residue"
                                                                  'note= "conserved Cys residue'
                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto HY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sensitivity of a plant to light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                             96WO-US18291.
                                                                                                                                                                                                                                                                                                              96US-0023502
95US-0006315
                                                                                                                                                                                                                                                                                                                                                                                                   Bugos RC, Rockholm DC,
                  Misc-difference 175
                                                  Misc-difference 190
                                                                                                                                                                                                                                                                                                                                                                (CALJ ) CALGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-281036/25
                                                                                                                                                      Misc-difference 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT66241.
                                                                                   Misc-difference
                                                                                                                     Misc-difference
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07-NOV-1995;
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                                                                                                                                                                        PRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFE 180
                                                                     Gaps
                                                       MALSLHTVFLCKEEALNLYARSPCNERFHRSGQPPTNIIMMKIRSNNGYFNSFRLFTSYK 60
                                                                                                                                                                                   NSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWY ITSGLNPTFDA
                              ;
0
   Length 473;
                              Indels
Query Match 33.3%; Score 2498; DB 18; Best Local Similarity 99.6%; Pred. No. 9.2e-187; Matches 471; Conservative 0; Mismatches 2;
 Query Match
Best Local (
                                                                                                                                          61
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241 fdcqlhefhmendklvgnltwriktldggfftrsavqtfvqdpdlpgalynhdneflhyq
                                          301 DDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVG
                                                                        361 RDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLF
421 ORLLEGFKELQQDEENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLR 473
                                                                                                                              Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin;
                                                                                                                                                                                                                                                                                                                                                                                                                                        364.462 ______/label= Highly-charged_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "conserved Cys residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                  114.185
/label= Cys-rich_domain
                                                                                                                                                                                                                                                                                                                                                                 /label- Transit_peptide
                                                                                                                                                                                                                                                        Arabidopsis violaxanthin de-epoxidase.
                                                                                                                                                                                                                                                                                                                                                                                      /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                          AAW09876 standard; Protein; 462 AA.
                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana var. columbia
                                                                                                                                                                                                                                                                                                                                                                                                           "Claim 8"
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                             .462
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                                                                                                                                                                                                                                                                                                    xanthophyll
                                                                                                                                                                                                               AAW09876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1011 RPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1071 ACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1251 NKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDN 1310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 32.2%; Score 2417; DB 18; Length 462; Local Similarity 99.8%; Pred. No. 1.9e-180; les 461; Conservative 0; Mismatches 1; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 41pp; English
96WO-US18291
                                               96US-0023502
95US-0006315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 461; Conservative
                                                                                                                                (CALJ ) CALGENE INC.
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07-NOV-1996;
                                                  06-AUG-1996;
07-NOV-1995;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 63310.
       AAG49996 standard; Protein; 525 AA.
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99US-0129845.
99US-0130077.
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990S-0130510.
990S-0130891.
990S-0131449.
990S-0132407.
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99US-0132486.
99US-0132487.
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99US-0134256.
99US-0134218.
99US-0134219.
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99US-0134370.
99US-0134768.
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99US-0135124.
99US-0135353.
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99US-0136392.
99US-0136782.
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99US-0137528.
99US-0137502.
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99US-0138094.
99US-0138540.
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99US-0127462.
99US-0128234.
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                                                                                                                                                                                                         99US-0126264
                                       (first entry)
                                                                                         termination sequence.
                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                         05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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04-JUN-1999;
07-JUN-1999;
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                                       18-OCT-2000
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04-MAY-1999;
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01-APR-1999;
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16-APR-1999;
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25-MAR-1999
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                        AAG49996;
AAG49996
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270 FFTRSAVQTFVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAW 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 AEEGEKILIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----psldeasfs--rrgrttvvr----vletekstkiekpeppv--klial 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 212.5; DB 21; Length 525; 20.2%; Pred. No. 4.5e-08; Live 98; Mismatches 215; Indels 235;
    990S-0149929.
990S-0149902.
990S-0150566.
990S-0150884.
990S-0151065.
990S-0151066.
990S-0151089.
990S-0151303.
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990S-0153070.
990S-0153788.
990S-0154018.
990S-015479.
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Best Local Similarity
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                             611 LKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFN 670
                                                                                                                                          710 WFITRGLNPTFDAFDCQLHEFH-------TEENKLVGNLSWRIRTPDGGF 752
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                                                                                                                                                                                                                                                           753 FTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVENSPEDYIFVYYK 805
                                                                                                                                                                                                                                                                         806 GRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKTDNTCGPEPPLVE 863
447 EILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWG 506
                                         507 WEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPK 566
                                                                                    567 GNSGCKFPKDVALMV-----WEKWG----QFAKTAIVAIFILSV-----ASKADAVDA 610
                                                                                                  671 ECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK--------709
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                   128 ramn-ltgelngtdilvvva--------vnnsesv-
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                                                                                                                                                                                                                                                                                                                                                                                                                                         107 werrnsddirfcllviinayirpvpvlqnlrsk----gfstlscmvkncgpqilnclld 161
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                                                                                                                                                                                                                                                                                                                                                                          % Match 2.8%; Score 207; DB 21; Length 428; Local Similarity 23.5%; Pred. No. 8.9e-08; es 86; Conservative 48; Mismatches 124; Indels 108;
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990S-0160814.
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99US-0157865.
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20-AUG-1999;
    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 3068.
                                                                                                                                                                                                                                                                                                                            990S-0121825

990S-012180

990S-0123548

990S-0125788

990S-0125785

990S-0125785

990S-0128714

990S-0128714

990S-0130871

990S-0130891

990S-0130891

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990S-0139468
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                17-OCT-2000 (first entry)
                                                                                                                                                                      Arabidopsis thaliana.
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The present sequence is a MIM protein from Arabidopsis thaliana, which contributes to recombination repair of DNA damage in plant cells. The protein was tracked down with the help of a T-DNA tagged Arabidopsis mutant showing hypersensitivity to methyl methanesulphonate (MMS). It shows homology to a member of SMC (Structural Maintenance of Chromosomes) protein family and confers hypersensitivity to treatment with MMS, X-rays, UV light or mitomycin C. The present sequence is useful for DNA repair in plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= DA-box
/note= "conserved motif which harbours a Walker B type
NTP binding domain"
830 IIPELQTAAQKVG-RDFNTFIKTDNTCGPEPPLVERLEKKVEEGER-----TIIKEVEEI 883
                                                                    372 ekerlqsalekcgikewelf-avdncscenppl----gipqqsrlhsrisiieepdse 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Arabidopsis polynucleotide encoding protein useful for assisting recombinant repair of DNA damage in plants -
                                                                                                                                                                                                                                                                                                              MIM: recombination; plant; DNA repair; hypersensitivity; SMC protein family; Structural Maintenance of Chromosomes; MIM; methyl methanesulphonate; irradiation; mitomycin C.
                                                                                                                                                                                                                                                                                      Arabidopsis thaliana recombination repair protein, MIM
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/label= NTP_binding_domain
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/label= Hinge/spacer
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99US-0161406.
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                                  99US-0151080
                                                                                                                    99US-0153758
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     99US-0151065
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                                                                                                                                            16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
04-OCT-1999;
05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                               13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
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08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
                                           30-A0G-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
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21-OCT-1999;
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25-OCT-1999;
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21-OCT-1999;
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                         WYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 syi-----leck-----gn----sssflrnllg---gvndllg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESIIPNLQKAAK -----SVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVEIEEEVEKEVEKVRDT-------EMTLFQRLLEGFKE------LQQD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EENFVRELSKEEKEILNELQMEATEVEKLFGRALP 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 570 GCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCI 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GNLSWRIRTPDG-GFFTRSAVQKFVQD-PKYPGILYNHDNEYLLYQDDWYILSSKVE 793
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                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 siyehltkataivd-----elentikpiekeiselrgk------iknmegv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 -----tlrgcaneanyrnlki-----ijydfsrprlniprhmypqtehpti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 FGSIVVAKICSS-RRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNS
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                                                                             Query Match 2.0%; Score 151; DB 21; Length 1055; Best Local Similarity 19.3%; Pred. No. 0.0084; Matches 182; Conservative 119; Mismatches 306; Indels 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              904 GFKELQRDE----ENFLRELSKEEMDVLDGLKMEATEVEKL 940
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Sequence
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pre-erythrocytic liver stage antigen. 3 (LSA-3) protein. The encoding gene sequence was isolated by screening a P. falciparum strain T9/96 library with serum from a missionary treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones isolated, clone 7295 was used to screen a library generated from Thai strain K1. One clone contained 6.85 kb insert including the genomic sequence AAT/8867. The gene comprises a 1.8 kb region encoding 3 major blocks of tetrapeptide repeats (especially the amino acid sequence VEES, VEEN, VEEI, VAPE, etc.) and a 3' hydrophobic region corresponding to a glycosyl-phosphatidyl- inositol membrane anchoring sequence. The inositol membrane anchoring sequence. The firm the LSA-3 protein with the exception of the peptides AWW24/91-4. The LSA-3 peptides can be used to raise antibodies and as vaccines for
                                                                                                                                                        prophylaxis; Thai strain; gene organisation; exon; intron; hydrophobic; glycosyl-phosphatidylinositol membrane anchoring sequence; antibody; vaccine; immunotherapy; malaria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                          Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum poly:peptide(s) and related nucleic acids -derived from the liver stage antigen-3, useful for malaria vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%; Score 147.5; DB 18; Length 1786; Best Local Similarity 18.1%; Pred. No. 0.035; Matches 207; Conservative 155; Mismatches 374; Indels 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence corresponds to a Plasmodium falciparum strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 SIIPNLQK-AAKSVGRDFN-----NFITTDNSCGPEPPLVE
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/note= "repeat region
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                                                                                                                                                                                                                                                                                                                                     /note= "repeat region
AAW24790 standard; Protein; 1786 AA
                                                                                                     falciparum liver stage antigen-3.
                                                                                                                                                                                                                                                              Location/Qualifiers
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/note= "re
279..818
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                                                                                                                                                                                                                             Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT78868.
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                                                                     08-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-1996
                                    AAW24790;
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the mammalian mitosin. Mitosin is involved in the regulation of the mammalian mitotic cell cycle. Mitosin as with EZF-1 (see AAR72824) interacts with the retinoblastoma tumour suppressor gene product). Mitosin is first synthesised at the G1/S boundary, it is then phosphorylated from S through M phase, and during mitosis, is closely associated with the centromeres/Kinetochores at the mitotic spindle poles. Mitosin is necessary for a cell to advance on to the next stage. Mitosin is thus necessary for a cell to advance on to the next stage. Mitosin is thus useful for ocntrolling cell growth as overexpression of mitosin prevents cell from exiting the M phase.

The mati-mitosin antibody antibody fragment or a phosphorylated mitosin mutein (or nucleic acid encoding it) can also be used to inhibit cell division which is particularly useful for the study of the cell cycle. A further use is to control hyperpolificative cells, and so control diseases such as psoriasis and breast cancer. It can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443; Indels 434; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purified mammalian protein mitosin and agents that bind it and inhibit its action - used to promote cell growth or to inhibit cell division and/or proliferation
                                                                                                                                          Cell cycle; M phase; mitosin; retinoblastome; mitosis; cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.0%; Score 147; DB 16; Length 2482; Best Local Similarity 18.4%; Pred. No. 0.064; Matches 240; Conservative 188; Mismatches 443; Indels 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              block gametogenesis of an immature gamete.
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/label= internal_repeat
1660..1839
                                                                                                                                                                                                                                                                                                        /label= internal_repeat
AAR72826 standard; Protein; 2482 AA.
                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0141239.
                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US12162.
                                                                      27-FEB-1996 (first entry)
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N-PSDB; AAQ86851.
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                                                                                                          Human mitosin.
                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1993;
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                                                                                                                                                             inhibition.
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                                    AAR72826;
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οy	501	×	551
qq	490	kseagglkqeimtlkeeqnkmqkevndllqeneqlmkvmktkhecqnlesepir	543
ογ	552	HNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDAL	611
qq	544	:::::nsvkereserng-cnfkpgmdlevkeisldsynaglvqleamlrnkelklgese	296
٥y	612	KTCTCLACAAN	637
qq	597	kekeciqhelqtirgdletsnlqdmqsqeisglkdceidaeekyisgphelstsqndnah	929
οy	638	VAC-LQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDF-	689
QQ	657	lgcslqttmnklnelekiceilgaekyelvtelndsrsecitatrkmaeevgkll	711
ογ	069	PVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDC	725
QQ	712	nevkilnddsgllhgelvedipggefgegpneghpvslapldesnsyehltlsdkev	768
δ	726	QLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQD	783
QQ	769	qmhfaelqekflslqsehkilhdqhcqmsskmselqtyvdsl	810
οy	784		826
qq	811		898
δy	827		873
QQ	869	eqtgdmsllsnlegavsanqcsvdevfcsslqeenltrketpsapakgveeleslcevyr	928
ΟŊ	874		922
QQ	929	qslekleekmesqgimknkeiqeleq11sserqeldc1rkqylseneqwqqkltsv	984
ζō	923		096
g	985	tlemesklaaekkqteq1slelevar1q1qg1d1ssrs11g1dtedaiqgrnescdiske	1044
ōλ	961		1002
QQ	1045	htsettertpkhd-vhqicdkdaqqdlnldiekitetgalkptgecsgeqspdtnye	1100
οy	1003	SRTGGRSSRPLSAFRSGFSKGIFDIVPLPSK	1033
QQ	1101	ppgedktqgsseciselsfsgpnalvpmdflgnqedihnlqlrvketsnenlrllhvied	1160
οy	1034	LIVPSADAVDALKTCACLLKGCRIELAKC	1084
QQ	1161		1199
οy	1085	FENSVVDEFNECAVSRKKCVPRKSDLG-	1143
QQ	1200		1212
ογ	1144	EFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGN	1197
QQ	1213	kleyfscdhqellqrvetseglnsdlemhadkssredigdnvakvn	1258
δy	1198	ISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENK	1252
Ср	1259	alyleadlevvqteklclekdnenk	1310

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1253 P-----EDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFI 1306
           1307 RIDNICGPEPALVERIEKTVEEGERIIVKEVEEIBEE---VEKEVEKVGRIEMTLFORLA 1363
                                                    This is the amino acid sequence for mitosin, a phosphoprotein necessary for the cell to ente mitosis. The protein's degradation is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated mitosin protein and gene - useful for, e.g. developing products for therapy and diagnosis of hyper-proliferative disorders such as cancers or psoriasis
                                                                                                                                                                                                                                           Mitosin; phosphoprotein; mitotic cell cycle; antibody; analogue; inhibition; M phase; Antagonist; hyperproliferative cell; cancer; leukaemia; lymphoma; chromosome segregation.
                                                                                 1364 EGFNELKQDEENFVRE-----LSKEEMEFLDEIK-MEASEVEK 1400
                                                                                            /label- "Bipartite targeting motif"
/note= "Optionally C or G"
2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= "Bipartite targeting motif"
/note= "optinally A or T"
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1885..1962
2146..2188
2165..2187
/note= "leucine heptad repeat"
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                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
258..280
                                                                                                                                                                                                                       Human mitosin amino acid sequence.
                                                                                                                                                        AAW23996 standard; Protein; 2482
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93US-0141239.
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N-PSDB; AAV09076.
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                                                                                                                                     RESULT 13
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also necessary for the cell to advance into the next stages of mitosis.

The mitosin protein, can be used to control the growth of cells. An anti-mitosin antibody, a muturn or a non-functional analogue of mitosin can inhibit the mitotic cell cycle by preventing the cells from entering the M phase, and over expression of mitosin or its functional equivalent, would inhibit the cycle by preventing cells from leaving the M phase. Antagonists to this protein can be used to control hyperproliferative cells in, (e.g. thyroid hyperplasia, Grave's disease, psoriasis, benign prostatic hypertrophy, Li-Fraumeni syndrome, breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, cupplementation of lost mitosin function by introduction of the protein or nucleic acid encoding the protein into a cell can restore defective chromosome segregation, which is a marker of progressing malignancy. Malignant proliferation of cells can then be halted. The protein can also be used for the detection and diagnosis of hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 ereksiselsdgykgeklillgrceetgnayedlsgkykaageknsklecllnectslce 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 240; Conservative 188; Mismatches 443; Indels 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 147; DB 19; Length 2482; 18.4%; Pred. No. 0.064;
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                                    985 tlemesklaaekkgteglslelevarlglggldlssrsllgidtedaiggrnescdiske 1044
                                                                                                        1045 htsettertpkhd-vhqicdkdaqqdlnldiekitetgalk---ptgecsgeqspdtnye 1100
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                                                                                                                                                                                                                   -----NELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKC 1084
                                                                                                                                                                                                                                                     -----kieac----ieleki 1199
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                                                                                                                                                                                                                                                                                                                                                                                                1213 kleyfscdhgellgrvetse-----glns----dlemhadkssredigdnvakvn 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                      ISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLH-----YQDDWYILSSKIENK 1252
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----- 0FTS-- 960
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                                                                    -----PCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPI-----QSADL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum chromosome 2 related protein SEQ ID NO:182
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                                                                                                                                              1003 ----RTTGGRS-----SRPLSAFRSGFSKGIFDIVPLPSK-
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                                                                                                                                                                                                                                                     1161 rdrkveslinemkeldskihlqevqlmt-----
                                                                                                                                                                                                                                                                                                                               v-----gel----
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   923 EMDVLDGLKMEATEVEKLF----
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200025728-A2.
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Wed Nov

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Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
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Disclosure; Page 410-414; 577pp; English.

by chromosome 2 of the human malarial parasite, the parameter of the human malarial parasite, the processing and the parasite in the coding (1); and (2) vaccines against P. falciparum infection comprising (1) or (II).

1. and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (1), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rights or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in nection of the plasmodium encomesome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the subsequent identification of proteins encoded by it will help to complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to ABB1832 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. The present invention describes proteins and their fragments (I) encoded

1558 AA; Sequence

50; | ::|::|::| ::| ::| | 3.40 ekinetvfntvldkveetveisgeslennemdkaf----fseifdnvkgigenlltg-- 792 793 -----mfrsietsivigsee--kvdlnenvyssildn--ienmkegllnklenisst 840 792 -VENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESI--IPELQTAAQKVGRDFNTF 848 849 IKTDNTCGPEPPLVERLEKKVEEGE--RTIIKEVEEI----EEEVEKVRD-----K 893 391 EKILIKEAVEIEEEVEKEV----EKVRDTEMTLFQRLLEGFKELQQD----EENFVREL 441 SKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHK 501 RFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHG----KHNLSPA 557 558 HSINQNVPKG-NSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTC 616 617 LLKECRLELAKCISNPACAANVACLQTCNNRPDETECQ---IKCGDLFENSVVDEFNECA 673 674 VSRKKCVPRKSDVGD--FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH 731 -----ekedltdkmidaveesieiss-dskeet------ekedltdkmidaveesieiss-dskeet 732 TEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSK 791 841 egvqetvtehveqnvyvdvdvpamk----dqf------lgilneagg-----DB 21; Length 1558; Indels 413; Ouery Match 1.9%; Score 143.5; DB 21; Best Local Similarity 17.9%; Pred. No. 0.059; Matches 206; Conservative 153; Mismatches 377; 347 SIIPNLQK-AAKSVGRDFN-----NFITTDNSCGPEPPLVE-: = :. 502 683 442 ŏ ò g g ò g ò a ò a õ g ò g δ

(GENE-) GENELABS TECHNOLOGIES INC.

WPI; 1997-393672/36. N-PSDB; AAT75237.

Dolganov G;

96US-0592126

26-JAN-1996;

an	IO4/ Idakd	ditekvieeemuiiliidevveikuveeukiekvauikuieuiik 1037
Qy	894	-TLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRAL 945
qq	1098	evkeikeleseiledykelktietdileekkeiekdhfekfeeeaeeikdleadilkevs 1157
Qy	946	-PIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL 994
QQ	bb 1158 sleveeekkleevhelkeevehiisgdah-	: 189 hiisgdahikg 1189
Qy	995	PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACA 1054
Op	Db 1190leeddleevddlkgsildmlkgdmelgdmd-	:
Qy	1055	FLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQICN NRPDETECQIK 1112
qq	1231	gerveslkdvlssalgmdeegmktrkkaqrpkleevilk 1269
Qy	1113	CGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGL 1172
Dp		: : kkitkkk 1292
Qy	1173	NPTEDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHD 1232
qq	Db 1293 epkdeivevemkdedided	iedveed1319
ΟŸ	1233	NEYLHYODDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELE 1292
qq	Db 1320ieedkvedidedid	edide 1334
Qy	1293	KAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIE 1341
qq	1335	didedigedkdevidlivgkekriekvkekkkklekkveegvsglkkhvdevmkyvqkid 1394
ΟŸ	1342	EEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKM 1393
qq	Db 1395 kevdkevskaleskndvt	nvlkqnqdffskvknfvkkykvfaapfisavaa 1445
Qy	OY 1394 EASEVEKLF 1402	
Dβ	Db 1446 fasyvvgff 1454	
RES	RESULT 15.	
AAW ID	AAW22//5 ID AAW22775 standard; Protein;	; 1312 AA.
A X	XX AC AAW22775;	
X E	XX DT 21-DEC-1998 (first entry)	
X D X	XX DE Human RAD50. xv	
KKK	KW Human; RAD50; DNA repair; t KW central nervous system.	tumour suppression; cancer; Septin-2;
×× s	XX OS Homo sapiens.	
V A	AA WO9727284-A2.	
7 G X	XX PD 31-JUL-1997.	
PF	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	.6
PR PR	AA 17-JUL-1996; 96US-0687080	0.

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Search completed: November 6, 2001, 04:59:38 Job time: 7622 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

November 6, 2001, 05:01:12 Run on:

; Search time 90.8 Seconds (without alignments) 349.941 Million cell updates/sec

US-09-075-375A-4
7495
1 MALSLHTVFLCKEEALNLYA.....MEASEVEKLFGKALPIRKVR 1412 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

212252 seqs, 22503292 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 8. Appli	9	148		~	~	7	28,	28,	28,	6, A	9	Sequence 6, Appli	6	6	7,	7	12,	35,	2, 1	7	4	4	4	4	Sequence 184, App	19
SUMMAKIES	ID	US-08-973-462-8	US-08-328-254-6	US-08-592-126-148	US-08-687-080-51	US-08-021-601-2	US-08-082-849B-2	PCT-US94-01624-2	US-08-404-531B-28	US-08-476-900A-28	US-08-488-546A-28	US-08-404-531B-6	US-08-476-900A-6	US-08-488-546A-6	US-08-574-959A-9	US-09-357-014-9	US-08-574-959A-7	US-09-357-014-7	US-08-836-567-12	US-08-968-542C-35	æ	US-08-125-077-2	US-08-460-309-4	US-08-125-077-4	US-08-568-459A-4	US-08-487-826B-4	US-08-755-587-184	US-08-482-728A-19
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ф	Query Match	2.0	2.0	1.8	1.8	1.8	1.8	1.8	1.7	1.7	1.7	1.7	1.7	1.7	1.6	1.6	1.6	1.6	1.6	1.6	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5
	Score	147.5	147	135.5	135.5	132	132	132	124	124	124	124	124	124	119	119	119	119	117.5	117.5	115.5	115.5	115.5	115.5	115	115	114.5	114
	Result No.		7	es	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27

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ALIGNMENTS

RESULT 1 (S-08-073-462-8 (S-08-073-462-8 (S-08-073-462-8 (S-08-073-462-8 (S-08-073-462-8 (SERNEAL INFORMATION: MALLEREE, PIERRE APPLICANT: DAUBERSIES, PIERRE APPLICANT: DAUBERSIES, PIERRE TITLE OF INFORMATION: MALLEREE FILENCE CURRENT FILING DATE: 1998-06-12 CURRENT FILING DATE: 1998-06-12 EARLIER FILING DATE: 1998-06-13 SEATILER FILING DATE: 1998-06-13 NUMBER OF SEQ ID NOS: 29 SEQ ID NOS: 29 SEQ ID NOS: 29 COHER INFORMATION: DESCRIPTION OF ARTIficial Sequence: Polypeptide SEQ ID NOS: 29 SEQ ID NOS: 29 COHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: PRATURE: CORANISM ARTIFICIAL SEQUENCE SEQ ID NOS: 29 SEC ID NOS: 29 SEC ID NOS: 29 SEG ID NOS: 29
SGUT 1 -08-973-462-8 Sequence 8, Application US/08973462B Sequence 8, Application US/08973462B Sequence 8, Application US/08973462B SEQUENT NO. 6191270 APPLICANT: DAUBERIES, PIERRE TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC FILE REFERENCE: 0660-0125-0 PCT CURRENT APPLICATION NUMBER: US/08/973,462B CURRENT FILING DATE: 1996-06-12 EARLIER APPLICATION NUMBER: FR 95/07007 EARLIER APPLICATION NUMBER: PR 95/07007 EARLIER APPLICATION
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                                                                                                      1110 -LKEMFFULEDVFKS----ESDVITVEEIKDEPVQKEVEKETVSIIEEMEENIVDVLEE-- 1163
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617 LLKECRLELAKCISNPACAANVACLQTCNNRPDETECQ---IKCGDLFENSVVDEFNECA 673
                                                                                                                                                                                                                   674 VSRKKCVPRKSDVGD--FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH 731
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APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campbell and Flores
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STREET: 4370 La Jolla Village Drive, Suite 700

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374 EREKSISELSDQYKQEKLILLQRCEETGNAYEDLSQKYKAAQEKNSKLECLLNECTSLCE 433
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                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: US/08/141,239
FILING DATE: 22-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                          COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 DEENFVRELS---KEEKEIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                            COMPUTER READABLE FORM:
CITY: San Diego
STATE: California
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                                                      USA
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                                                      COUNTRY:
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1045 HTSETTERTPKHD-VHQICDKDAQQDLNLDIEKITETGALK---PTGECSGEQSPDTNYE 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                874 RIIIKEVEEIBEEVEK---VRDKEVTLFSKLFEG-----FKELORDEENFLRELSKE 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      923 EMDVLDGLKMEATEVEKLF-----GRALPIRKLMAVATH------CFTS-- 960
                                                                                                                                                                                         827 PE----SIIPELQTAAQ----KVGRDFNTFIKTDNTCGPEPPL----VERLEKKVEEGE 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              929 QSL----EKLEEKMESQGIMKNKEIQELEQLLSSERQELDCLRKQYLSENEQWQQKLTSV 984
                                                                                                                                                                                                                                                                                  APPLICANT: Gregory Dolganov TITLE OF INVENTION: Transcripts Encoding Immunomodulatory TITLE OF INVENTION: Polypeptides NUMBER OF ENCORESPONDENCES: 151
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1428 ----QLNKEKELLVKESESLQARLSESDYEKLNVSKALEAALVEK 1468
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5821091
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 VRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFL-----ANHETIKY 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 ---LSKKQ----NELKNVKYELQQLEGSSDRILELDQELIKAERELSKAEKNSNVETLKM 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 135.5; DB 2; Length 1312;
19.7%; Pred. No. 0.02;
tive 95; Mismatches 218; Indels 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; INDIVIDUAL ISOLATE: Rad50.pro-translation of SEQ ID NO:54 US-08-592-126-148
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
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                                                                                                              NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REPERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 124; Conservative
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                                                                      CLASSIFICATION:
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                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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RESULT

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669 FITQL----TDENQSCCPVCQRV-----FQTEAELQEVISD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                 924 MDVLDGLKME------ATEVEKLF 941
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APPLICATION UNMBER: US/08/021,601
FILING DATE: 19930212
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08021601
Patent No. 5591631
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NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leppla, Stephen H. APPLICANT: Klimpel, Kurt R. APPLICANT: Nichols, Peter J.
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                840 KVGRDFNTFIKTD----
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CITY: Atlanta
STATE: GAT
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              639 ESDLDRLKE
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US-08-021-601-2
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                                                                                                              Human RAD50 Gene and Methods of Use Thereof 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.8%; Score 135.5; DB 2; Length 1312; Best Local Similarity 19.7%; Pred. No. 0.02; Matches 124; Conservative 95; Mismatches 218; Indels 191;
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                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sholtz, Charles K.
REGISTATION NUMBER: 38,615
REFERENCE/PLOCKET NUMBER: 4600-0111.30
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
                                                              APPLICANT: Gregory Dolganov
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and M
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY AGENT INFORMATION:
                   Sequence 51, Application US/08687080 Patent No. 5965427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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INDIVIDUAL ISOLATE:
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US-08-687-080-51
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Best Local Similarity 17.2%; Pred. No. 0.017;
Matches 139; Conservative 117; Mismatches 254; Indels 300; Gaps
                                                                                                                                                                                                                                                                                                                                                          701 ----LOSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPMROSIIDLKEKEIPELRNKLQ 755
-:: | : : | :
--EIEKSSKQRAMLAGATAVYSQ 668
                                                                                                                                                                                                                                                                         783 DDWYILSSKVENSPEDYIFV--YYKGRNDAWDGYGGSVLYTRSAV-LPESIIPELQTAAQ 839
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                                                                                                           723 FDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQ 782
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APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogendra
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: RELATED METHODS
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951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
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                                LSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNT 847
                                                                                                                                                                                                                                                                                                                                    237 APEAFNYMDKFNEQEINLSLEELKDQRMLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKL 296
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                                                                                                                                                                                                                                         177 IKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLY 236
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                                                                                                                                           L---VIQSSEDYVENTEKALN-------VYYEIGKILSRDILSKINQPYQKFLDVLNT
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APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Alora, Naveen
APPLICANT: Alora, Naveen
APPLICANT: Nichols, Peter J.
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor

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951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
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297 QIPIEPKKDDIIHSLSQEEKELLKRIQIDSSDFLSTEEKEFLKKLQIDIRDSLSEEKEL 356
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amino acid
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San Francisco
                                    California
                                                                              AY: USA
94111-3834
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                                                                              COUNTRY:
ZIP: 941
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788 LSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNT
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                         848 FIKTDNTCG---
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                                                                                                                     1223 NQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTR--S 1280
                                                                                                                                                                                                                                                                                                                                                                                                                               1338 ------EEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRE----- 1379
                                                                                                                                                                                                                                                                          1281 SVLPNSIIPPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE-RIIVKEV-- 1337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                637 PNIAEQYTHQDEIYEQVHSKGLYVPESRSILLHGPSKGV-ELRNDSEGFIHEFGHAVDDY 695
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                                                                                                                                                                                         534 ----IIKQSEKEYIRI-DAKVVPKSKIDTKIQE----AQLNINQEWNKALGLPKYTKLIT 584
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    Matches 139; Conservative 117; Mismatches 254; Indels 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 132; DB 5; Length 776; 17.2%; Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: RELATED METHODS
TITLE OF INVENTION: RELATED METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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REGISTRATION NUMBER: 31.677
REFERENCE/DOCKET NUMBER: 15280-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1380 ----LSKEEME-----FLDEIKMEASEV 1398
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APPLICATION NUMBER: PCT/US94/01624
FILING DATE: June 25, 1993
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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GENERAL INFORMATION:
APPLICANT: JOSEPh Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor Patent No. 5863724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1338 ------EEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRE----- 1379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 -----DNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDNERLKWRIQLSPDTR 510
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                                                                                                                                                                                  177 IKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLY 236
                                                                                                                                                                                                                                                                                                                                                                237 APEAFNYMDKFNEQEINLSLEELKDORMLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LORDEENFLRELSKEEMDVLDGLKMEATEV----EKLFGRALPI------RKL 950
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                                                                                                ----PEPPLVERLEKKVEEGERTIIK--
                                                                                                                                                                                                                                                                              879 -----EVEEIEEEVEKVRDKEVTLFSKLFEGFKE--
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MEDIUM TYPE: Floppy disk
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
IITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,900A
FILLIG DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: BYLR-0027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-476-900A-28
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                   Patent No. 6031150
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    926 VLDGLKMEA--TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDD-----GIGRL 978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 FFTWTPDGIPTLSNITIRIPRGQLTMIVGQVGCGKSSLLLATLG-----EMQKVSGAVF 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 1.7%; Score 124; DB 2; Length 1498; Best Local Similarity 18.8%; Pred. No. 0.24; Matches 109; Conservative 72; Mismatches 221; Indels 178;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               947 RK---APEPS--QGLPRAMSSRDGLLLDEDEEEEEAAESE 981
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                                                                                    FILING DATE: 15-MAR-1995
CLASSIFITMENTON
                                                                                                                                                                                              NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0003
TELECOMMUNICATION:
TELEPHONE: 215-568-3100
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; Sequence 28, Application US/08476900A
; Patent No. 6031150
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1498 amino acids
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MOLECULE TYPE: protein
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and Method of Detecting Persistent Hyperinsulinemic Hypogly Infancy
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Sequence Encoding Mammalian Sulfonylurea Receptor
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                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6031150ris
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor Patent No. 6054313
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
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                                                1248 KIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIR 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : : ||| :| || 581 SLFHILVTPLFLLSSVVRSTVKALVSVQKLSEFLSSAEIREEQCAPREPAPQGQA----G 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 KLSQAQRTTL-----EYSNERLKQT---NEMLRGIKLLKLYAWENIFCSRVEKTRRK 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926 VLDGLKMEA--TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDD-----GIGRL 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        529 EMTSLRAFAVYTSISIFMNTAIPIAAVLITFV-----GHVSFFKESDFSPSVAFASL 580
                                                                                            ----ETVME 946
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846 STPMIVFLDDPFSALDVHLSDHLMQAGILELLRDDKRTVVLVTHKLQYLPHA-DWIIAMK 904
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18.8%; Pred. No. 0.24;
tive 72; Mismatches 221; Indels 178;
                                                                                          905 DGTIQREGTLKDFQRSECQLFEHW------KTLMNRQDQELEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6054313ris
STREET: Dietty Place 46th. Floor
CITY: Philadelphia
                                                                                                                                          1308 TDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKE 1347
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/488,546A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                US-08-488-546A-28; Sequence 28, Application US/08488546A; Pattent to . 6054313; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-
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SEQUENCE CHARACTERISTICS:
LENGTH: 1498 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 18.8
Matches 109; Conservative
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MEDIUM TYPE: Floppy
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ZIP: 19103
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor tent No. 5863724
1024 IFDIVPL-----PSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKG 1076
                                                                                                                                                                                                                                   1118 ENSVYDEFNECAVSRKKCVPRKSDLGEFPAPDP------SVLVQNFNI-SDF 1162
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                                                                                                                1205 -----LDSGF----FTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSS 1247
                                                                                                                                                                           685 FFTWTPDGIPTLSNITIRIPRGQLTMIVGQVGCGKSSLLLATLG-----EMOKVSGAVF 738
                                                                                                                                                                                                                                                                                                  739 WNSLPD-----SEGRRPQQPRAGDSGRFGCQEQRPCGYASQKPWLLNATVEENITFESPF 793
                                                                                                                                                                                                                                                                                                                                                                                                               794 NKQRYKMVIEACSLQPDIDIL------PHGDQTQIGERGINLSTGGQRPDQCRPEPST 845
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                                                        637 KYQAVPLKVVNRKRPAREEVRDLLGPLQ------RLTPSTDG-DADNFCVQIIGG 684
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CLASSIFICATION: 435
TORNEY AGGRESS
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MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
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CORRESPONDENCE ADDRESS:
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979 GITRKRINGTFLL-----KILPPIQ-----SADLRTTGGRSSRPLSAFRSGFSKG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         685 FFTWTPDGIPTLSNITIRIPRGQLTMIVGQVGCGKSSLLLATLG-----EMQKVSGAVF 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.7%; Score 124; DB 3; Length 1581;
Similarity 18.8%; Pred. No. 0.26;
09; Conservative 72; Mismatches 221; Indels 176
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                                                                                               BYLR-0027
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                                                                34,293
                                                                                         REFERENCE/DOCKET NUMBER: BY TELECOMMUNICATION: 215-568-3100 TELEPHONE: 215-568-3439
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                                                                                                                                                                                                                                                                           1581 amino acids
         ATTORNEY/AGENT INFORMATION:
                                 NAME: Beardell, Lori Y REGISTRATION NUMBER: 34
                                                                                                                                                                                  TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-476-900A-6
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CORRESPONDENCE ADDRESS:
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
TITLE OF INVENTION: and Method of Detecting Persistent Hyperinsulinemic Hypoglycen
TITLE OF INVENTION: Infancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .248 KIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIR 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            685 FFTWTPDGIPTLSNITIRIPRGQLTMLVGQVGCGKSSLLLATLG-----EMQKVSGAVE 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  794 NKORYKMVIEACSLOPDIDIL------PHGDQTQIGERGINLSTGGQRPDQCRPEPST 845
                                                                                                                                                            926 VLDGLKMEA--TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDD-----GIGRL 978
                                                                                                                                                                                                                                                                                                529 EMTSLRAFAVYTSISIFMNTAIPIAAVLITFV-----GHVSFFKESDFSPSVAFASL 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                739 WNSLPD----SEGRRPQQPRAGDSGRFGCQEQRPCGYASQKPWLLNATVEENITFESPF 793
                                                                                                                       968 KVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFK--ELQRDEENFLRELSKEEMD 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 846 STPMIVFLDDPFSALDVHLSDHLMQAGILELLRDDKRTVVLVTHKLQYLPHA-DWIIAMK 904
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                             637 KYQAVPLKVVNRKRPARBEVRDLLGPLQ------RLTPSTDG-DADNFCVQIIGG
Query Match
1.7%; Score 124; DB 2; Length 1581;
Best Local Similarity 18.8%; Pred. No. 0.26;
Matches 109; Conservative 72; Mismatches 221; Indels 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         905 DGTIQREGTLKDFQRSECQLFEHW-----KTLMNRQDQELEK--
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,900A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     947 RK---APEPS--QGLPRAMSSRDGLLLDEDEEEEEAAESE 981
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ADDRESSEE: No. 6031150ris
STREBT: One Liberty Place 46th. Floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08476900A
Patent No. 6031150
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NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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905 DGTIQREGTLKDFQRSECQLFEHW------KTLMNRQDQELEK-----ETVME 946
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                                                                                                                                                                                              US-08-574-959A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1163 NGKWY----ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKT-------- 1204
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581 SLFHILVTPLFILSSVVRSTVKALVSVQKLSEFLSSAEIREEQCAPREPAPQGQA----G 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      868 KVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFK--ELQRDEENFLRELSKEEMD 925
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Similarity 18.8%; Pred. No. 0.26;
09; Conservative 72; Mismatches 221; Indels 178;
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                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
E: No. 6054313ris
One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMOUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DAYS:
APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
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Matches 109; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                COMPUTER READABLE FORM:
                                              Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                               USA
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ADDRESSEE:
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                                                                                               COUNTRY:
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Best Local S
                                                                          STATE:
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1284 PNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERI------EKTVEEGERIIV 1334
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                                                                                                                                                                                                                                                                        APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.6%; Score 119; DB 2; Length 905; Best Local Similarity 31.0%; Pred. No. 0.28; Matches 39; Conservative 15; Mismatches 34; Indels 3
1308 TDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKE 1347
                                947 RK---APEPS--QGLPRAMSSRDGLLLDEDEEEEEAAESE 981
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/574,959A FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFN-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              Sequence 9, Application US/08574959A Patent No. 5962224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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APPLICATION NUMBER: US,
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AND USES THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSE: LAHVE & COCKFIELD

STRET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTR: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: THE PECONOMINATION:

OFFRATING SYSTEM: DC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/357,014

FILING DATE: 19-Jul-1999

PRIOR APPLICATION NUMBER: 08/574,959

FILING DATE: CURROWN-

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REFERENCE/DOCKET NUMBER: 36,207

REFERENCE/DOCKET NUMBER: 36,207

TELECOMMUTICATION NOW: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 905 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.6%; Score 119; DB 4; Length 905; Best Local Similarity 31.0%; Pred. No. 0.28; Matches 39; Conservative 15; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: November 6, 2001, 05:01:26
Job time: 7515 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-09-357-014-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1395 ASEVEK 1400
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

6, 2001, 05:02:57 November Run on:

; Search time 82.15 Seconds (without alignments) 1309.294 Million cell updates/sec

1 MALSLHTVFLCKEEALNLYA..........MEASEVEKLFGKALPIRKVR 1412 US-09-075-375A-4 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

pirl:* pir2:* pir3:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	violaxanthin de-ep			- o		hypothetical coile		rved hyp	reticulocyte-bindi	hypothetical prote	0.	heavy	myosin beta heavy	nuclear migration	DNA topoisomerase	hypothetical prote	RESA-H3 antiqen PF		hypothetical prote	cag island protein	myosin beta heavy	hypothetical prote		surface-located me	hypothetical prote	probable membrane	hypothetical prote		phosphoprotein pho
SUMMARIES																														
SUMM	QI	T03750	T00708	A84606	T28677	T28676	T38077	T30822	H69378	A42771	H36812	T18372	A59286	A37102	857976	S54174	G70163	B71603	F75103	T29145	A71928	806006	T32650	C70319	JC6009	F64508	S54044	T05113	\$38173	A40801
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	Query Match Length	478	462	522	2269	2401	1957	1365	988	2829	2469	1939	1935	1935	2748	839	2166	1558	880	1199	1819	1935	5105	1002	1302	800	02	2712	1875	1109
dР	Query	34.1	32.4	2.8	5.6	2.5	2.1	2.1							1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.8	1.8
	Score	2557	2430	210	194.5	167.5	158.5	156	155.5	155.5	155	151	148.5	146	146	144.5	14	143.5	142.5	142.5	142.5	142.5	142.5	141	140.5	140	139.5	139	137.5	137
	Result No.	1	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

594 VAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETEC 653

534 RICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAI 593

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774 HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 833

714 RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773

654 QIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT 713

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probable centromer	hypothetical prote	ORF MSV156 hypothe	dystrophin, muscle	myosin heavy chain	conserved hypothet	major merozoite su	hypothetical prote	_			chromosome assembl	anthrax toxin leth	hypothetical prote	chromosome segreda	major merozoite su
E71410	T18427	T28317	S02041	I38055	A70387	805603	T20978	148153	T25592	C71622	B70356	JQ0032	A72287	E69444	SAZQK1
7	~	N	Н	~	~	~	~	7	7	7	7	-	7	~	-
1676	3724	1127	3660	1937	978	1639	2261	1934	1624	1979	1156	808	1170	1156	1631
1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.7	1.7
137	136.5	136	135	134.5	134	134	134	133.5	133	133	132.5	132	131.5	131	130.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 103750
violaxanthin de-epoxidase precursor - common tobacco
C; Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000 C:Accession: T03750
R; Buqos, R.C.; Hieber, A.D.; Yamamoto, H.Y.
J. Biol. Chem. 273, 15321-15324, 1998
A; Title: Xanthophyll cycle enzymes are members of the lipocalin family, the firm
A;Reference number: Z15054; MUID:98288256 A;Accession: T03750
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-478 <bug></bug>
A; Cross-references: EMBL: U34817; NID:q1463122; PIDN: AAC50031.1; PID:q1463123
A; Experimental source: strain Xanthi; tissue-type leaf
C;Genetics:
A; Gene: TVDE1
C; Function:
A; Description: violaxanthin de-epoxidase and zeaxanthin epoxidase catalyze the
d in protecting the photosynthetic apparatus from excessive light
A; Note: established as member of the lipocalin family
F;1-134/Domain: transit peptide (plastid) #status predicted <tnp></tnp>
F;135-478/Product: violaxanthin de-epoxidase #status predicted <mat></mat>
Query Match 34.1%; Score 2557; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.4e-142; Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A74 MATA DISCONDER A MITTING TO THE TOTAL POPULATION OF THE TOTAL AND TH
CY +/+ MALLPETONE LANNELINIX VOSKILPCENTKESWGWEDIYEGSLOVGKILCENTRETKERS 533
Db 1 MALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSP 60

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hypothetical protein At2g21860 [imported] - Arabidopsis thaliana C. Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: A84606
R:Lin, X: Kaul, S: Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.: VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Niarman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Accession: A84420; MUID:20083487
A; Accession: A84420; MUID:20083487
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-522 <STO>A; Cross-references: GB:AE002093; NID:94417279; PIDN:AAD20404.1; GSPDB:GN00139
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T2867; C4551; C4551
Mol. Biochem. Parasitol. 65, 171-177, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TEENKLVGN 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 SPAHSINQNVPKGNSGCKFPKDVALMV-----WEKWG----QFAKTAIVAIFILSV--- 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602 ---ASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         659 DLFENSVYDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK------ 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 LFVGWLGELEWSWRVVAGQNPAYDQFPCQYQLFYRGKGKSSFWYEPVFQVRTLEEKLV-- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          741 LSWRIRTPDGGFFTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVE 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 --WRRR------RYSVKR----GKIPATFRFSVLDNGVVSNEF------WTIVD--VS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKT 851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 PEPPV--KLIALVGKGEVSPLK-STSWEEVMLHTARRLKWVD------EGYEMLVFDD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 ENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVG 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 PEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVROTEMTLFQRLLEGFKELQQDE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 2.8%; Score 210; DB 2; Length 522; Similarity 21.1%; Pred. No. 8.3e-05; Conservative 77; Mismatches 186; Indels 194;
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Cipacies: Arabidopsis thaliana (monse-ear cress)
Cipaces: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
Cipaces: 100008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1011 RPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1071 ACLIKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1191 DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1251 NKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDN 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1311 TCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELK 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 DNKLYGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 360
                                                                                                                         834 LQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDK 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 60
                                                                                                                                                                                                                                                                                              894 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 950
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.4%; Score 2430; DB 2; Length 462; Best Local Similarity 100.0%; Pred. No. 1.1e-134; Matches 462; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    violaxanthin de-epoxidase homolog F22013.3 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1371 ODEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 QDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 72/3; 128/2; 160/3; 292/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: ATSP: F22013.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Map position:
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RESULT A84606

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A;Title: A;Referen	A.Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii. A;Reference number: 220508; MUID:95021522	QY	902	FEGF
A; Status:	A:Accession: T286/7 Status: preliminary; translated from GB/EMBL/DDBJ	QQ	733	GNLF
A; Residue	e type: DNA 1 1 2 2 6 9 KBES SECTION TO THE SECTION OF THE SECTION	QY	926	HCFT
R; Keen, J	ererences: Embi-12/838; NID:945/145; FID:945/140; FIDN:AAA21304.1 .; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.	QQ	792	HDDD
A;Title:	Moi. Blocken. Parasitor. 42, 241-246, 1990 A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple cd	ΟŊ	1016	FRSG
A; Accessi	Af MacLetence number: A4351; MUID:91101000	QQ	843	SQNH
A; Molecul	A; Status: preliminary A; Molecule type: DNA A: Doctation: 0.101 0.000	QY	1043	LLLK
A; Cross-r	A;KcSIQUeS: Z131~Z209 <kez> A;Cross-references: GB:M34283</kez>	qq	900	:: VIKK
Z :	2 69. GOODS 104 5. DB 2. Tonneth	Qy	1100	CNNR
Best Lo	5 607	QQ	939	-NIL
Marches 0	Vallve ZIS; MISHBICKHES 430; INGELS 485; GB	Qy	1129	1 1
Cy 304 Db 34		qq	966	KSHK
"	AK SVÇDDBINIPTIFITINISC ÇDBDDI VIDDI BKFA ABBCBVI	Qy	1176	FDAF
		qa	1048	- E
•		Qy	1230	NHDN
	DEBAVEN	qq	1083	-IKN
	KKELEKNNATIDELANÇSPIKVIGILENKNILINILKSIFDQIYEGDIDIFINELSSIVK	QY	1285	N
	E-ILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYV	qq	1119	IKIN
	EDPIDDIE-DKTKLENLRSKIDNVYDKIQKMEIETVKSHLNNIETNNKLPNTILEIKKYI	Οy	1332	IIVK
0y 494	GSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSH 549	qa	1176	- -
Db 255	; YDEISKELNKMLEDFKNKEKELSNKISDYDKKREQL-SEYKSKMLEIRNHYNSQ 307	ò		KEEM
Qy 550)GRHNLSPAHSINQNVP	3 2		- 7
DP 308	TNVDNIKEEEBAKONYDKSNEHMITIPINEDEISKIISEVKIMKDEILSKVNIYIDFNKKY 367	200		T.A.V.
0у 578	ALMVWEKWGOFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAAN 637	RESULT	ULT 5	
Db 368		T286/b rhoptr	T28676 rhoptry pr	protei
Ov 638		S (C)		Pla -Oct
		C',	ccessio	
76E aa		R;S Mol	R;Sinha, K.A.; Mol. Biochem.	. A.; em.
Oy 686	5VGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEE- 734	A; T	itle: C	ompa
Db 453		A A	ccessio	
Qy 735		A;S	A; Status: prel A; Molecule typ	prei typ
Db 508		A A	esidues ross-re	: 1- fere
Qy 791	KVENSPEDYIFGY 814	R; K Mol	R;Keen, J.; H Mol. Biochem.	J.; Ho ochem.
Db 553		A;T	A;Title: Ident A:Reference nu	dent e nu
	THE PROPERTY OF A PROPERTY OF	A; A	A; Accession: A	n: A
UY 613 Db 613		A A Y	A;Molecule typ A;Molecule typ A;Residues: 22	typ: 22
Qy 850	KTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKL 901	A;C	A;Cross-refere	fere
Db 673		a	Query Match	tch

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SPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSA 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCQLHEFHTEGDNKLVGNISWRIK-----TLDSGFFTRSAVQKFVQDPNQPGVLY 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLP---- 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISI------IPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGER 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :||| :: | |:| |: ::::: : | EIRTKSDDCLKETNDLEKQISNLSIDTQETKLTEN--GKQLKTLEELLESLKKQK- 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIAN---PACAANVACLQT 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVEEIEEEVEKEVEKVGRTEMTLFQR-----LAEGFNELKQDEENFV---RELS 1381
                                                                                                                                      KKCHDKSK--NHKENISDIYDKSSKIIQDF-----SRESDINDIKNKLQKNVSE 842
                                                                                                                                                                                                                                         ------LKECRSKINSTLDDKDIDECIKNINVLKK 938
KELQRDEENFLRELSKEEM----DVLDGLKMEATEVEKLFGRALPIRKLMAV--AT 955
                             LE-QIDEEKKKAENTIKSMEAYIDDLDNIKKKSQEIETEMDIKMDINKEMEALKIS 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKSNGYKTEADQNKKAIQKNKELFEQYKEEVTVLLNKYYAVELKNK-----
                                                                                                                                                                                                         FS-----KGIFDIVPLPSKNELKEL----
                                                                                                                                                                                                                                                                                                                                                                                                                      PDETEC--QIKCGDLFENSVVDEFNEC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n - Plasmodium yoelii (fragment)
                                                                                                                                                                                                                                                                                                                                                                  IEGDLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFL 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :
Оні 1239
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issmodium yoelii 1-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000 128676; A45521 ; Keen, J.K.; Ogun, S.A.; Holder, A.A. Parasitol. 76, 329-332, 1996 arison of two members of a multigene family coding for high-molecular ma

iminary; translated from GB/EMBL/DDBJ e: DNA

ences: EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1 older, A.; Playfair, J.; Lockyer, M.; Lewis, A. Parasitol. 42, 241-246, 1990 t. Liffication of the gene for a Plasmodium yoelii rhoptry protein. Multiple number: A45521; MUID:91101660

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1227	Oy 983 KR Db 1281 KN	1043	1315	Oy 1086 ANI Db 1363 ISI	1122	1423	OY 11// DA. Db 1481 DN	Qy 1237 HY(Qy 1297 SI Db 1569	Oy 1348 VEI Db 1612 LN	RESULT 6 T38077 hypothetics	C;Species: Sc C;Date: 03-Da C;Accession: R;Connor, R.	submitted to A;Reference A;Accession: A;Status: pr	A; Molecule ty A; Residues: A; Cross-refel A; Experimenta	C;Genetics: A;Gene: SPDB A;Map positio	Query Matcl Best Local Matches 2	Qy 59 YK	119	Db 354 -	Qy 176 GDI	221
Best Local Similarity 16.7%; Pred. No. 0.21; Matches 260; Conservative 274; Mismatches 498; Indels 525; Gaps 71;	QY 23 PCNERFHRSGQPPTNIIMMKIRSNNGYFNSFRLFTSYKTSSFSDSSHCKDKSQICSID 80	Db 453 PPNEMKYQKPSIEIKIMKDEFLSKVNKYNDFDKVYKEKVESEHNKFTELTNKIKTE 508	QY 81 TSFEEIQRFDLKRGMTLILEKQMRQFIQLAIVLVCTFVIVPRVDAVDALKTCACLLKECR 140	OY 141 IELAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFENSVVD 185 DD 556 LNFNELTYNCHNKOLTIKDK.NONIKTIKEFNSIDKIYTDKENITED 603	186 QFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWY	: : : : : : Db 604 KKTELETKFTGLSLNNHESNNKELLTYFYDLKANLGKNKENMLYKQFNEKEKAVE 658	QY 230 ITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPGAL 289 : :: :	-SQIENKPDDYIFVYYRGRNDAWD :: : : LNEIKEKLKDYDFODF	GYGGSVIXTRSPTLPESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEG	QY 391 EKLLIKEAVEIEBEVEKEVEKVROTEMTLRQRLLEGFKELQQDEEN 436 : : : : : : : :	QY 437FVRELSKEEKEILNELQMEATEVEKLFGRALPIRK 471 1 :: : : : : : :	QY 472 LRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAK 518 ::	QY 519 ICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVA 578	QY 579 LAVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISN 631	QY 632 -PACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSD 685	QY 686 VGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRI 745	OY 746 RIPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYK 805	806 GRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERL		QY 866 EKKVEBGERTIKEVEBIBEBEVEKVRDKEVTLFSKLFEGFKELQRDEBNFLRELSKEEMD 925 Db 1100 IFFER STANDARM PROGRAMMETER STANDARM PARKET ST	. 926 VLD-GLKMEATEVEKLEGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITR
	J	Ц	о п	O D	a	Д	<u> </u>	<u> </u>	G D	O D	о п	G D	3 4	σд	σд	σд	0 0	. 0		0	

qq	1227	ILDIQLSVEPFKIKFLKIKDLRTKSDDCLKETKDIETKISNLSIDTQETKL-IEN 1280
Óγ	983	KRINGTFLLKILPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAP 1042
QQ	1281	KNILNT-LEKLLESLKNQKKNIEDQKKELDEVNSK 1314
Qy	1043	LLLKLVGVLACAFL
Dp	1315	IKNIESNVNQHKKNYEIGIVEKINE
ΟŶ	1086	ANPACAANVACLQTCNNRPD-ETECQIKCGDLFENSV :
qq	1363	ISPFKANDLEGIDTNKNLGKYNTEMNNIYEEFIKSYDLITHYLETVSKEPITYEQIKNKR 1422
Øγ	1122	
QQ	1423	ITAQNELLTNIKNVNKAKSYLDDIEANEFDRIVTHFKNKLNDVNDKFTNEYSKVNKGF 1480
Qy	1177	DAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYL 1236
qq	1481	LNQTKE
Qy	1237	HYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAK 1296
QQ	1523	YEAENIFINIPK
Qy	1297	KTDNTCGPEPALVE
qq	1569	DTLTFIPSPEKTSETYTKISDSYNTLLDILKRSQELQKKEQQA 1611
Qy	1348	VEKVGRTEMTLFORLAEGENELKODEENFVRELSKEEMEFLDEIKMEASEVEKL 1401 ::: : : ::: ::: : :::
3	7101	
RES T38 hyp	RESULT (138077) hypothetic	omyces pomb
1;C	Date: 0. Accessic	nge 03-Dec-
R;C Sub	Connor, omitted	R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. to the EMBL Data Library, April 1996 Se number, 791747
A A	Accessic tatus:	on: 138077 preliminary; translated from GB/EMBL/DDBJ
A A	folecule Residues	E type: DNA 5: 1-1957 <con></con>
∀ •	ross-re	eferences: EMBL:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
, O &	C;Genetics: A;Gene: SPD	S: S: PDB:SPACIF3:06c
A;	A; Map posi	position: 1
ОЩΣ	Query Match Best Local S Matches 265	Match 2.1%; Score 158.5; DB 2; Length 1957; Local Similarity 17.6%; Pred. No. 0.54; Les 265; Conservative 227; Mismatches 503; Indels 511; Gaps 68;
Οy	59	
qq	305	HWANYSDAIVHKDK-LIEDLSTRISEFDNLKSERDTLSIKNEKLEKLLR 353
Qy	119	IVPRYDAVDALK TCACLLKECRIELAKCIANPSCAANVACLQTCUNRPDETECQIKC 175
οg	354	NTIGSLKDSRTSNSQLEEEMVELKESNRTHHSQLTDAESKLSS 396
Qy	176	GDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVQNFN 220
qa	397	ONNLSSKDKMVKQVSSQLEEARSSLAHATG
Οy	221	MKDFSGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDG-GFFTRSAV 276

qq ,	457 IKDFE	KIEQDLRACLNSSSNELKEKSALIDKKDQELNNLREQIKEQKKVSESTQSSL 51	13
δy	277 QTF	OTEVODPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSV 336	36
qu .	514 QSL	QSLQRDILNEKKKHEVYESQLNELKGELQTE544	4 4
ογ	337 IYT	IYTRSPTLPESIIPNLQKAAKSVGRDFNNPITTDNSCGPEPPLVERLEKTAEEGEKLLIK 396	96
qa	545	ISNSEHLSSQLSTLAAEKEAAVATNNELSESKNSLQT 581	81
Qy	397 EAV	EAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILN 450	20
QΩ	582 LCN	LCNAFQEKLAKSVMQLKENEQNFSSLDTSFKKLNESHQELENNHQTITKQL-KDTSSKLQ 640	40
οy	451 ELQ	ELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGS 495	95
qq	641 QLQ	: :	95
Qy	496 KLP	55	52
Ор	969		56
δŏ		ALMVWEKWGOF	02
වූ	727 ETL	ETLEAQRNDLHSSLSDAKNTNAILSSELTKSSEDVKRLTANVETLTQD 774	74
δ		DAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIK 656	26
q	775 SKA	SKAMKQSFTSLVNSYQSISNLYHELRDDHVNMQSQNNTLLESESKLK 821	21
Qy	657 C(-CGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDP 694	94
qq	822 TDC	TDCENLTQONWTLIDNVQKLMHKHVNQESKVSELKEVNGKLSLDLKNLRSSLNVAISDND 881	91
δλ	178 S69	SVLVQKFDM-KDFSGKWFIIRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIR 746	46
QQ	882 QIL	QILTQLAELSKNYDSLEQESAQLNSGLKSLEAEKQLLHTENEELHIRLDKLTGKLK 937	37
δλ	747 TPD	z	90
qq	938		9/
Qy	807 RND	RNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLE 866	99
qq	977 KLDE	ETLSKSSKL-EADIEHLKNKVSEVERNALLASNERLM 1017	517
δy	867 KKVI	KKVE-EGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQRD 911	11
qq	1018 DDL	::	071
δy	912 EENI	EENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHC 957	57
q	: . 1072 KTN(: : : : : : :	124
δy	958 FTS	FTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD 1001	001
qq	1125 -SKI	SKKQHDLCANFVDDLKEKSDALEQLTNEKNELIVSLEQSNSNNEALVEERSDLANKLSD 118:	183
ΟY	1002 LRT	LRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSA 1061	191
qq	1184 MKKS	ii i l	902
Óγ	1062 DAVI	DAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSV 1121	121
qq	1207 DEL	: DELDTLK	240
οy	1122 VDE	VDEFNECAVS-RKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYIT-SGLNPTFD 1177	177
qq	1241 EESI	EESFNKYAVSLRELCTKSEIDVPVSEILDDNFVFNAGNFSELSRLTVLSLENYLD 129	295
δλ	1178 AFD	LVGNI	237
q	1296 AFN		330

Oy 4	1238 YQDDWYILSSKI 1331 EUDDWII	29
8 6		
QQ	:: 1349 SEKNF	LRKEAEMTENIH-SLEEGKEETKKEIAELSSRLEDNQLATNKLKNQ 1398
ΟŸ	1346KEVE	- KEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEA 1395
qq	1399 LDHLNQEIRLKE	LDHLNQEIRLKEDVLKEKESLIISLEESLSNQRQKESSLLDAKNELEHMLDDTSRKNS 1456
Qγ	1396 SEVEKL 1401	
qq	1457 SLMEKI 1462	
RESU T308	ULT 7 822	,
Lmp. C; Sp	d protein - Mycopla pecies: Mycoplasma ate: 22-0ct-1999 #e	sme hominis Abominis revision 22-00+-1000 #+00+ phenso 07-noc-1000
C; Ac R; Je	ccession: T30822 ensen, L.T.; Ladefo	evision is our issuericamente of bec issue Birkelund, S.; Christiansen, G.
Infe A;Ti	ect. Immun. 63, 333 itle: Selection of eference number: 71	995 a hominis PG: D.95369882
A; Ac	ccession: T30822 tatus: preliminary;	translated from GB/EMBL/DDBJ
A; Re A; Re A; Cr C; Ge	A; Molecule type: DNA A; Residues: 1.1365 <jen> A; Cross-references: EMBL:U21962 C; Genetics: A; Gene: lmp1</jen>	N> BL:U21962; NID:G790243; PID:G790244; PIDN:AAA81013.1
A; Ge	enetic code: SGC3	
n O R	Query Match Best Local Similarity 16.8 Matches 200. Conservative	18; Score 156; DB.2; Length 1365; 38; Pred. No. 0.46; 18. Missian Ann. Tadala 220. Cana
Å0		DLPGALYNEDNEFLHYODDWYILSGOIENKPDDYIEVYYRGRNDAWDG 331
qa		
Qy	332 YGGSVIYTRSPT	YGGSVIYTRSPTLPESII-PNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEK 385
qq	320 SNKSDIESANTE	SNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVSNANTLSA 369
Qy	386 TAEEGEKLLIKE	TAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFORLLEGFKELOODEENFVREL 441
qq	370 KLTDKDNTIQQA	KLTDKDNTIQQAKTELEKEVQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETF 425
QY	442 SKEEKEILNELQ	SKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHK 501
qq	۰ ۵	2TRNQIQEF 446
Qy	502 RFSWGWEDYFGS	RFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHS-I 560
qq	447	INTNKNNPNYSELISQLTSKRDSKNSVTDSSNKSDIESA
ΟŊ	561 NQNVPKGNSGCK	NQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKE 620
qq	490 KOALAKAN	DNLAKS 509
ΟŊ	621 CRLELAKCISNP	CRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCV 680
QQ	510 IKEQLNNSVSN-	ANTLSAKLTDKDNTIQQAKTE 541
ΟŊ	681 PRKSDVGDFPVPI I	PRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEBNK 736
qq	542 LEKE	VQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETFNKDKEA 588

in the

27;

C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

ΛĊ	737		196
_ q ₀	589	KFNELKQTRNQIQEFININKNDPNYSELISQLTSKRDS 6	626
δλ	797	EDYIFVYXKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIK 8:	850
QQ	627		676
δý	851	LVERLEKKVEGGRRTIKEVEEIEEEVEKVRDKEVTLF : : : : : : :	868
Ор	677		726
δλ	899	GRALPIRKLMAVAT	955
QQ	727	727 AKVAEITKKLETFNKDKEAKFNELKQIRNQIQEFINTNK7	765
δy	926	HCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRS	1009
qq	166	: : : : : : : : : : : : : : : : : : :	814
οy	1010		1049
οp	815	SSIDNELRPLKNDLQSKIEEFGPIRNTNFSWISSKLETTKNKLAEELT 8	862
οy	1050	VLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCN	1101
qq	863		206
٥y	1102		1155
Db	806	SNIGYRLFKLAQAEQFNNSDVDKLKNAWEEKQTLLSKKQKLGNQSTKDYLTQLSTEMSTQ 9	296
οy	1156	NFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTR-	1212
Db	896	ESTIKKVIVNIQAHIRNNLNSQYRLEAD-KLIAN	1009
οy	1213	SAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRN	1265
QD	1010	GIESLQKW-QDLMDDSVLSVDDSLKDDFNKALRVLVGDYTKNPPVSSWFINKRNRS	1064
δy	1266	-DAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGR	1300
Ob	1065	I ENYQNERNETELVRENETELDEAKDEDERRAEKTIKFVDENINSLDQRAKREKQETENAKN	1124
Qγ	1301	DESTFIRVEBIEEEVEKIEKTVEEGERIIVKEVEBIEEEVEKEV	1348
qq	1125	DLSNFTLNHQKNQFTAKDITPKISLLENKLNEINQYLLPIIKEKAVSKISEIEKN-KKEL	1183
οy	1349	EKVGRTEMTLFORLAEGFNELKODEBNFVRELSKEEMEFLDEIKME 1394	
QQ	1184	1184 EDIIRSNFYLWEKVEINKYISELTNKQVELRSNINFE 1220	
PESITLE	£.	a	

conserved hypothetical protein AF1032 - Archaeoglobus fulgidus
C.Species: Archaeoglobus fulgidus
C.Species: Archaeoglobus fulgidus
C.Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C.Accession: H69378
R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A.Reference number: A69250; MUID:98049343
A.Reference number: A69250; MUID:98049343
A.Accession: H69378
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Status: Drall A.Sesidues: Lase A.Sesidues: 1-886 (KLE>
A.Cross-references: GB:AE001032; GB:AE000782; NID:92689355; PIDN:AAB90211.1; PID:9264956

reficulocyte-binding protein 1 - Plasmodium vivax
C.Species: Plasmodium vivax
C.Species: Plasmodium vivax
C.Species: Plasmodium vivax
C.Species: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C.Accession: A42771
B.Galinski, M.R.: Medina, C.C.: Ingravallo, P.: Barnwell, J.W.
B.Galinski, M.R.: Medina, C.C.: Ingravallo, P.: Barnwell, J.W.
A.R.: Medina, C.C.: Ingravallo, P.: Barnwell, J.W.
A.R.: Mediculocyte-binding protein complex of Plasmodium vivax merozoites.
A.R.: A.A.Ccession: A42771
A.A.Ccession: A42771
A.R.: Medicule type: DNA
A.M.: Medicule type: DNA
A.M.: Medicule type: DNA
A.R.: Medicule type: DNA
A.R.: Medicule type: Balem strain, merozoites
A.R.: Medicule type: Balem strain, merozoites
A.R.: Medicule type: Balem strain, merozoites
A.R.: Medicule type: DNA
A.R.: Medicule type: Balem strain, merozoites
A.R.: Medicule type: DNA
A.R.: Medicule type: Balem strain, merozoites
A.R.: Medicule type: DNA
A.R.: Me -----DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYN-- 1230 1289 PELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEV 1348 968 FFSSDDGIGRLGITRKRINGTFLLKILPPIQSA--DLRTTGGRSSRPLSAFRSGFSKGIF 1025 1026 DIVPLPSKNELKELTAPL------LLKLVGVLACAFLIVPSADAVDALKTC 1070 1071 ACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130 1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190 1231 --HDNEYLHYQDDWY1LSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSII 1288 1349 EKVGRTEMTLFQRLAEGFN---ELKQDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKA 1405 512 SSHDAE-----KLSAESEE----YRKVKERLDGLRGQQKILLSSA---SRI 550 594 ------QSLRPFYNKWLELKDAESRLESELKRRE-KLEDEISEAIAKLEEANGKA 641 330 D-----TLKPKMDRMQGIK-- 372 ----AKLEEKNLTPDKVE---KMYDLLSKAKEEE-KEITE 404 405 KLKKLIAKKSSLKTRGAQLKKAVEE-----LKSAERTCPVCGRELDEEHRKN 451 452 IMAEYTREMKRIAEELAKADEIEKKLKERLEKVEKALEKQETVLKYROMVDELKALENEL 511 551 KELKSSLREI-------EEAL-KNVESERGELHRKIREEGFESLEELEREV 593 -----SILEKLLSEINQALRDVEKREGDLTREAAGIQAQLKKAEE 329 797 EDYIFVYYKGRNDAWDGYGGSV--LYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTD-N 853 854 TCGPEPPLVERLEKKVEEGERTI ---IKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQR 910 911 DEENFLRELSKEEMDV---LDGLKMEATEVEKLFGRALPIRKIMAVATHCFTSPCHDRIR 967 152 EDY-----ENAWKNLGAVIRMLEREKERLKEFLSQEEQIKROKEEK-----KAEIE 197 85; Mismatches 221; Indels 221; Gaps Length 886; Query Match 2.1%; Score 155.5; DB 2; Best Local Similarity 20.6%; Pred. No. 0.27; Matches 137; Conservative 85; Mismatches 221; 1406 LPIR 1409 642 EEIR 645 373 ----1191 RESULT A42771 g g pp Qy qq qq qq q ò g δλ g QΥ δ qq δy g QΥ δy δ Qγ

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Application of the EMBL Data Library, January 1992
A; Description: Primary structure of the herpesvirus saimiri genome.
A; Reference number: A36806
A; Accession: H36812
A; Molecule type: DNA
A; Residues: 1-2469 - AALB>
A; Residues: 1-2469 - AALB>
A; Cross-references: GB:X64346; NID:g60320; PIDN:CAA45687.1; PID:g60385
B; Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; J. Virol. 66, 5047-5084, 1992
A; Title: Primary structure of the herpesvirus saimiri genome.
A; Reference number: A37309; MUID:9233588
A; Contents: annotation; protein-coding frames
A; Note: neither protein nor nucleotide sequence is given
C; Genetics: A; Reference is given
A; Genetics: A; Reference is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: saimiriine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
C;Accession: H36812
R;Albrecht, J.
                                                                                                                                                                                                                               995 PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNE----LKELTAPLLLKLVGV 1050
                                                                                                                                                                                                                                                                                                                                               1051 LACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2313 SVNDHMHSMEAEMIKNGLKYTPESVQNINNIYSVIEAEVKTLEEIDRDYGDNYQIVEEHK 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1302 --FSTFIRTDNTCGPEPALVERIEKTVEEGE----RIIVKEVEEIEEEVEKEVEKV--GR 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2373 KQFSILIDRTN-----ALMDDIEIFKKENNYNLMEVNTETIHRVNDYIEKITNKLVQAK 2426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1354 TE-----EFLDE 1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2427 TEYEQILENIKQNDDMLQNIFLKKVSIIEYFENVKKKKESILNDLYEQERLLKIGEHLDE 2486
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1111 IKCGDLFE--NSVVDEFNECAVSRKKCVPRKSDLG-EFPAPDPSVLVQNFNISDFNGKWY 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1168 ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGV 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1268 ------WDGYGGAVVYTRSSV--LPN--SIIPELEKAAKSIGRD------ 1301
                                                                                                                                                                      2041 -ELENL-----KKMVTIY-----RDKKSERESGLQEM---ENEMN-TYSNSI- 2077
881 EEIEEEVEKVRDKEVTLFSKLFEGFKELQRDE-----ENFLRELSKEEMDVLDGLKMEA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                         2253 LYDKLNEEKREMDELYRNISETKLKQMEHSTDVFKPMIELHKGMNETNNKSLLEKEKKLK
                                                                                                                                                                                                                                                                   2078 --TQLEGIVVSAGESKE------DIEKLERSNEEMRNISEKISTIDSK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     935 TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1%; Score 155; DB 2; Length 2469;
Best Local Similarity 17.3%; Pred. No. 1.2;
Matches 230; Conservative 208; Mismatches 497; Indels 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ORF64 – saimiriine herpesvirus 1 (strain 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1228 LYNHDNEYLHYQDDWYILSSKIENKPEDY-----IFVYYRGRNDA----
                                                   1992 NEFNEKLEEAKNKEEVVSEKVREALKRLSQVEGIRCHFENFHRLLDNTE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1391 IKMEASE 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2487 IKRNVTE 2493
                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                  QQ
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Wed Nov 7 09:24:00 2001

	0y 1:	1207	SGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYY 1261
		1083	: ; ; ;:
-	Qy 1:	1262	RGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAK 1296
-	Db 1.	1125	: : : : : :
		1297	SIGRDFSTFIRTDNT-CGPEPALVERIEKTVEEGERIIVKEV 1337 :+ : : : : : : :
-	Dp 1	1185	NIGHELSILSQALNSKTLPEAVVGTSLEQHAAKFSCMFKTLEATWHDHQVDTRTKIDEYI 1244
		1338	
	Dp 13	1245	
	Qy 1:	1389	DEIKMEASEVE 1399
	Db 1:	1305	- ENTVKAAELQ 1314
	RESULT	11	
	repeat	org	anellar protein – Plasmodium chabaudi Dlasmodium chabandi
	C; Date	15	-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
	R; Wern	er,	E.B., Taylor, W.R.; Holder, A.A.
	A; Titl	e: A	Farasitol. 94, 183-196, 1998 Plasmodium chabaudi protein contains a repetitive region with a predicted processing and predicted and predicted and predicted are predicted as a predicted and predicted are predicted as a predicted are predicted as
	A; kere A; Acce	ssic	e number: 218922; MULD:98418/65 n: T18372
	A;Stat: A;Mole	us: cule	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DBP A; Docidinor, 1-10-10, American
	A; Cros	s-re	i 1353 NMEAN TERBL:U43145; NID:gl151157; PID:gl151158; PIDN:AAC63403.1
	Quer; Best	y Ma Loc	Query Match 2.0%; Score 151; DB 2; Length 1939; Best Local Similarity 17.5%; Pred. No. 1.5;
	Matci	hes	vative 167; Mismatc
	δλ	380	VERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRILEGFKELQQDEEN 436
	qq	95	VKEYEVKIEBLEKELKLEKEKQINKEYEKELNEKSEFIKRQMELLKEKELNINLKEN 151
	, YO	437	FVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHE 487
	qq	152	KINNKEIITLKREEKLNDIESEYIEKNKEKEKLNYEVTNIKMSLD 196
	, ко	488	TIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLF 547
-	q a	197	KLTCEVQEKKDNLEKINKKVIEKENNLRELKEFMKEKNEIIESLDG 242
	δλ	548	SHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADA 607
	qq	243	TINDKKNAYEKLEISFEEKKM 264
	. Qy	809	VDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVD 667
	qq	265	IEMLDSKLIEKEENFAN
	Oy (668	EFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQL 727
	qa	288	KENEIIIEKLKDIESREKDFKSKEEKFASMENEL 321
	δλ	728	HEFHTEENKLYGNLS-WRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWY 786
	qq	322	- >
	δλ	787	ILSSKVENSPEDVIEVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN 846
_	qq	366	KINNMKEKLSSINDKGIDNTVLHSEEKI-NKLLKEKETELNEIHKKYN 413

δλ	847 TFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVT 896	0y
qq	414 LEIETIKNELNEKEEELEKNKKAHTVEVTNLTKEIK 449	qa
Οÿ	897 LFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMA 952	QY
q	450 LLEKKTEDAKEGHKNELNELNNQLSKLNKEKDNIKNENTEL 490	qa
δλ	953 VATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRP 1012	δδ
qq	491NDKISSLNSEVNILNKDKQTLG 512	q _Q
δλ	1013 ISAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCAC 1072	0λ
Op	513DLINNLKN 527	q _Q
δλ	1073 LLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVD 1123	QY
qa	528VID 558	qa
δλ	1124 EFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTF 1176	δō
QQ	559 BIEKKYKNEIFMLEEKLKEKENYADLNDEISILRNSIYVKEKEFI 603	q _Q
Οy	1177 DAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDN 1233	QY
qq	604EMKEFYENKINLFNKNFEEKKNIYENELNSLELKYDNEQ 642	qa
δλ	1234 EYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEK 1293	QY
qq	643 GLIKQIDELNIQKLKTEEKYLQLYNDN	qa
δλ	1294 AAKSIGRDFST-FIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEVEK 1350	QY
qq	688 IKGSDLVDFVTAYIKRRDESSSDANPDTTHKEMVAELEKRHAAIVAELEEKHKEEIAK 745	q _C
οy	1351 VGRTEMTLFQRLABGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEKLFG 1403	QY
qq	746 LGEGHKEVVLRLGEQHKEFTIILEEKHKDVYRKLGEQHKENIIKLEEEHKDVVTKLG 802	q _O
RESUI	12	Qy
A5928	5 1 heavy chain beta chain, cardiac - nig	qa
C; Spe C; Dat	C;Species: Sus screfa domestica (domestic pig) C;Date: 09-Jun-2000 #sequence revision 09-Jun-2000 #text change 08-Sen-2000	QY
C; Acc	X.L.	අය
subm	tted to Genbank, October 1996 prence number: A59286	οy
A; Acc A; Sta	ession: A59286 tus: preliminary; not compared with conceptual translation	ପ୍
A; Mol	Molecule type: mRNA Residues: 1-1915 < Mol>	Oy
A; Crc	Cross-references: GEU75316; NID:g1698894; PIDN:AAB37320.1; PID:g1698895 Experimental source: strain domestica	qa
C; Sup	Superfamily: myosin heavy chair; myosin motor domain homology Kewwords: cardiac muscle, heart	QY
F; 88-	88-766/Domain: myosin motor domain homology <mmo></mmo>	q _Q
Эnŏ	2.08;	ογ
Bes	Similarity 16.7%; Pred. No. 2; 8; Conservative 220; Mismatches 555; Indels	qa
οy	/SRKKCVPRKSDVGEFPVPDRNAV	QY
Q	: ::: : 375 PDGTEEADKSAYLMGLNSADLIKGLCHPRVKVGNEYVTKGQNVQQVMYATGALA 428	ପ୍ର
οy	217 ONFWAKDFSGKWYITSGLNPTFDAFDCQLHEFHMENDKL 255	δo d
QQ	429 KAVYEKMENWAVTR-INTTLETKQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKL 485	g

Oy Ph	256	VGNLTWRIKTLDGGFFTRSAVQTFV 2 VGNLTWRIKTLDGGFFTRSAVQTFV 2 VGNLTWBFTDEPOWDEN S	280
3		GMD LYAC TO LIER FROM THE LEE BOME FOR	
QY	QY 281 QDPDLPGALY-NHDNEFLHYQDDWYILSSQ : : Db 544 TDMTFKAKLYDNHLGKSNNFQKPRN	LSSQIENKPD-DYIFVYYRGRNDAWDGYGG 3 : : : -PRNIKGRPEAHFALIHYAGTVDYNIIGW 5	34
δλ	335 SVIYTRSPTLPESIIPNLQKAA-K	SVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKL 3	93
οp	594 LOKNKDPLNETVVDLY	AGADTP-VEKGKGKAKKGSSF	644
οy	394	LIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKE 4	47
οp	Db 645 QTVSALH-RENLNKLMTNLRST		685
Oγ	OY 448ILNELOMEAT-EVEKLFGRALP	IRKLRMALAPHSNFLANHETIKYY 4	92
qq	989	NPLVMHQLRCNGVLEGIRICRKGFPNRILYGDFRQRYRILNPAAIPEGQFIDSRKGAEKL 7.	45
δŏ	493	VGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKH 5	52
qq	746 LGSLDIDHNQYKFGHTKVF	FKAGLLGLLEEMRDERLSRIITRIQAQSRGVLSRMEFKK 8	803
ΟŊ	553 NLSPAHS	INQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVD 6	609
Ор	Db 804 LLERRDSLLIIQWNIR	AFMSVKNW-PWMKLYFKIKPLLESAETEKEMA 8	20
Οy	Qy 610 ALKTCTCLLKECRLELAKCI:	SNPACAANVACLQTCNNRPDETECQIKCGDLFE	662
qq	851 TMKEEFGRLKEALEKSEA	RRKELEEKMVSLLQEKNDLQLQVQAEQDNLSDSEERCDQLIK 91	10
QY	VSN E99	FD 7	02
QQ	911 NKI	OLEAKVKEMTERLEDEEEMNAELTAKKRNVEDECSELKRDIDDLELTLAKVEKEK- 9	99
οy	703 MKDF	SGKWFITRGLNPTFDAFDCQLHEFHTBENKLVGNLSWRIRTPDGGFFTRSAVQKFV 7.	62
qq	696 qq	HATENK-VKNLTEEMAGLDEIIAKLT 9	93
δλ	763 QDPKYPGILYNHDNEYLLYQDDWY	ILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTR 8:	822
qq	Db 994 KEKKALQEAHQQALDDLQAEEDKVNTLTKAKVKLEQHV	DDLAGSLEQEK	104
QY	823 SAVLPESII	PELQTAAQKVGRDFNTFIKTDNTCGP 8	857
qq	Db 1043 KVRMDLERAKRKLEGDLKLTQESIMDLENDKQQLDERLKKKDFELNALNARI		10
οy	858 EPPLVERLEKKVE		83
QQ	1103 QLQKKLKELQARIEELEEEL-	EAERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQI 1:	16.
οy	068	VRDKEVILFSKLFEGFKELQRDEENFLREL 91	19
QQ	1162	:	22
QY	920 S	OIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLG 97	79
Dp	Db 1222 SEFKLELDDVTSNMEQIIKAKANLEKM	CRTLEDQMNEHRSKAE 1	76,
οy	QY 980 ITRKRINGTFLLKILPPIQSADLRTTGGRSSRPL	SAFRSGFSKGIFDIVPLPSKNEL 1	03(
Dp	Db 1265 ETQRSVNDLTSQRAKLQTENGELSRQL	DEKEALISQLTRGKLTYTQQL 1	31.
ΟY	1037	PACAANVAC 1	960
QQ	Db 1313 EDLKROLEEEVKAKNALAHALQSARHAADLLREQYEEETETKAELQRYLSK	ANSEVAQ 1	37(
ΟŻ	1097	LQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDFSVLVQN 11	156
g	Dh 1371 WPT	-KYETDATORTELERAKKKI AORIODARE1	40,

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R;Saez, L.J.; Gianola, K.M.; McNally, E.M.; Feghali, R.; Eddy, R.; Shows, T.B.; Leinw Nucleic Acids Res. 15, 5443-5459, 1987
A;Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
A;Reference number: A93669; MUID:87260010
A;Accession: A27858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Construction of a human ventricular cDNA library and characterization of a b A;Reference number: S02229; MUID:87192738
A;Accession: S02229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amp position: 14912-14912
A; Introns: 67/3; 115/3; 168/1; 1548/3; 266/1; 299/1; 333/3; 380/1; 419/3
A; Introns: 67/3; 115/3; 168/1; 1548/3; 1719/3; 1761/3; 1853/3; 1865/3; 1930/3
24/3; 1390/2; 1507/1; 1548/3; 1651/3; 1719/3; 1761/3; 1853/3; 1865/3; 1930/3
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
F; 88-766/Domain: myosin motor domain homology < WMOT>
F; 88-766/Domain: myosin motor domain more domain more domain more domain more domain more domain more domain motif A (F-loop)
F; 848-586/Region: actin binding #status predicted
F; 655-677/Region: actin binding #status predicted
                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1854-1865, A, 1867-1935 <SAE>
A; Residues: 1854-1865, A, 1867-1935 <SAE>
A; Cross-references: GB:X05631; GB:Y00362; NID:934643; PIDN:CAA29119.1; PID:934644
A; Cross-references: GB:X05631; GB:Y00362; NID:934643; FICHTER, P.; Vosberg, H.P.
Hum. Genet. 81, 214-220, 1999
A; Tille: Isolation and characterization of the complete human beta-myosin heavy chain
A; Reference number: 154254; MUID:89154425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: B23767
A; Molecule type: mRNA
A; Rolecule type: mRNA
A; Residues: 'LiGVGELASG', 1311-1312, 'G', 1314-1355,'R', 1357-1358,'GD', 1361-1438,'LQ', 14
A; Note: the first ten codons of the sequence figure show the reverse complementary st
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
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A;Residues: 1393-1702, DR, 1705-1935 <JAN>
A;Cross-references: EMBL:X06976; NID:934860; PIDN:CAA30039.1; PID:9825694
R;Saez, L.; Leinwand, L.A.
Nucleic Acids Res. 14, 2931-2969, 1986
Nucleic Acids Res. 14, 2931-2969, 1986
A;Fitle: Characterization of diverse forms of myosin heavy chain expressed in adult la. A;Reference number: A93616; MUID:86176778
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F;1297/Modified site: N6.N6.N6-rimeUnyllysine (Lys) #status predicted
F:184/Rinding site: ATP (Lys) #status predicted
F;695,705/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.9%; Score 146; DB 1; Length 1935; Best Local Similarity 16.9%; Pred. No. 2.9; Matches 238; Conservative 207; Mismatches 529; Indels 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;839-1935/Domain: coiled coil #status predicted <COI>F;839-1279/Region: S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GDB:120215; OMIM:160760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MayJulus myosin beta heavy chain, cardiac and skeletal muscle - human Nocontains myosin ATPR28 (EC 3.6.1.32)

N.Contains: myosin ATPR28 (EC 3.6.1.32)
C.Species: Homo saplens (man)
R.Jadenicke, T.; Diederich, K.W.; Haas, W.; Schleich, J.; Lichter, P.; Pfordt, M.; Bach, A; Title: The complete sequence of the human beta-myosin heavy chain gene and a comparation of the luman beta-myosin heavy chain species: Homo saplens (GB: MG); Yamauchi: Takhara, K.; Kellam, B.; Anderson, D.H.; Lin, L.; Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross_references: GW_M11665

• A;Note: the authors translated the codon AGC for residue 108 as Arg
R;Lichter, P.; Umeda, P.K.; Levin, J.E.; Vosberg, H.P.
R;Lichter, P.; Umeda, P.K.; Levin, J.E.; Vosberg, H.P.
A;Title: Partial characterization of the human beta-myosin heavy-chain gene which is exp
A;Reference number: A24997; MUID:87030293
                                                                                                                                                                                                                                          1217 KFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVV 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1277 YTRSSVLPNSIIPELE-----KAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE 1330
                           1157 FNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQ 1216
                                                                                                                                      -----VERSNAA 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1478 STELFKLKNAYEESLEHLETSKRENKNLQEEISDLTEQLGSSGKTIHELEKVRKQLEAEK 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : :|| | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :|
                                                                                                                                                                                                                                                                                                                              1439 AAALDKKQ----RNFDKILAEWKQKYEESQSELESSQKE-------ARSL 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1331 RIIVKEVEELEEEVEKEVEKVGRTEMTLFQ-----RLAEGFNELKQDEENFVRELS-- 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KEEME-FLDEIKMEASEVEKLFGKA 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1598 QTSLDAETRSRNEALRVKKKMEGDLNEMEIQLSHANRMAAEA 1639
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A,Molecule type: mRNA
A,Residues: 1412-1518,'R',1520-1574,'NV',1577-1935 <KUR>
                                                                                                                                1403 -----AVEAVNAKCSSLEKTKHRLQNEIEDLMVD-----
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A;Residues: 682-721;975-1112;1854-1935 <LIC>
A;Cross-references: GB:X04627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A92770; MUID:88299163
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51;

DUGGEPUPDRNAVYQNFUMKDFSGKWYITSGLNPTFDAFDCQLHEP

qq	
QY	1171 GLNPTFDAFDCQLHEFHTEGDNKLYGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYN 1230
qq	
Qy	1231 HDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPE 1290
qq	1449 FDKILAEWKQKYEESQSELESSQKEARSLSTELFKLKNAYEES 1491
δ δ	1291 LEKAAKSIGRDESTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEV 1344
9	
Oy Dp	1345 EKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELS 1381 1 1 1 1 1 1 1 1 1 1
ò	KEEME-FIDEIKMEASEVEKIECKA 1405
G G	612 LRVKKKMEGDLNEMEIQLSHANRMABEA 163
RESULT	ULT 14
nuc. N;A	2017.70 nuclear migration protein NUM1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YD8358.06; protein YDR150w
ς Ω Ω	pecies: Saccharomyces cerevisiae ate: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
R.;A	
subi A; R	submitted to the EMBL Data Library, July 1995 A; Reference number: 557971
A X A	ccession: S5/9/6 General type: DNA Seiding: 1.2740 vmms
2 G 6	Solutes: 1-2/40 kmuk> TOSS-references: EMBL: 250046; NID:9899393; PID:9899399; MIPS:YDR150w
K X;	Aperimental Source: Strain Abs/1 Ormanec, J.; Schaptenschlaeger, I.; Zimmermann, F.K.; Perecko, D.; Kuentzel
A; R	tile: Nuclear migration in Saccharomyces cerevisiae is controlled by the highly re- afference number: S1905; MUID:92079907
A; Ac	Accession: S19052
A ; R.	A:Residues: 1-1569, V, 1571-1821, K', 1823-1959, RHL', 1963-1970, RN', 1973-2048, 'N', 205 A:Tross-references: WMI:X61236, NIP. A4071, PIRM. CAAA3564, 1. PIR. 2073
, o	MAT
A; C;	A.Cross-references: SGD:S0002557; MIPS:YDR150w A.Map position: 4R
QAR	Query Match 1.9%; Score 146; DB 2; Length 2748; Best Local Similarity 17.9%; Pred. No. 4.7; Matches 283; Conservative 232; Mismatches 781; Indels 486; Gans 72.
QY	DSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQF1QLAIVLVC 115
QQ	
Qy	116 TEVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDET 169
qq	801 LAYLVEHAKATDHHLLSDSAYEELVKCKENPDMEFLKEKSAKLGHTVVSNEAYSEL 856
Οy	SVVDQFN
qq	857 EKKLEQPSLAYLVEHAKATDHHLLSDSAYEDLVKCKENSDV-EF 899
Qy	216 VONFUMKDESGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSA 275
Op	900LKEKSAKLGHTVVSNEAYSELEKKLEQPSLAYLVEHAKATDHHLLSDSA 948

Oy 325 R OD 1003 Tr OY 364 - OY 364 - OY 409 - OY 409 - OY 7409 -	
364 1063 409 1123	TNHHII,SDSAYEDI,VKCKENPDMEFLKEKSAKLGHTVVSNEAYSELEKKLEOPSLEYLVE 1062
1063	
1123	HAKATNHHLLSDSAYEELVKCKENPDVEFLKEKSAKLGHTVVSNEAYSELEKKLEQPSLE 1122
1123	댐
	CEK
1179	RALPIRKLRWALAPHSNFLANHETIRXYVGSKLPGHKRFSWGWEDYFGSIVVAK
Oy 519 -	PRICC
Db 1218 E	EFLKEKSAKLGHTVVSNEAYSELEKKLEQPSLAYLVEHAKATDHHLLSDSA 1268
565	
Db 1269 Y	YEDLVKCKENPDMEFLK-EKSAKLGHTVVSNEAYSELEKKLEQPSLEYLVEHAKATNHHL 1327
Oy 618 I J Db 1328 I	LKECRLE-LAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFN 670 :
Qy 671 F	ECAVSRKKCVPRK-SDVGDFPVPDPSVLVQKEDMKDFSGKWFITRGLNPTFDAF 723
Db 1378 F	SKLOKLEY
Qy 724 [DCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQD-PKYPGILYN 773
Db 1436 I	SNFNSPILKFI
Qy 774 B	HDNBYLD 798
Db 1483 B	DLNRIATTPSKEEIDNFCKQIGCYALDSKEYERL
QY 799 1	QKVGRDFNTFI
Db 1543 I	LVLVDKTEYQAMKD 1576
856	ERTIIKEVEEIEEEVEVRDKEVTLFSKLFEGFKELQRD
Db 1577	-PAPQLASAEKSSLQKRTLSDIENELKALGYVAIRKENLPN 1616
	EENFLRELSKEEMRALPIR 948
Db 1617	LEKPIYDNASKNDVLNICSKFSLYPLSTEEYDNMRKEHTKILNILGDPSIDFLKEKCEKY 1676
Qy 949 I	GRLGIT
Db 1677 (QMLIISKHDYEEKQEAIENPGYEFILEKASALGYELVSEVELDRMKQMIDSPD 1729
Qy 1002	LRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSA 1061
Db 1730	ARNEMVLLRNEEKEALQKKIEYPSLTFLIEK
, Qy 1062	DAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCG 1114
Db 1771 (GMNKILVDQIEYDETIRKC1RKCNHPTRMELEESCH 1802
Qy 1115 1	DLFENSVVDEFNECAVSRKKCVPRK-SDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLN 1173
1174	NATOR THE TREE TREATMENT OF THE TREE TREET AND THE TREET A

qa	1856	
QY	1230	NHDNEYLHYQDDWYILSSKIENKPEDXIEVYYRGRNDAWDG 1270
QQ	1897	KAVLNNHILIKE
Qy	1271	AAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE 133
QQ	1951	HPTVIHLSEKASLLNKVLVDKDDFATMSRSIEKPTIDFLSTKALSMG- 1997
Qy	1331	80 1
QΩ	1998	KILVNESTHRRNEKLLSEPDSEFLTMKAKEQGLIIISEKEYSELRDQIDRPSLDVLKEKA 2057
δλ	1386	EFLDEIKMEASEVEKLFGKALP 1407
ΩD	2058	AIFDSIIVENIEYQQLVNTTSP 2079
RESULT	٦	iΩ
S54	174 topois	omerase (EC 5.99.1.2) - malaria parasite (Plasmodium falciparum)
	ate: 00	C;Date: 09-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jun-2000
R; TC	osh, K	nn. Solari T.; Kilbey, B.J.K. T. the PMRE Data Library. January 1995
A; De	escrip	tion: Isolation and characterisation of the topoimerase 1 gene from Plasmodi
A; R A; A	eferenc	e number: S54174 on: S54174
A;S;	tatus:	preliminary type: DNA
A; R	esidue	1-839 <tos></tos>
A;Cross-rere C;Superfamil C;Keywords:	ross-ru uperfar eyword:	rences: Embi.Acc/Jos; NAL'9/Yortor, FIU'9/Yortor, y: enkaryotic type I DNA topoisomerase DNA binding; DNA replication; isomerase
ć	Ouerv Match	.h 1.9%;
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i i	Ċ	
g G	4.4	. !
Qy	410	LFGRALPI 46
qq	79	SKRKSNELKEKNNLKEGKKKYVEKKSRTVKDETKLTNVIKKETQNNKKPK 128
Qy	470	RKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYF 529
Dp	129	KLLKKSEENFEPINRW-WEKIDDQTDIQWNY158
QY	530	GKHNLSPAHSINQNVPKGNS
QQ	159	: : : : : : :
QY	590	KTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKC:
Db	189	: :
Οy	650	ETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDV
qq	232	ENETKLKKGDISNFKFIDFMPIKDHLLKLREEKLNKTKEE 271
QY	704	KDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAV 758
qq	272	KEEEKKMRMEKELPYTYALVDWIREKISSNKAEPPGLFRGRGEHPKQGLLKKRIFPEDVV 331
Qy	759	QKFVQDPKYPG

₹	Op	332	332 INISKDAPVPRLYDNMCGHNWGDIYHDNKVTWLAYYKDSINDQIKYTFLS	381
	ΟŊ	807	RNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLV	862
•	Ор	382	AQSKFKGYKDLMKYENARKLKSCVHKIREDYKNKMKNKNIIDKQLGTAVYLI	433
	δλ	863	ERLEKKVEEGGRTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKE	922
	QQ	434	DFLALRV-GGEKDIDEEADTVGCCSLRVEHISFAHDIPFF	472
	ογ	923	EMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLG	616
	qq	473	SVDSKEQKTNDEKVNKIPLPTNLESISSEDCYITLDFLGKDSIRYFNT	520
	Qy	980		1038
	qq	521	VKIDKQAYINIIIFCKNKNRDEGVFDQITCSKLNEYKE	559
	οy	1039	LTAPLLLKLVGVLACAFLIVPSADAVDAL KTCACLLKGCRIELAKCIANPACAANVAC	1096
	qq	260	INPTLSARVERTYNASITLDQQLKRIKEVYGKTTYSLYSG-ETELHKSK	209
	Qγ	1097		1152
	qq	608	KRKSSHLTSDTNILSDASDSTINDVNNEYDENGINKKLSYATTVGKENDVDDKNSP-IEV	. 999
	Οy	1153	LVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTR	1212
	qq	199		703
	Óγ	1213	SAVQKFVQDPNQPGVLYNHD-NEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGY	1271
	Op	704	SKIKKQIELYNEDIKEYKKYLQHLKKNSDKKFIFV	738
	ογ	1272	GGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGER	1331
	qq	739	SKVSTLDGTLRPNKVKENMK	758
	δ	1332	IIVKEVEEIEEEVEKEVEKVGRTEMTLFORLAEGFNELKODEENFVRELSKEEMEFLDE-	1390
	QQ	759		802
	δy	1391	IKMEASEVEKLFGKALPIR 1409	
	qq	803	ITVAFCKKFEIPIEKVFNRSLRLK 826	

Search completed: November 6, 2001, 05:03:18 Job time: 6742 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

November 6, 2001, 05:14:41; Search time 67.97 Seconds (without alignments) 711.619 Million cell updates/sec Run on:

Perfect score: Title:

US-09-075-375A-4 7495 1 MALSLHTVFLCKBEALNLYA......MEASEVEKLFGKALPIRKVR 1412 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	r i	O10411 schizosacch	Q00798 plasmodium				Q00402 saccharomyc	_	Q12176 saccharomyc		P11533 gallus gail				P13540 mesocricetu	P15917 bacillus an		P47460 mycoplasma	P34529 caenorhabdi	Q13439 homo sapien		Q39565 chlamydomon		sndouax	074712 candida alb	-	P57235 buchnera ap	aquifex a		Q58445 methanococc	Q58357 methanococc	Q28178 bos taurus	Q03640 saccharomyc	P53804 homo sapien
SUMMARIES	ID	YD86_SCHPO	RBP1_PLAVB	TEGU_HSVSA	MYSB_PIG	MYSB_HUMAN	NUM1_YEAST	MYSB_RAT	MK21_YEAST	MLP1_YEAST	DMD_CHICK	MYSP_HUMAN	MSP1_PLAFK	MSP1_PLAFW	MYSB_MESAU	LEF_BACAN	YIO9_YEAST	HMW2_MYCGE	YM68_CAEEL	GOG4_HUMAN	USO1_YEAST	DYHB_CHLRE	NISB_LACLA	TANA_XENLA	HIS2_CANAL	POL1_GFLV	SYGB_BUCAI	METE_AQUAE	DMD_MOUSE	RPA1_METJA	SYI_METJA	TSP1_BOVIN	YMH2_YEAST	TTC3_HUMAN
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277 QTFVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSV 336

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SO		chizosaccha	romyces	qшod	_ 0	ission yeast).			
888		Eukaryota; Fungi; Ascomyc Schizosaccharomycetales; Schizosaccharomyces,	ingi; A romycet romyces	scomy ales;	Scl	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.	: SS		
X O		NCBI_TaxID=4896;	396;						
RP		SEQUENCE FROM	FROM N.A.						
R. R.	_	STRAIN=9/2; Connor R., Cl	9/2; R., Churcher	Ċ.₩.,		Barrell B.G., Rajandream M.A.,	n M.A., Walsh	sh S.V.;	
RL		red	PR-1996) to .	the		•		
888		This SWISS-PROT entry is	ROT ent	ry is	S	copyright. It is produced through	Ų,	collaboration	ion
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N OS		Hypothetical SEQUENCE 19	1957 AA;		785	222785 MW; 3F480CA06171D9DA CRC64	CRC64;		
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, o	Matches		Conservative	ative	,	255; Conservative 22/; Mismatches 503; Indels 511; G VKTSSFSDSSHOKDKSOTCSTDMSFERFTORFDIRECMMILITEROMBORIOLALVIVOMEN	Indels 511	1; Gaps	68;
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δλ qd		119 IVPRVDAVDALK- : : 354NTIGSLKD	1 0	-TCACI - STSNS	CLKE	CRIELAKCIANPSCAANVAC : :: EMVELKESN	LQTCNNRPDETECQIKC : :: :: :: :: :: :: ::	CQIKC 175	
!			1	1	1	No.	er terocent		
Οy		176 GDLFENSY	OGA/	FNECA	/SRF	GDLFENSVVDQFNECAVSRKKCVPRKSDVG	-VGEFPVPDRNAVVQNFN	VONEN 220	

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λ D	337	IYTRSPTLPESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIK : : : : : : : : : : :	396 581
οy	397		450
Op	582	LCNAFQEKLAKSVWQLKENEQNFSSLDTSFKKLNESHQELENNHQTTTKQL-KDTSSKLQ	640
QY Dh	451	ELOMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGS : :	495 695
3 8	1 20 4	VI DOUWDDOGGOUDDDADOCTUVANI TOCODI DDADDVODI TOCCI DISPANDADOGGOUDDDADOCU	5.7.5 5.7.5
<u>8</u>	969	ALFORNIA STANDARD STA	726
οy	553	NLSPAHSINQNVPKGNSGCKFP	602
Op	727	ETLEAQRNDLHSSLSDAKNTNAILSSELTKSSEDVKRLTANVETLTQD	774
δλ	603	SKADAVDALKTCTCLLKECRLELAKCISNPACAANV	929
οg	775	SKAMKQSF	821
δy	657	CGDLFENSVVDEFSDVGDFPVPDP	694
qq	822	TDCENLTQQNMTLIDNVQKLMHKHVNQESKVSELKEVNGKLSLDLKNLRSSLNVAISDND	881
ογ	695		746
qq	882	QILTQLAELSKNYDSLEQESAQLNSGLKSLEAEKQLLHTENEELHIRLDKLTGKLK	937
QY	747	TPDGGFFTRSAV	806
qq	938	IEESKSSDLGKKLTARQEEISNLKEENMSQSQAITSVKS	926
Qy	807	RNDAWDGYGG	998
qq	977	KLDETLSKSSKL-EADIEHLKNKVSEVEVERNALLASNERLM	1017
δý	867	KKVE-EGER	911
qq	1018	DDLKNNGENIASLQTEIEKKRAENDDLQSKLSVVSSEYENLLLISSQTNKSLE-D	1071
δλ	912	EENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHC	957
Ωp	1072	KTNQLKYIEKNVQKLLDEKDQRNVELEELTSKYGKLGEENAQIKDELLALRKK	1124
οy	958		1001
gg	1125	SKKQHDLCANFVDDLKEKSDALEQLTNEKNELIVSLEQSNSNNEALVEERSDLANRLSD	1183
οy	1002	LRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSA	1061
qq	1184	:::	1206
Οy	1062	DAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSV	1121
QQ	1207	DELDTLKKDKDSLSTQYSEVCQDRDDLLDSLKGC	1240
δy	1122		1177
g.	1241		1295
οy	1178		1237
Q	1296	AFN-QVNFKKMELDNEKLTTTDAEFTKVVADLEKLQH	1330
δy	1238	YQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSI 	1297
qq	1331	EHDDWLIDLEKALKD	1348

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS.
-!- SUBUNIT: HOMODIMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1349 SEKNF------LRKEAEMTENIH-SLEEGKEETKKEIAELSSRLEDNQLATNKLKNQ 1398
                                                           ----KEV---EKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFL--DEIKMEA 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 IVLVCIFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 CQIKCGDLFE--NSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNA---VVQNFNM-KDF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 TSYKTSSFSDSSHCKDKSQICSIDTSFEEI-----QRFDLKRGMTLILEKQWRQFIQLA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1150 TSNKNEILKSVKEVEDKLNLVEQNEDYKKVKNPENEKQLEAIRGSMSKLKE------
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CELL ATTACHMENT SITE (POTENTIAL).
330213 MW; B9DBE442205EBGFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 2869;
                                                                                                                                                                                                                                                                                                                                                     Plasmodium vivax (strain Belem).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
RETICULOCYTE BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.: "A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 155.5; DB 1; Length 2 llarity 17.4%; Pred. No. 0.86; Conservative 242; Mismatches 573; Indels
1298 IGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIBEEVE---
                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
RETYCULOCYTE BINDING PROTEIN 1 PRECURSOR.
                                                                                                                                                                                                                                      2869 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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MEDLINE=92315338; Pubmed=1617731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M88097; AAA29743.1; -. HSSP; P36956; 1AM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  merozoites.";
Cell 69:1213-1226(1992).
                                                                                                                                                                                                                                         STANDARD;
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1457 SLMEKI 1462
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2808
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RBP1_PLAVB
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Matches
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ά	225		
9	1297	AGKVVEEMNSLKTKIEKLIQETSDDSQNELVTTSITKHLENAKG13	
λ	283		
ą	1341	:	
λ	342		
ą	1369	KKLVQQVNMNLQSAIQGNAGISKELNELKGVIELLISTINTSSILEYVKKNSSESVRFSQL 1428	
λ	373		
ą	1429	ANGEFTKAEGEEKNASARLAEAEKLKEQIVKDLDYSDIDDKVKKIEGIKREILKMKES 1486	
λ	416		
ą	1487	ALTEWBE-SEKFKGMCSSHMENAKEGKKKIEYLKNNGDGGKANITDSQMEEVGNYVSKAE 1545	
⋩	456	ATEVEKLFGR	
ą	1546	HAFHTVEAQVDKTKAFCESIVAYVTKMDNLFNESL	
λ	493	VGSKLPGHKRFSWG	
q	1599	-SAKL	
χ.	553	NLSPAHSINONVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALK 612	
ą	1644		
⋩	613	TCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQ-IKCGDLFENSVVDEF 669	
ą	1700	AAKESYEKNLETVQNEMSRINVEEGSLTDIDKKITDIENDLLKMKQYEEGLLQKI 1755	
ζ	670	NECAVSRKKCVPR-KSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT	
ą	1756	KENADKRKSNFELVGSEINALLDPSTSIFI-KLKLKEYD	
Ϋ́	729	EFHTEENKLVGNLSWRI	
ą	1807	EIHGEFTKSYNLIETHLSNATDYSVTFEKAQSLRELAEKEEEHL	
<u>~</u>	761	. FVQDPKYPGILYNHDNEYLLYQDDWYILS789	
ą	1867	VESLKLLKEMMKKVSAEYEGMKRDHTSVSQLVQDMKTIVDELKTLNDISECSSVLNNVVS 1926	
Σ	790	FVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQK	
ą	1927	IVKKVKESKHADYRRDANSMYESMYTLANYFLSDEAKISSGMEFN 1971	
≿	847	TFIKTDTICGPEPPLVERLEKKVEEGERTIIKEV 880	
ð	1972	AEMKSNFKTDLELEIFSVISNSNELLKKIEQDSNDVIQKERESEQLAKDATDIYNVIKLK 2031	
Ž.	881	EEIEEEVKKUKEVKLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEA 934	
ą	2032	NEFNEKLEEAKNKEEVVSEKVREALKRLSQVEGIRCHFENFHRLLDNTE 2080	
Δī	935	FGRALPIRKLMAVATHCFTSPCH	
Q	2081	-ELENLKDYKKATIYRDKKSERESGLQEMENEMN-TYSNSI- 2117	
<u>≯</u>	995	PPIQSADLRITGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKKLVGV 1050	
ą	2118	TQLEGIVVSAGESKE2157	
<u>≯</u>	1051	LACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ 1110	
ā	2158	VIEMNSTIDELYKLGKNCQAHWISLISYTANMKTSKKLIMINKEKENTE 2206	

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               2207 -KCVDYIKDNSSSTDGYVETL------KGFYGSKLIFSSASEIVQNADTYSVNFAKH 2256
                                                                                                                                                                                                2353 SVNDHMHSMEAEMIKNGLKYTPESVQNINNIYSVIEAEVKTLEEIDRDYGDNYOIVEEHK 2412
                                                                                                                                                                                                                                                                                          1354 TE-----EPLDE 1390
                                                                                                                                    2413 KOFSILIDRTN-----ALMDDIEIFKKENNYNLMEVNTETIHRVNDYIEKITNKLVQAK 2466
                                                                                                                                                                                                                                                                                                              1111 IKCGDLFE--NSVVDEFNECAVSRKKCVPRKSDLG-EFPAPDPSVLVQNFNISDFNGKWY 1167
                                                       1168 ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGV 1227
                                                                                                                                                                             .-- 1301
                                                                                                                                                                                                                                   --FSTFIRTDNTCGPEPALVERIEKTVEEGE----RIIVKEVEEIEEEVEKEVEKV--GR 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92333688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.,
                                                                         LYNHDNEYLHYQDDWYILSSKIENKPEDY -----IFVYYRGRNDA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
                                                                                                                                                                          ---WDGYGGAVVYTRSSV--LPN--SIIPELEKAAKSIGRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE LARGE TEGUMENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpesvirus saimiri (strain 11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X64346; CAA45687.1; -. EMBL; M86409; AAA46140.1; -. PIR; H36812; H36812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      1391 IKMEASE 1397
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Q01056;
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w	SEQUENCE 2469 AA; 280165 MW; D2B4BBDC08644CDB CRC64;	
Query Best Matcł	Query Match Best Local Similarity 17.3%; Pred. No. 0.75; Matches 230; Conservative 208; Mismatches 497; Indels 396; Gaps 58;	ko da ko
	271 FTRSAVQTEVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIEVYYR 323 	G 6
	324 -GRNDAWDGYGGSVIYTRSPILPESIIPNLQKAAKSVGRDFNNFI 367 	
	368 TTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTL 419 : : ::	
	420 FQRLLEGFKELQQDEENFVRELSKEEKEILNELQMEATEVEKL 462	Š Š Š
Qy	463 FGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVA 517 : :	
	518 -KICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVFKG 567	RE MY
	568 NSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAK 627	
	628 CISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVG 687 ::	
	688 DFPGKWFITRGLNPTF 720 : : :	
	721 DAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPG 769 :	
Qy	770 ILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVL 826	
QY	827 PESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTI-IKEVEE 882	
Oy Db	883 IEBEVEKVRDKEVTLFSKLFEGFKELGRDEENFLRELSKEEMDVLDGLKMEATEVEKLFG 942	
Qy Dp	943 RALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQ 998 	
O.	999 S-ADLRTIGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLL 1045 : : : :	
. dy	1046KLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC 1096 :: :: :: :: :: ::	
• •	1097 LQTCNNRPDETECQIKCGDLFBNSVVDEFNECAVSRKKCVPRKSDLGEFPAPD 1149	<u>—</u>

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-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBDINIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-!- SUBDINIT: MUSCLE MYOSIN IS A HEXALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-!- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|| : | : | : | : : | : : | : : | : : | : : | : : | 1185 NIGHELSLLSQALNSKTLPEAVGTSLEQHAAKFSCMFKTLEATWHDHQVDTRTKIDEYI 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1338 EEIEEEVEK----EVEKVGR----TEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFL 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:: :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
--KMEVDSF-VPT 1027
                                                                                                               1150 PSVLVQNF -- NISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDN-KLVGNISWRIKTLD 1206
                                                                                                                                                                                                                                                                                                                                         1207 SGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIF-----VYY 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KIQSAFQDLNFSILI------PDDWLSL-AKEYTRPKSTLFTVIGPILL 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1125 KFVEEVLESVKNLKEAKLKSLLPNGPVFTPPKFDWIHYYESNVNFHLKTINLPKVSTVAH 1184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                          1028 PSRDVKTFIQNAPSMKAKQYAKKALKDQIQAMEIDVDPESVIEDNIKANGQKAWQ----
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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MISCELLANBOUG: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYCSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1935 AA.
           --TAVDRPLKRELYNVIRKLQKQLKTLLEQQEFDNW-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 PDGTE-----EADKSAYLMGLNSADLLKGLCHPRVKVGNEYVTKGONVQQVMYATGALA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 QDPDLPGALY-NHDNEFLHYQDDWYILSSQIENKPD-DYIFVYYRGRND----AWDGYGG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 SVIYTRSPTLPESIIPNLQKAA-KSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 ---ILNELOMEAT-EVEKLFGRALP------IRKLRMALAPHSNFLANHETIKYY 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VDEFNECAVSRKK-----CVPRKSDVGDFPVPDPSVLVQKFD 702
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                                                                                                                                                                                                                                                                                                                                                                                                                459; Gaps
                   InterPro; IPR002928; -.
Pfam; PF00512; IQ; 1.
Pfam; PF001576; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
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                                                                                                                                                                        RODLIKE TAIL (S2 AND LMM DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                           2.0%; Score 148.5; DB 1; Length 1935; 16.7%; Pred. No. 1.3;
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                                                                                                                                                                                                                                                                        METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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Matches 248; Conservative 220; Mismatches 555; Indels
                                                                                                                                                                                                                                                                                                                            149CDBFD910DBB08 CRC64;
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                                                                                                                                      ATP-binding; Methylation; Alkylation; Multigene family. DOMAIN 1 838 GLOBULAR HEAD (S1).
                                                                                                                                                                                                          COILED COIL (POTENTIAL).
ATP (POTENTIAL).
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763 QDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTR 822
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Flordt M., Bach A., Vosberg H.P.;
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313 EDLKRQLEEEVKAKNALAHALQSARHAADLLREQYEEETETKAELQRVLSK--ANSEVAQ
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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VARIANT CMH1 TRP-719.
VARIANTS CMH1 GLU-256 AND ARG-741.

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                                                                                                                                                                                                                                                                                                                                     VARIANTS CMH1 GLN-249; GLN-403; CYS-453 AND MET-606.
MEDLINE=92204193; PubMed=1552912;
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MEDLINE=92346810; PubMed=1638703;
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MEDLINE=93038688; Pubmed=1417858;
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VARIANT CMH1 GLN-403.
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MEDLINE=94110336; PubMed=8282798;
Anan R., Greve G., Thierfelder L., Watkins H., McKenna W., Solomon S., Vecchio C., Shono H., Nakao S., Tanaka H., Marsa A. Jr., Towbin J.A., Spirito P., Roberts R., Seidman J.G., Seidman C.E.;
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Matches 238; Conservative 207; Mismatches 529; Indels 434; Gaps
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    MEDLINE=95179132; PubMed=7874131;
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MEDLINE=96209901; PubMed=8655135;
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                                                                                            -CAVSRK----KCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGL 716
                                                                                                                                                                               717 NPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDN 776
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                                           865 KSEARRKELEEKMVSLLQEKNDLQLQVQAEQDNLADAEERCDQLIKNKIQLEAKVKEMNE 924
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                                                                                                                                                                                                                                                                                                                                                                     825 ---VLPESIIPELQTAAQKVG-----RDF-----NTFIKTDNTCGPE-----PPLVE
                                                                                                                                                                                                                                                                           777 EYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSA---
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                                                                                                                                   925 RLEDEEEMNAELTAKKRKLEDECSELKRDIDDLELTLAKVEKEK ----
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01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FWBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72;
                                                                                                                                                                                                                                                                           MISCELLANEOUS: ADDITIONAL REGIONS OF LOWER HOMOLOGY TO THE REPEAT CONSENSUS (ALMAYS STARTING WITH PROLINE) ARE FOUND IN BOTH FLANKING DOMAINS OF THE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 SSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQF-----1QLAIVLVC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      748 SAYEDLVKCKENPDV-----EFLKEKSAKLGHTVVSSEEYSELQRKYSELEKEVEQPS 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 TFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSC-----AANVACLQTCNNRPDET 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 LAYLVEHAKATDH----HLLSDSAYEELVKCKENPDMEFLKEKSAKLGHTVVSNEAYSEL 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECQI-------KCGD--LFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAV 215
                                                                                                                                                                               hly repetitive 313 kDa NUM1 protein.";
Gen. Genet. 230:277-287(1991).
FUNCTION: CONTROLS NUCLEAR MIGRATION. NUM1 SPECIFICALLY CONTROLS THE INTERACTION OF THE BUD NECK CYTOSKELETON WITH THE PREDIVISIONAL G2 NUCLEUS PERRAPS BY RECOGNIZING G2-SPECIFIC CYTOPLASMIC MICROTUBULI OR OTHER COMPONENTS OF THE NUCLEAR
                                                                                                                                                               "Nuclear migration in Saccharomyces cerevisiae is controlled by the highly repetitive 313 kDa NUM1 protein."; Mol. Genet. 230:277-287(1991).
                                        dukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582; Indels 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.9%; Score 143; DB 1; Length 2748; 17.9%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 PH DOMAIN.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
                                                                                                                                Kormanec J., Schaaff-Gerstenschlaeger I., Zimmermann F.K.,
Perecko D., Kuentzel H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B2FBD67C9F6211AE CRC64;
                                                       Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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             NUM1 OR YDR150W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 28383 / FL100;
MEDLINE-92079907; PubMed=1145235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231;
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NUCLEAR MIGRATION PROTEIN NUM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X61236; CAA43554.1; -.
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                                                                    NCBI_TaxID=4932;
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SEQUENCE
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Matches 26
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1617 LEKPIVDNASKNDVLNLCSKFSLVPLSTEEYDNMRKEHTKILNILGDPSIDFLKEKCEKY 1676
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                                                                                                                                                                                                                                                                276 VQTFVQDPDLPGALYNHDNEFLHYQ------DDWYILSSQIENKPDDYIFVYYRG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 RND---AWDGYGGSV-----IYTRSPTLPESIIPN----LQKAAKSVGRDF--- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 ----NNFITTDNS-----CGPEPPLVERLEKTAEEGEKLLIKEAV-EIEEEVEKE--- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILNE--LQMEA-TEVEKLF 463
857 EKKLEQPSLAYLVEHAKATDHHLLSDSAYEDLVKC------KENSDV-EF----- 899
                                                                                        216 VONFNMKDFSGKWYITSGLNPTFDAFDCOLHEFHMENDKLVGNLTWRIKTLDGGFFTRSA 275
                                                                                                                                                                            ----LKEKSAKLGHTVVSNEAYSELEKKLEQ-----PSLAYLVEHAKATDHHLLSDSA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 GRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAK----
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------NHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDG 1270
                                                                                                                                                                         1897 SEKIDHIVVPLSEYNLMVTNYRNPSLSYLKEKAVLNNHILLIKEDDYKNIL-----AVSE 1950
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                                                                  1174 PTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLY---- 1229
                                                                                                     1271 YGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE 1330
                                                                                                                                                                                                                                                                                RIIVKEV----EEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEM 1385
                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryotą; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahdavi V., Periasamy M., Nadal-Ginard B.;
"Molecular characterization of two myosin heavy chain genes expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISCUSSION OF SEQUENCE.
MEDLINE-90133919; PubMed-2614840;
MCMALLY E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
"Full-length rat alpha and beta cardiac myosin heavy chain sequences."
Comparisons suggest a molecular basis for functional differences.";
J. Mol. Biol. 210:665-671(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. Heart J. 5:181-191(1984).
-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBBNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF ;
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
"Complete nucleotide sequence of full length cDNA for rat beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1935 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiac myosin heavy chain.";
Nucleic Acids Res. 17:7529-7530(1989).
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MEDLINE=85179510; PubMed=6241892;
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                                                                                                                                                                                                                                                                                                                                                                      2058 AIFDSIIVENIEYQQLVNTTSP 2079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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P02564;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAR PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.
PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUITED FOR MYOSIN ATPAGE ACTIVITY.
MISCELLANBOUS: EACH WYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED
SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                          SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES, WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
                                                                                                                                                                                         MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MIXOSIN, WHILE THE BETA ISOFORM IS A 'SLOW, AIPASE. MISCELLANEOUS: THERE AFE 10 OF MORE MYOSIN HEAVY CHAIN GENES IN THE RAI, TWO OF WHICH ARE SPECIFIC FOR ADULT CARDIAC MYOSIN HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 PDETECQIKCGDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRN------AVV 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 QNFNMKDFSGKWYITSGLNPT-------FDAFDCQLHE---FHMENDKL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00193; MYOSINHEAVY.
PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Methylation; Alkylation; Multigene family.

DOMAIN

1 839

RODLIKE HEAD (S1).

BAND LMM DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIN-EINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
IRK -> VRR (IN REF. 3).
IR -> VRR (IN REF. 3).
IR -> K (IN REF. 3).
I -> N (IN REF. 3).
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-> K (IN REF. 3).
-> N (IN REF. 3).
-> K (IN REF. 3).
C8376C324A7BDB2B CRC64;
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16.7%; Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
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EMBL; J00752; AAA41654.1; -.
EMBL; M32698; AAA41659.1; -.
PIR; S06006; S06006.
PIR; A02999; A02999.
HSSP; P08799; 1MND.
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Interpro; IPR001609; -.
Interpro; IPR002928; -.
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1935 AA;
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CONFLICT
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Oy Db	256 486	VGNLTWRIKTLDGGFFTRSAVQ-TFVQ
. do	283	PDLPGALY-NHDNEFLHYQDDWYILSSQIENKPDDYIFVYRGRNDAWDGYGGSVI 337
Q7 Op	338 595	YTRSPILPESIIPNLOKAA-KSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIK 396
Qy Db	397	EAVEIEEEVEKEVEKVRDTEMTLFORLLEGFKELQQDEENFVRELSKEEKE
Qy	448	ILNELOMEAT-EVEKLFGRALPIRKLRWALAPHSNFLANHETIKYYVGS 495 :::: :
Qy Db	496 749	KLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLS 555 ::
QY	556 807	PAHSINONVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILLSVASKADAV 608
Qy	609	DALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFE 662
Qy Dp	663 911	NSVVDEFNE
Qy	703	MKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLYGNLSWRIRTPDGGFFTRSAVQKFV 762
Qy	763	QDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAMDGYGGSVLYTR 822 ::
QQ Dp	823	SAVLPESIIPELQTAAQKVGRDFNTFIKTDNTGGP 857 : : : KVRMDLERAKRKLEGDLKLTQESIMDLENDKQQLDERLKKKDFELNALNARIEDEQALGS 1102
Oy Dp	858 1103	EPPLVERLEKKVEEGGRTIIKEVEBIEEEVEK 889 : : ::: QLQKKLKELQARIEBLEEEL-EAGRTARAKVEKLRSDLSRELEBISERLEEAGGATSVQI 1161
Qy	890 1162	
Qy Db	920	SKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLG 979 :::::
QQ Dp	980 1265	ITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNEL 1036 :::
Q7 Dp	1037 1313	KELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC 1096
ζς, qα	1097	LQTCNNRPDETECQIKCGDLFENSYVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQN 1156 : : 1 WRT

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157 FNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQ 1216
                                                                    ----VERSNAA 1438
                                                                                                                                         1217 KFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVV 1276
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MEDLINE-99003341; PubMed=9786894;
Bdakkes H.K., Ohtake Y., Wickner R.B.;
Bdakkes H.K., Ohtake Y., Wickner R.B.;
maklip of Saccharomyces cerevisiae, a homolog of human CAATT-binding protein, is essential for 60 S ribosomal subunit biogenesis.";
J. Biol. Chem. 273:28912-28920(1998).
--- PUNCTION: REQUIRED FOR 60S RIBOSOMAL SUBUNIT SYNTHESIS.
--- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-96381250; PubMed-8789263;
Brandt P., Ramlow S., Otto B., Bloecker H.;
"Nucleotide sequence analysis of a 32,500 bp region of the right arm of Saccharomyces cerevisiae chromosome IV.";
Yeast 12:85-90(1996).
                                                                                                                                                                                           1439 AAALDKKQ----RNFDKILVEWKQKYEESQSELESSQKE-----ARSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RIBGEOME BIOGENESIS PROTEIN MAK21.
MAK21 OR YDR060W OR D4237 OR YD9609.14.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1598 QTSLDAETRSRNEALRVKKKMEGDLNEMEIQLSHANRMAAEA 1639
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                                                                        ---AVEAVNAKCSSLEKTKHRLQNEIEDLMVD---
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EMBL; Z4436; CAA98878.1; -.
EMBL; Z49209; CAA89089.1; -.
EGB; S0002467; MAK21.
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                                                                            1403 -----
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Q12176;
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                                                                                                                                                                                                                                                                                          -FVRELSK--EEKEILN------ELQMEATEVE-----KLF-----GRALPIR 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       692 PDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH----TEENKLVGNLSWRIRT 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   775 PDLGLFTLSHFLDRFVYRSAKQTNTARGTSIMQPLFSGSRVNDSVLVKASDIMHD-QGPV 833
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                                                                                                    Gaps
                                                                                                                                     345 PESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEI--- 401
                                                                                                                                                                                                                                                   460 PNADYHTTYYSVITLNQTILKRSEDSVANKLVK---TYFTLFEKFL----INTDKDNTN 511
                                                                                                                                                                                                                                                                                                                             512 GVVKSNSKSYEEKRKKNFKKGKHGGKSVKIEKTENEVLDEKNSKLFSALLTGINRAFPFA 571
                                                                                                                                                                                                                                                                                                                                                                 471 KLRMA------LAPHSNF-----LANHETIKYYVGSKLPGHKRFSWGWEDYF 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572 KFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 PACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPV
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
NCBL_TaxID=4932;
                                                              Length 1025;
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       1025 AA; 116676 MW; FB80378727ED71D8 CRC64;
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                                                          1.9%; Score 139.5; DB 1; 20.9%; Pred. No. 1.8; ative 94; Mismatches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 YQDDWYILSSKVEN-SPEDYIFVYY------KGR----
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15-JUL-1998 (Rel. 36, Last annotation update)
MYOSIN-LIKE PROTEIN MLP1.
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                                                                                                  Matches 159; Conservative
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15-JUL-1998
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Q02455;
       SEQUENCE
                                                            Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 CQIKCGDLFENSVVD-----QFNEC------AVSRKKCVPRKSDVGEFP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 ALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPES 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.8%; Score 137.5; DB 1; Length 1875; Best Local Similarity 17.5%; Pred. No. 5.1; Matches 252; Conservative 240; Mismatches 525; Indels 421; Gaps
                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-94205265; PubMed=8154186; Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G., Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.; Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.; "The complete sequence of a 15,820 bp segment of Saccharomyces cerevisiae chromosome XI contains the UBI2 and MPLI genes and three
                                                                                                                                                                                                                                                                                                                                   FUNCTION: MYOSIN-LIKE PROTEIN THAT IS PROBABLY INVOLVED IN DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 CSLEQVKSFDGDVVKHLNDKLLQFNELKSENLKVTVSFDELKASSLKKIDGLKTEM-ENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 DCQLHEFHM---END-----KLVGNLTWRIKTLDGGFFT-----RSAVQTFVQDPDLPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 DERLKEIELVRVENNRSNSECKKLRSTIMDLETKOOGYITNDLNSRTELERKTOELTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 DSLNSEKQEF-SAEMSLKQRLVDLLESQLNAVKEELNSIRELNTAKVIADDSKKQTPENE
                                                                         Koelling R., Nguyen T., Chen E.Y., Botstein D.; "A new yeast gene with a myosin-like heptad repeat structure."; Mol. Gen. Genet. 237:359-369(1993).
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MW; 683A0D34C9066867 CRC64;
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EMBL; X75541; CAA51948.1; -.
EMBL; Z28320; CAA82174.1; -.
STR: S38173; S38173.
SGD; S0001803; MLP1.
Myosin; Heptad repeat pattern; Colled coil; DNA repair.
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COILED COIL (POTENTIAL).
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-!- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1".
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                                    STRAIN=5288C;
MEDLINE=93247549; PubMed=8483450;
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301 30
1875 AA;
[1]
SEQUENCE FROM N.A.
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1015 KSEY-----ESKLSKIQNDL-----DQQTIYANTAQNNYEQELQKHADVSKTISELRE 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               885 ------EDKIRLHTYNVMDETINDDSL-RKELEKSKINLTDAYSQIK--EYKDLYET- 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    720 TILKQDSKTHETLNEYVSCKSKLSIVETELLNLKEE------QKLRVHLEKNLKQEL 770
506 GWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVP 565
                                                                               402 HLONQIETFIVELEHKVPIINSFKERTDMLENELNNAALLLEHTSNEKNAKVKELN---A 458
                                                                                                                                                                       566 KGNSGCKFPKDVALMVWEKW--------GOFAKTAIVAIFILSVASKA 605
                                                                                                                                                                                                                                                                                                                                      606 DAV----DALKTCTCLLKECR--LELAKCISNPACAANVACLQTCNNRPDETECQIKCG- 658
                                                                                                                                                                                                                                                                                                                                                                                                                      517 DSTITESDSQKVVTERLVEFKNIIQLQE-----KNAELLKVVRNLADKLESKEKKSK 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          659 ---DLFENSVVDEFNECAVSRKKCVPRKSDVGD------FPVPDPSVLVQKFD 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         569 QSLQKIESETVNEAKEAIITLKS---EKMDLESRIEELQKELEELKTSVPNEDASYSNVT 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703 MKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFV 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             626 IKQ------LTETKRDLESQVQDLQTRISQIT-----RESTEN-----MSLLNKEI 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 763 QDPKYPGILYNHDNEY-----LLYQDDWYILS----SKVENSPEDYIFVYYKG 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 QD-----LYDSKSDISIKLGKEKSSRILAEERFKLLSNTLDLTKAENDQLRKRFDYLQN 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----RNDAWDGYGG-----SVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTD- 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 NTCGPE-----PPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKL 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       771 NKLSPEKDSLRIMVTQLQTLQKEREDLLEETRKSCQKKIDELEDALSELK-KET---SQK 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           902 FEGFKELQRDE-----ENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVA 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               827 DHHIKQLEEDNNSNIEWYQNKIEALKKDYESVITSVDSKQTDIEKLQYKVKSLEKEIE-- 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------DEKTS 964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 KNOKLVECENDLQTLTKQRLDLCRQIQYLLITNSVSNDSKGPLRKEEIQ--FIQNIMQED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             933 --TSQSLQQTNSKLDESFKDFT----NQIKNLT------
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for Emblance and the EMBL outstation is the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89210800; PubMed-3072195; Lemaire C., Helilg R., Mandel J.L.; "The chicken dystrophin cDNA: striking conservation of the C-terminal coding and 3' untranslated regions between man and chicken.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODRIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and 3' untranslated regions between man and chicken."; 7:4157-4162(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 3660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85493DAF6D5B6D4A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                Lemaire C., Heilig R., Mandel J.L.;
"Nucleotide sequence of chicken dystrophin cDNA.";
Nucleic Acids Res. 16:11815-11815(1989).
                     01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 135;
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                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89098331; PubMed=3062582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422874 MW;
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PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
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IPRO01715; -.
IPRO02017; -.
IPRO02349; -.
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HSSP; Q01082; 1AA2.
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Muscle;
                                                                                                                DYSTROPHIN.
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Pred. No. 17;

Best Local Similarity

3660 AA

STANDARD;

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•	Matches 245; Conservative 196; Mismatches 482; Indels 472; Gaps 64;	
Oy	71 KDKSQICSIDTSFEEIQRFDLKRGMTLI-LEKOWROFIOLAIVLVC 115	Oy 978 LGITRKRINGTFLLK
q α •		Db 2807 LHLSLQELLAWLQLKEDEI
Oy	116 TFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLOTCNNRPDETECOIKC	Qy 1017 RSGFSKGIFDIVPLE
qq	:: : : 13 14 15 17 1983 TTFVMTESMTVETTYVPSTYLAEI-LQLLQALSEVEERLNSPVLQAKDC	Db · 2867 RLFLADQPVEGLEKVYPEF
δλ	176 GDLFENSVVDQFNECAVSRKKCVPRKSDVGEFFVVPDRNAVVQNFNMKDF	1064
QQ	2031 EDLLKQEECLKNIKDCLGRLQGHIDIIHSKKTPALQSATPRETANIQD-KLTQL 2083	2927
ΟY	225 SGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLT 260	1113
qu	2084 NSQWEKVNKMYRDRQARFDKSKEKWRLFHCEMKSFNEWLTETEEKLSRAQIEAGDVGHVK 2143	2960
QY	261 WR-IKTLDGGFFTRSAVQTFVQDPDLPG	1164
qq	2144 TKOFLQELQDGIGRQQTVVKTLNVTGEEIIEQSSAADANVLKEQLGNLNTRWQEICR 2200	
ΟŶ	288	QY 1220 QDPNQPGVLYNHDNE 123
qa	2201 QLVEKRKRIEBEKNILSEFQEDLNKLILWLEETENVIAIPLEPGNEDQLRDCLGKVKLRV 2260	SOOF ISENAVELLINGELY
Qγ	341 SPTLPESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKL	RESULT 11
qa	2261 BELLPHKGILKRLNETGGTTLGSASLNPERKHKLESTLKEASRRLLKVSRD 2311	MYSP_HUMAN ID MYSP_HUMAN STANDARD;
Qy	401 IEEEVEKEVEKVRDTEMTLFQRLLEG	
qq	2312	DT 15-JUL-1998 (Rel. 36, La DT 01-OCT-2000 (Rel. 40, La
Qy	. 461KLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFG 512	
qq	2345	
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0λ		RC TISSUE=Skeletal muscle; RX MEDLINE=90323631; PubMed
qo	2408 AINHLILQLKEK-PTFGEPALTSPGVLT-SGQTVAVDTQARVTKETTSFTP	
QY	633 ACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKS 684	
q	2457 EMPSSVLLEVPALADFNKAWAELTDWILSRIDREIKAORV	
٥y	685 DVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCOLHEFHTEENKLVGNLSWR	
q	2496 TVGDLDDINDMIIKQKANMQDLEQRRPQLDELITAAQNLKNK	RA Stedman H H Rubingtein
Qy	745 IRTPDGGFFTRSAVQKF-VQDPKYPGILYNHDNE-YLLYQDDWYILSSKVENSPEDYIFV	
qa	(4	
ΟÝ	803 YYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN- 846	RP SEQUENCE OF 502-1937 FRO TISSUE-Skeletal muscle:
q	: :: : :: 2595 QAKAKLESWKEISYTVEALKKONSELKQFSKEIRQWQMN	MEDLINE-90235863 Bober E., Buchbe
Qy	847TFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVE 881	Arnold "Ident
q	: : 2651 DDTRKVELMTDNINATWATINKRVSEREAALESALLMLQEFYLDLEKFLAWLTEAE 2706	RT myosin heavy chains."; RL Eur. J. Biochem. 189:55-
Qy	882 EIEEEVEKVRDKEVTLFSKLFEG	RN [4] RP SEQUENCE OF 860-1937 FRO
qq	::	RX MEDLINE=89234168; PubMed RA Feghali R., Leinwand L.A
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qq	2767 EDAVLLQRRLDNMNFRWSELRKKSLNIRSHLEASTDQWKR 2806	RL J. Cell Biol. 108:1791-1 RN [5]

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PRDLSPEERAQNVTKVLRRQADDVRTEWDKLNLRSADWQKKI 2926
-----ILPPIQ-----SADLRTTGGRSSRPLSAF 1016
                     P---SKNELKELTAPLLIKLVGVLACAF--LIVPSAD----A 1063
                                                                                                                                     AKCIANPACAANVACLQTCNNRPDETECQIK----- 1112
                                                                                                                                                             )LHEFHTE-GDNKLVGNISWRIKTLDSGFFTRSAVQ---KFV 1219
                                                                                                                                                                                                                                                                                                      developmentally controlled isoforms of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l=7601129;
, Pompidou A.J., Hoffman R., Schiaffino S.,
i N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  criterization of a developmentally regulated neavy chain.";
797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rdata; Craniata; Vertebrata; Euteleostomi;
nates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1=1691980;
dl A., Braun T., Singh S., Goedde H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-2373371;
Jaali R., Shows T.B. Jr., Leinwand L.A.;
Pngth human perinatal myosin
YA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan perinatal myosin heavy-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reated)
ist sequence update)
ist annotation update)
INATAL SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1937 AA.
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1=2715179;
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              ESSET K., Tidhar A., Myszkowski M.;
"Isolation and characterization of the human perinatal MHC promoter.";
submitted (MAX-1998) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: MISCLE CONTRACTION.
                                                                                SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) and 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                          SUBFRAGMENT (S2).
SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
                                                                                                                                                                                CHARACTERISTIC FOR ALPHA HELICAL COLLED COLLS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE

SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50U96; 10; 1.
Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding;
ATP-binding; Methylation; Alkylation; Heptad repeat pattern;
                                                                                                                                                                                                                                                                                                                             WHICH DICTATE THE ALPHA-HELLICAL COILED-COIL STRUCTURE, ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RODLIKE TAIL ($2 AND LAM DOMAINS) COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
E -> Q (IN REF. 1).
M -> N (IN REF. 1 AND 4).
N -> H (IN REF. 1 AND 4).
MC -> DGG (IN REF. 3).
E -> G (IN REF. 3).
K -> Q (IN REF. 1 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHYLATION (TRI-) (POTENTIAL).
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EN -> AH (IN REF. 1 AND 4).
E -> D (IN REF. 1 AND 4).
D -> H (IN REF. 2).
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Pfam; PF01876; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF067143; AAC21557.1; -. PIR; A30220; A30220. HSSP; P13538; 2MXS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M36769; AAC17185.1; -. EMBL; Z38133; CAA86293.1; -. EMBL; X51592; CAA35941.1; -. EMBL; M35250; AAA36346.1; -.
SEQUENCE OF 1-46 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000048; -.
InterPro; IPR001609; -.
InterPro; IPR002928; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  972 -------HATENK-VKNLTEEMAGLDETIAKLSKEKKALQE-----THQQTLD 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    718 PTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNE 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     778 YLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTA 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663 TNLRSTHPHFVRCIIPNETKTPGAMEHELVLHQLRCNGVLEGIRICRKGFPSRILYGDFK 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 ----KLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYF---GSIVVAKICSSR 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 RIPRYFRKSPRICCGLDSR------GLQLFSHGKHNLSPAHSINQNVP 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783 KLAQIITRIQAVCRGFLMRVEYQKMLQRREALFCIQYNVRAFMNVKH--WPWMKLFFKIK 840
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                                                                                                                                                                                                                                                                        133 ACLLKECRIELAKCIANPSCAANVACLQTCNN---RPDETECQIKCGDLFENSVVDQFNE 189
                                                                                                                                                                                                                                                                                                                                                                                                                 396 ADLLKALCYPRVK-VGNEYVTKGQTVQQVYNAVGALAKAVYEKMFLWMVTR-INQQLDTK 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 OPROYFIGVLDIAGFEIFDFNSLEQLCINFTNEKLOOFFNHHMFVLEQEEYKKEGIEWTF 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 VQ-DPDL-----PGALYN-----HDNEFLHYQDDWYILSSQIENKPDDYI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 IDFGMDLAACIELIEKPLGIFSILEEECMFPKATDTSFKNKLYDQHLGKSANFQKPK--- 570
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                                                                                                                                                                         99 LEKQWRQFIQLA-----AVDALKTC 132
                                                                                                                                                                                                                     282 AERSYHIFYQITSNKKPDLIEMLLITTNPYDYAFVSQGEITVPSIDDQEELMATDSAIDI 341
                                                                                                                                                                                                                                                                                                                    342 LGFTPEEKVSIYKLTGAVMHYGNMKFKQKQREEQAEPDGTEVADKA-----AYLQSLNS 395
                                                                                                                                                                                                                                                                                                                                                                     190 CAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGK------WYITSGLNPT---- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------FDAFDCQLHE---FHMENDKLVGNLTWRIKTLDGGFFTRSAVQ-TF 279
                                                                                                                        239 VRNDNSSRFGKFIRIHFGTTGKLASADIETYLLEKSRV------TFQLK----- 281
Best Local Similarity 17.0%; Pred. No. 7.8;
Matches 280; Conservative 243; Mismatches 597; Indels 529; Gaps
                                                                          43 IRSNN----GYFNSFRLFTSYKTSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLI 98
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1113 ELQARIEELGEEIEAERASRAKAEKQRSDLSRELEEISERLEEAGGATSAQVELNKKREA 1172	890	928 DGLKMEATEVEKLEGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRING 987 	988 TFLLKILPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLL 1044 1:	LKIVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRP 110	137	IIOO DETECQIACGOLEENSYVDEENECAVSKAKCYPRKSDLGEEPAPDPSYLYQNENISDENG IIO4 	1165 KWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQ 1224	1225 PGVLYNHDNEYLHYQDD#YILSSKIENKPEDXIFVYYRGRNDAWDGYGGAVYYTRSSVLP 1284	1285 NSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEV 1344 : : : : : : :	1345 EKEVEKVGRTEMTLFQRLAEGFNELKODEENFVRELS	2KEEME-FLDEIKMEASEVEKLFGKAL 1406 :: : ::: : : ::	1615 LRVKKKMEGDLNEMEIQLNHANRLAAESL 1643	PILZE PILZE MSPI_PILAFE MSTANDARD; PRT; 1630 AA. MSPI_PILAFE MSF04923; 13-AUG-1987 (Rel. 05, Created) 01-FEB-1996 (Rel. 34, Last sequence update) 01-FEB-1996 (Rel. 34, Last annotation update) MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS) (PMMSA) (P190). MSP-1. Plasmodium falciparum (isolate K1 / Thailand). Plasmodium falciparum (isolate K1 / Thailand). SEQUENCE FROM N.A. SEQUENCE FROM N.A. MSP-1. FINITARID=5839; [1] MSROYA: MSP-1. FORMAD M. Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Stunnachergy H., Bujard H.; FOLYMOTPHISM OF the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985). PREVISIONS, SEQUENCE FROM N.A. PRAM W., TOLLE R., Bujard H.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases. SUBMITCH AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SCHIZONT. FRAM AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SCHIZONT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 134; DB 1; Length 1630;
Local Similarity 18.0%; Pred. No. 6.7;
les 246; Conservative 207; Mismatches 473; Indels 444; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 VDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWYITSGLNPTFDAFDC 243
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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N-LINKED GECUNC.
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981 LE-EDINKL-----KKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLT---LL 1029
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637 NIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPST 696
                                           652 ECQI------KCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQ-- 699
                                                                                                                                                                                                                                            799 YIF------VYYKGRNDAWDGYGGSV-----LYTRSAVL-----PESIIPELQTAAQ 839
                                                                                    697 EGEITGQATTKPGQQAGSALEG---DSVQAQAQEQKQAQP-----PVPVPVPEAKAQVP 747
                                                                                                                               700 -------KFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRI 745
                                                                                                                                                                        748 IPPAPVNNKTENVSKLDYLE------NTSYIC 779
                                                                                                                                                                                                                   746 RIPDGGFFTRSAVQKFVQDPKYPGILYNHD--NEYLLYQDDWYILSSKVEN----SPED 798
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5848;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                    Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246; Conservative 207; Mismatches 473; Indels 444; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: MEROZÓITE SURPACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURPACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                               Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
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                                                                                       "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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MEROZOITE SURFACE PROTEIN 1.
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SEQUENCE FROM N.A. MEDLINE=86014355; PubMed=2995820;
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                                                                                                                             Nature 317:270-273(1985).
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1071 -----IAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASL 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990 LE-EDINKL-----KKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLT---LL 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     992 KILPPIQSADLRTTGGRSSRP---LSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLV 1048
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                                                                                                                                                                                                                                             596 KITKDENKPDEKILEV----SDIVKVQVQKVLLM-----NKIDELKKTQLILKNVELKH 645
                                                                                                                                                                                                                                                                                                                                                                                             652 ECQI------KCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQ-- 699
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                                                                                              515 VVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGC--- 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 EVEKLFGR--ALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDY-FGSI
                                               508 NFEKAMGKRYSYKVEKL----THHNTFASYENSKHNL-EKLTKALKY---MEDYSLRNI
                                                                                                                                                                                                                                                                                                                                            646 NIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPST
                                                                                                                                                                                                                                                                                                                                                                                                                                               706 EGEITGQATTKPGQQAGSALEG---DSVQAQAQEQKQAQP-----PVPVPVPEAKAQVP
                                                                                                                                       559 VVEKEL-----KYYK------NLISKIENEI---ETLVENIKKDEEQLFEK
                                                                                                                                                                                                                                                                                               ----LAKCISN-----PACAA-----NVACLQTCNNRPDET
                                                                                                                                                                                                 572 -----KFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLE-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
DOMAIN: THE RODLIKE TALL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FIB; TISSUE=Liver;
MEDLINE=95115033; PubMed=7815459;
Wang R., Sole M.J., Cukerman B., Liew C.-C.;
"Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain gene from Syrian hamster.";
J. Mol. Cell. Cardiol. 26:1155-1165(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
MISCELLANBOOK: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MERONYCSIN (LMM), AND 1 HEAVY MERONYCSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS ($1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 962-1935 FROM N.A.
MEDILINE-88247788; PubMed=3380703;
Jandreski M.A., Sole M.J., Liew C.-C.;
"Sequence of cDNA encoding the Syrian hamster cardiac beta-myosin heavy chain.";
                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RODLIKE TAIL (S2 AND LMM DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFRAGMENT (S2).
SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding; Methylation; Alkylation; Multigene family, DOMAIN 1 838 GLOBULAR HEAD (S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL)
                               P13540; Q60540;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.
PRT; 1934 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 16:4737-4737(1988).
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Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L12104; AAA62313.1; -. EMBL; X07273; CAA30256.1; -. PIR; A28298; A28298.
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00612; IQ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                 Mesocricetus
      MYSB_MESAU
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DD 1004 QALDDLQAEEDKVWILTKSKVKIEGOVDDLEGSLEGEKKVRENDLERAKERS QY 814 AVLPESIIPELGTAGAVGG
. 63; . 63; . 66 63; . 77 7 66 . 68 8 8 8 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
28 METHYLATION (TRL-) (POTENTIAL). 04 ALKYLATION (SH-1) (POTENTIAL). 05 ALKYLATION (SH-1) (POTENTIAL). 06 D > E (IN REF. 2). 17 B T > Y (EN REF. 2). 18 E -> O (IN REF. 2). 19 D -> N (IN REF. 2). 17 D -> N (IN REF. 2). 18 E -> O (IN REF. 2). 19 D -> N (IN REF. 2). 17 D -> N (IN REF. 2). 18 E -> O (IN REF. 2). 19 D -> N (IN REF. 2). 10 D -> N (IN REF. 2). 11 D -> N (IN REF. 2). 12 D -> N (IN REF. 2). 13 D -> N (IN REF. 2). 14 D -> N (IN REF. 2). 15 D -> N (IN REF. 2). 16 D -> N (IN REF. 2). 17 D -> N (IN REF. 2). 18 E -> O (IN REF. 2). 19 D -> N (IN REF. 2). 19 D -> N (IN REF. 2). 222928 MM; PEDGAC9310B0B57D CRC64; 11 D -> N (IN REF. 2). 222928 MM; PEDGAC9310B0B57D CRC64; 11 D -> N (IN REF. 2). 222928 MM; PEDGAC9310B0B57D CRC64; 222928 MM; PEDGAC9310B0B57D CRC64; 223928 MM; PEDGAC9310B0B57D CRC64; 23 D -> N (IN REF. 2). 24 D -> N (IN REF. 2). 25 D -> N (IN REF. 2). 26 D -> N (IN REF. 2). 26 D -> N (IN REF. 2). 27 D -> N (IN REF. 2). 28 D -> N (IN REF. 2). 29 D -> N (IN REF. 2). 21 D -> N (IN REF. 2). 22928 MM; PEDGAC9310B0B57D CRC64; 21 D -> N (IN REF. 2). 22928 MM; PEDGAC9311GALAKSVERNEN-INVERCIPE SEEPERPLY COLVOCEPTRENTY CO
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128 128 ALKTLATIO 704 704 ALKTLATIO 705 966 D -> E (I) 986 986 E -> Q (I) 1008 1014 DLQAEED -> Y (I) 1060 1060 D -> Y (I) 1051 1057 D -> Y (I) 1051 1057 D -> Y (I) 1051 1057 D -> Y (I) 1217 1217 E -> D (I) 1217 1217 E -> D (I) 1218 1328 C -> R (I) 1328 1358 C -> R (I) 1358 1358 C -> R (I) 1358 1359 C -> R (I) 1556 1556 N -> K (I) 1557 N -> K (I) 1556 N -> K (I) 1556 N -> K (I) 1557 N -> K (I) 1557 N -> K (I) 1558 N -> K (I) 1559 N -> K (I) 1550 N -> K (I) 155
121 195 96 97 97 97 98 105 105 1121 122 123 123 123 123 123 123 123 12

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RKLEGDLXLTQE 1063
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|KLKELQARIEEL 1117
                                                                                                                                                                                                                                                                  NNRPDETE--CQ 1110
:||| :
EQYEEETEAKAE 1355
                                                                                                    KREAEFQKMRRD 1176
                                                                                                                          MDVLDGLKMEAT 935
::: | :
LELDD----VTS 1232
                                                                                                                                                                                        :|
SVNDL----- 1272
                                                                                                                                                                                                                     APLLLKLVGVLA 1052
                                                                                                                                                                                                                                                                                                                APDPSVLVQNFN 1158
                                                                                                                                                                                                                                                                                                                                                             SGFFTRSAVQKF 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIEKTVEEGERI 1332
:| | :| :
KIRKQLEAEKME 1538
                                                                                                                                                                                                                                              RQL----- 1318
                                                                                                                                                                                                                                                                                                                                                                                   --- VERSNAAAA 1439
                                                                                                                                                                                                                                                                                                                                                                                                          AWDGYGGAVVYT 1278
                                                                                                                                                                                                                                                                                                                                                                                                                           : |
-----ARSLST 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFVRELS---- 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :| :
RNHLRVVDSLQT 1598
                              ----PPLVERL 865
                                                                             688 -----
                                                                                                                                                                        RINGTFLLKILP 995
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951 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                             Kochi S.K., Schlavo G., Mock M., Montecucco C.;
"Zinc content of the Bacillus anthracis lethal factor.";
FEMS Microbiol. Lett. 124:343-348(1994).

-i. FUNCTION: ONE OF THE THEE PROTEINS COMPOSING THE ANTHRAX TOXIN,

-i. FUNCTION: ONE OF THE THEE PROTEINS COMPOSING THEA NATHRAX TOXIN,

AGENT WHICH INFECTS MANY MAMMALIAN SPECIES AND THAT MAY CANSE

DEATH. LE IS THOUGHT TO BE A LETHAL FACTOR THAT, WHEN ASSOCIATED

WITH PA, CAUSES DEATH. LE IS NOT TOXIC BY ITSELF. PA IS THOUGHT TO

BIND TO RECEPTORS OF SENSITIVE EUKARYOTIC CELLS, THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 APEAFNYMDKFNEQEINLSLEELKDQRMLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 ---LQRDEENFLRELSKEEMDVLDGLKMEATEV----EKLFGRALPI------RKL 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: ::: ||:|| ::| |::| |::| |::| |: || ::| |: || ::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
                                                                                                                                                                                                                                                                                                                                                                                                                                         FACILITATING THE INTERNALIZATION OF LF OR EF.
SUBUNIT: SECRETED ANTHRAX TOXIN IS COMPOSED OF THREE DISTINCT
PROTEINS, A PROTECTIVE ANTIGEN (PA), A LETHAL FACTOR (LF) AND AN
EDEMA FACTOR (EF). NONE OF THESE IS TOXIC BY ITSELF.
SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: THE PA-BINDING REGION IS FOUND IN BOTH B.ANTHRACIS EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNT 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L---VIQSSEDYVENTEKALN------VYYEIGKILSRDILSKINOPYOKFLDVLNT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 IKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLY 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733 EENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHD---NEYLLYQDDWY--I 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 EMYKAIGG---KIYIVDGDITKHISLEALSEDKKKIKDIYGKDALLHEHYVYAKEGYEPV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000130; -.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Toxin; Signal; Repeat; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 132; DB 1; Length 809;
Best Local Similarity 17.2%; Pred. No. 3.4;
Matches 139; Conservative 117; Mismatches 254; Indels 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA-BINDING REGION (POTENTIAL) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC (CATALYTIC) (POTENTIAL).
8C16B4D7277310AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (POTENTIAL)
                                                                                 Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO PEPTIDASE FAMILY M34 (ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       848 FIKTDNTCG-----PEPPLVERLEKKVEEGERTIIK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EVEEIEEEVEKVRDKEVTLFSKLFEGFKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LETHAL FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                          MEDLINE-95154669; PubMed-7851740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809 LE
293 PA
420 RE
719 ZI
720 PO
723
93786 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M29081; AAA79216.1; -. EMBL; M30210; AAA22569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METALLOPROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JQ0032; JQ0032.
MEROPS; M34.001; -.
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34
300
719
720
723
809 AA;
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND LF
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METAL
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.223 NQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTR--S 1280
                                                                                                                                                                                                                                                                                                                     1050 VLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETEC 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1165 KWYITSGLNPTFDAFDCQLHEFHTEGDNKLV--GNISWRIKTLDSGFFTRSAVQKFVQDP 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1281 SVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE-RIIVKEV-- 1337
MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
                                                                                                                                                               1007 GRSSRPL------SAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVG 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1110 QIKCGDLFENSVVDE--FNECAVSRKKCVPRK---SDLGEFPAPDPSVLVQNFNISDFNG 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 FNVHNRYASNIVESAYLILNEWKNNIQSD------LIKKVTNYLVDGNGRFVFTDITL 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      670 PNIAEQYTHQDEIYEQVHSKGLYVPESRSILLHGPSKGV-ELRNDSEGFIHEFGHAVDDY 728
                                                                           390 L------NRIQVDSSNP-----LSEK--EKEFLKKLKLDIQPYDINQRLQDTG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDNERLKWRIQLSPDTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567 ----IIKQSEKEYIRI-DAKVVPKSKIDTKIQE----AQLNINQEWNKALGLPKYTKLIT
                                                                                                                                                                                                                                          430 GLIDSPSINLDVRKQYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1338 ------EEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 AGYLENG---------KLILORNIGLEIKDVQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1380 ----LSKEEME-----FLDEIKMEASEV 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: November 6, 2001, 05:15:07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              729 AGYLLDKNQSDLVTNSKKFIDIFKEEGSNL 758
                                                                                                                                                                                                                                                                                                                                                                                                                 -----GADLVDST-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Job time: 646 sec
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4' 10

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November 6, 2001, 05:13:08 ; Search time 119.14 Seconds (without alignments) 1568.027 Million cell updates/sec
                                                                                                                                                                                                        US-09-075-375A-4
7495
1 MALSLHTVFLCKEEALNLYA......MEASEVEKLFGKALPIRKVR 1412
                                                                                                                                                                                                                                                                                                                                                                                                           425026
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                          425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL_16:*

1: Sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_invertebrate:*
5: sp_mnmal:*
5: Sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                          Run on:
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3: Sp_fungl:*

4: Sp_maman:*

5: Sp_maman:*

6: Sp_mamman:*

7: Sp_mnc:*

8: Sp_organelle:*

9: Sp_organelle:*

10: Sp_plant:*

11: Sp_unclassified:*

12: Sp_unclassified:*

13: Sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	% Query Match	Length DB	DB	ID	Description
1	2557	34.1	478	10	040593	O40593 nicotime +
7	2508	33.5	473	10	040251	
m	2430	32.4	462	10	039249	
4	1604.5	21.4	472	10	09SM43	
S	1300	17.3	244	10	9053D9	
9	1219.5	16.3	289	10	O9FUS5	
7	210	2.8	522	10	098313	
œ	194.5	5.6	2269	Ŋ	026223	
σ	161.5	2.2	2771	S	026216	026216 plasmodium
10	156	2.1	1365	7	049525	049525 mycoplasma
11	156	2.1	1933	13	090337	090337 evering ca
12	155.5	2.1	886	Н	029230	O29230 archaeoglob
13	151	2.0	1055	10	098722	09s722 arabidonsis
14	151	2.0	1939	2	025662	O25662 plasmodium
15	150.5	2.0	1332	4	. ОЭНАМ4	O9haw4 homo sapien
16	148.5	2.0	2473	11	090284	090284 mus musculu
17	147.5	2.0	1786	2	Q900P0	Oguđeo plasmodium
18	146.5	2.0	1387	2	09GZ76	Ogaz76 plasmodium
19	146	1.9	1935	4	Q9H1D5	

Q03767 saccharomyc Q9vnh4 drosophila Q26024 plasmodium O51465 borrelia bu	0996y2 homo sapien 096275 plasmodium 09w0m1 drosophila Q9uzc8 pyrococus P91349 caenorhabdi	0921v0 helicobacte 061201 caenorhabdi 099kr1 sus scrofa 065583 aquifex aeo 049547 mycoplasma		944 C
3 Q03767 5 Q9VNH4 5 Q26024 2 O51465		2 Q9ZLV0 5 O61201 6 Q9GKR1 2 O66583 13 O99675	1 059066 1 0900H3 10 09SB74 1 099996 1 09Y2L2	5 Q9N2M3 1 Q9UQQ4 1 O60772 5 Q00756 10 Q23332
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SEQUENCE FROM N.A.
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                                                                                         654 QIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT 713
                                                                                                                                                                                                                                                    774 HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 833
                                                                                                                                                                                                                                                                                                                                             LOTAAOKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDK 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MALSLHTVFLCKEEALNLYARSPCNERFHRSGQPPTNIIMMKIRSNNGYFNSFREFTSYK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bugos R.C., Yamamoto H.Y.; "Molecular cloning of violaxanthin de-epoxidase from romaine lettuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactuca sativa (Garden lettuce).
Bukaryota, Viridiplantae; Bnbryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
euasterids II; Asterales; Asteraceae; Lactuceae; Lactucea.
                                                                                                                                                                                                                                                                                                                                                                                                                                       894 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 950
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13, Last annotation update)
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Pred. No. 4.2e-135;
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Proc. Natl. Acad. Sci. U.S.A. 93:6320-6325(1996).
EMBL; U31462; AAC49373.1; -.
Mendel; 8691; Lacsa; Vdel;8691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 AA.
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100.0%; Pre
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MEDLINE-96270536; PubMed-8692813;
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01-MAY-2000
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951 MAVATHCFISPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 1010
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                                                                                                                                          241 FDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPGALYNHDNEFLHYQ 300
                                                                                                                                                                                                    301 DDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVG 360
                                                                                                                                                                                                                                                                                                                 361 RDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLF 420
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Welley Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 ORLLEGFKELQODEENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLR 473
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STRAIN-CV. COLUMBIA;
BUGOS R.C., Yammonto H.Y.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000566; -.
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462 AA;
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263 KTPDGGFFTRTAVQKFAQDFSQPGMLYNHDNAYLHYQDDWYILSSKIENQPDDYVFVYYR 322
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1143 GEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRI 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    968 FFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSAFRS-----GFSK 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 GEFPUPDPSVLVKSFNMADFNGKWFISSGLNPTFDAFDCQLHEFHLE-DGKLVGNLSWRI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1251 NKPEDYIEVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDN 1310
                                                                                                                                                                                                                                               1311 TCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELK 1370
                                                      SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
                                                                                                                     1191 DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 1250
                                                                                                                                                                                                 37 FLFQDDARRNIRFNDRKLSCTKFIGASEKLQ------HSKSPKSGLISCGWEVNSSK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%; Score 1604.5; DB 10; Length 472; 66.4%; Pred. No. 1.1e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and sequencing of Spinacia olercea violaxanthin de-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epoxidase.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 VIOLAXANTHIN DE-EPOXIDASE.
53658 MW; 12B4C8C69AB61E12 CRC64;
                                                                                                                                                                                                                                                                                                             1371 QDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
VIOLAXANTHIN DE-EPOXIDASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                               421 QDEENFVRELSKEEMFLDEIKMEASEVEKLFGKALPIRKVR 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Emanuelsson A.K., Eskling M., Akerlund H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spinacia oleracea (Spinach)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ250433; CAB59211.1;
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Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 4
472 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3562;
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1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1071 ACLIKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130
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                                                                                         1323 EKTVEEGERIIVKEVEEIEEEVEKUGRTEMTLFQRLAEGFNELKQDEENFVRELSK 1382
                                                                                                                      Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Leas C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence for Arabidopsis thaliana BAC T27G7 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaeae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 AA; 26631 MW; 4CD8221F444CF04C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1300; DB 10;
Pred. No. 9.8e-67;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             244 AA.
                                                                                                                                                                                                   1383 EEMEFLDEIKMEASEVEKLFGKALPIRKVR 1412
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                                                                                                                                                                                                                             PRT;
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Similarity 21.18;
                                                                                                                           Matches 122; Conservative
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                                                                                                  Query Match
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Q26223;
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STRAIN=CV. ZHENHII-249;
Lin R.-C., Xu C.-C., Li L.-B., Kuang T.-Y.;
Molecular cloning and expression of rice violaxanthin de-epoxidase.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288196; AAF97601.2;
                                                                                                                                                                                                                                                                                                                                                             1123 DEFINECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYIISGLNPTFDAFDCQ 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1243 YILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDF 1302
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MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Eujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                1183 LHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDW 1242
                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa subsp. indica.
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                              16.3%; Score 1219.5; DB 10; Length 289; 74.8%; Pred. No. 4.7e-62; Live 43; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1363 AEGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 AA; 33496 MW; B91C7BBD4CE1770D CRC64;
                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AT2G21860 PROTEIN.
                             289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 AA.
                                                                                        VIOLAXANTHIN DE-EPOXIDASE (FRAGMENT).
                             PRT;
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                                                                                                                                                                                                                                                                                                                                     Matches 217; Conservative
                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                       NCBI_TaxID=39946;
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SEQUENCE
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                                    Q9FUS5;
                       09FUS5
RESULT 6
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Q9SJ13
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"A gene coding for a high-molecular mass rhoptry protein of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                               375 PEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 ENFVRELSKEEKEILNELOMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 E----IVSSNDQRAMN-LTQELNQTDILVVVA-------VNNSESV---- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 -----NWIQTNSKNVKNMIC-----FESSPNLMNRLGG----- 178
                                                                                                                                                                                                                                                                                                                               77; Mismatches 186; Indels 194; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495 SKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNL 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 SPAHSINQNVPKGNSGCKFPKDVALMV-----WEKWG----QFAKTAIVAIFILSV--- 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 IDVGSVNKD------KEVTEVVKTVGDAWERRNSDDIRFCLLVIINAYIRPVPVL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602 ---ASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 QNLRSK-----GFSTLSCMVKNCGPQILNCLLDPNCRKALQCLNQCS--PVDQVCSYRCI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   659 DLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK------ 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 ASYEGPYFEAFSLCVLOKHNCLELDAKIPEKPYVPP-----MISFRGKELCHDTAED 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            710 -----TEENKLVGN 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 LFVGWLGELEWSWRVVAGONPAYDOFPCOYOLFYRGKGKSSFWYEPVFQVRTLEEKLV-- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     741 LSWRIRTPDGGFFTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVE 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 --WRRR------RYSVKR----GKIPATFRFSVLDNGVVSNEF-----WTIVD--VS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 DDLSWGLFHYHGAARVAGQSYTGAVLVTPDGSYPAEKDKERLQSALEKCGIKEWELF-AV 487
Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome II of Arabidopsis thaliana."; Nature 402:761-768(1999).
BMBL; AC007019; AAD20404.1.; --
SEQUENCE 522 AA; 59287 MW; 63EF3102F3E96C21 CRC64;
                                                                                                                                                                                                                                                                             Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium berghei yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2269 AA; 265158 MW; F3D8CB103FB9A6E1 CRC64;
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                                                                                                                                                                                                                                                                  2.8%; Score 210; DB 10;
21.1%; Pred. No. 0.0003;
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EMBL; L27838; AAA21304.1; -.
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Query Ma Best Loc	y Ma Loc bes	/ Match Local Similarity 18.4%; Pred. No. 0.017; ne 255; Concervative 213; Mismatchee 436; Indale 483; Gane 65;	
		SQUENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKA 355	
۵	34	: - : : : : : - : : : : : : : : : : : : :	
>-	356	AKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEI 401	
۵	88	EKEIRELFKKYLDEFABRKYLEGLKLELNKKIKDITAKIEYVKNTVEL 135	
٠ ۵	402	EEEVEK	
>-	447	E-ILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYV 493	
	196	::::: : :: : : : : :	
>-	464	GSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSH 549	
۵	255	YDEISKELNKMLEDFKNKEKELSNKISDYDKKREQL-SEYKSKMLEIRNHYNSQ 307	
> -	550	GKHNLSPAHSINQNVPKGNSGCKFPKDV 577	
Q	308	TNVDNTKEEEEAKQNYDKSNEHMTTIPTNEDEISKIISEVKTMKDEILSKVNTYIDFNKKY 367	
	578	TCLLKECRLELAKCISNPACAAN 6	
Д	368	KETVNSEHSQFTE LTDKIKAEVSDKELKK 396	
ъ д	638 397	VACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSD 685	
>	989	VGDFPVPDPSVLVOKFDMKDFSGKWFITRGLNPTFDAFDCOLHEFHTEE- 734	
	453	1.5	
×	735	KFVQDPKYPG	
Ω	508	IKYFSDEKANLGINEENMLYNQFTEKEKTFNDIKEKNIHINEEIS52	
γ	791	KVENSPEDYIFGY 814	
Q	553		
Α.	815	VLYTRSLPESIIPE	
q	613	:: ::	
χ.	850	KTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKL 901	
ą	673	SNDNVEGIKKKÇQIIVTKIDKKKNIYEEINKLISEISKIEKDNTSLEKVKDINLSYGQNL 732	
λ	902	FEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVAT 955	
۾	733	GNLFLE-QIDEEKKRAENTIKSMEAYIDDLDNIKKKSQEIETEMDIKMDINKEMEALKIS 791	
¥	926	HCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSA 1015	
۾	792	HDDDKKCHDKSKNHKENISDIYDKSKIIQDFSRESDINDIKNKLQKNVSE 842	
7 4 1	1016	FRSGFSTAP 1042 :: :- :: : :: : SONHNSTINDELNINSER 899	
r ⊵ g	1043	LELKLYGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLOT 1099 ::: : - - - - - - - - - - - - - - - - -	

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68;
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                                                                                                                                                                                                                                                                                          1285 ---NSI-----IPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGER 1331
                                                                                                                                                                                                                                                                                                                                                                    1332 IIVKEVEEIEEEVEKEVEKVGRTEMTLFQR-----LAEGFNELKQDEENFV---RELS 1381
                       939 -NILNEETNITNHFKNAEEYNKIVLSNFNNIEMADNKSQYILEIKKNNGTNDHDYNIKEL 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 YKTSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQFIQLAIVLVCTFV 118
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                                                                                                                                                                              1048 ---FD-----KTKNDSK---QIIKEIKDAHNYCTLESG------KSEKKMNE----
                                                                   -AVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPT
                                                                                                                                                                                                                   1230 NHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLP----
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Green J.L., Holder A.A.;
Structure of the E8 gene encoding a high molecular mass rhoptry
protein of Plasmodium yoelli.";
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                                                                                         998 KSHKDKSNGYKTEADQNKKAIQKNKELFEQYKEEVTVLLNKYYAVELKNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; U36927; AAB41263.3; -. SEQUENCE 2771 AA; 325640 MW; COCCB9AB6E7ACF36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
1100 CNNRPDETEC -- OIKCGDLFENSVVDEFNEC-----
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01-OCT-2000 (TrEMBLrel. 15, Last anno
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Mol. Biochem. Parasitol. 0:0-0(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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λ Q	119 915	IVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIK 174 :: : :	
γ	175 952	CGDLFENSYVDQFNECAVSRKKCVPRKSDVGEF 207	
ξ	208		
λ Q	268 1051	GGFFTRSAVQTFVQDPDLPGALYNHDNEFLHYQDDWYILS	
≿ q	309	QIENKPDDYIEVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDFNNFIT 368 : :	
λ Q	369 1139		
ž q	426	GFKELQQDEENLORD 454 ::: : : : : : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :	
ž q	455 1256	EATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFS504 	
<u>ک</u> و	505 1315		
Υ _α	557 1359	AHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTG 616 : : :	
ζi q	617 1397	LLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFEN 663	
Zi qi	664	SUVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAF 723 :	
દ્ર વ	724	TPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQD : : E	
λ. q	784	DWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGR 843 :	
<u>≽</u> . Q	844	DEWTFIKTDWTGGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFE 903	
Q	904	GFKELQRDEENFLRELSKEEMDVLD-GLKMEATEVEKLFGRALPIRKLMAVATHCFTS 960 :::: : : ::	
ξ. q	961 1630	PCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSAFRSGF 1020	
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2 ≱.	1064	1000 ARMIEDUNRELDEVNSKIRNIESNVNQHKKNYEIGIVEKINEIAKANKDØ 1/1/ 1064 VDALKTCACLLKGCRIELAKCIANPACAANVACLØTCNNRPD-ETECQIKCGDL 1116	

Ω	Db 1718	::::
a	Qy 1117	
Ω	Db 1771	ITHYLETVSKEPITYEQIKNKRITAQNELLTNIKNVNKAKSYLDDIEANEFDRIVTHFKN 1830
0 D	Oy 1158 Db 1831	NISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSA 1214 :: : : : : :
, oʻ	12	VQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGA 127
Ω	Db 1885	SKKYYSKKYEAENIFINIPKLANSLNIQIKSSSGI 1919
α 	Qy 1275	VVYTRSSVLP
Д	Db 1920	DLFKNINIAILPYLDSQKKDTLTFIPSPEKTSETYTKISD 1959
a	0y 1333	IVKEVEBIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEM 1385
Ω	Db 1960	SYNTLLDILKRSQELQKKEQQALNLIFENRLHDKVQATNELKDTLSDIKNKKE 2013
α	Qy 1386	EFLDEIKMEASEVEKL 1401
О	Db 2014	QILINKVKELEHKSNEENKE 2032
ж Ó i	95	
HĀ		25 PRELIMINARY; PRT; 1365 AA. 25:
ממ		01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
A A		(TrEMBLrel. 08, Last annotation
υ Ö		LMP1. Mycoplasma hominis
, o o	OC Bacte	Mycoplagmataceae; Mycoplasma. Mycoplagmataceae; Mycoplasma.
OR		_raxID=2098;
<u>α</u> α		SEQUENCE FROM N.A. STRAIN=MH56:
i izi i		9882; PubMed=7543881;
* 124	"Se	ion o
K K	in Inf	presence of monoclonal antibod Immun. 63:3336-3347(1995).
ωΩ	DR EMBL; SQ SEQUE	U21962 NCE 1
	Query Ma	h 2.18; So
	Best Local Matches 2	Similarity 16.8*; 09; Conservative 18
Qy	y 272	AVQTFVQDPDLPGALYNHDNEFLHYQDDWYILSSQ
qa	b 282	TRNQIQEFINTSKNNP-NYSELISQLTSKRDSKNSVTDS 319
δō	у 332	YGGSVIYTRSPTLPESII-PNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEK 385
qa	b 320	SNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVSNANTLSA 369
δō	у 386	TAEBGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVREL 441
qa	b 370	KLTDKDNTIQQAKTELEKEVQKADQAIKSNNTASMQSAKSSLDAKVAETTKKLETF 425
QY	y 442	SKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHK 501
É	h 426	NYDREE KENET, KOTEDNOTOER

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1301 DFSTFIR-----TDNTCGPEPALVERIEKTVEEGERIIVKE-----VEEIEEEVEKEV 1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1156 NFNISD--FNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTR- 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                    627 -----KNSVTDSSNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVS 676
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                                                                                                                                                                                                                                       681 PRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIIRGLNPTFDA----FDCQLHEFHTEENK 736
                                                                                                                                                                                                                                                                          542 LEKE-----VQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETFNKDKEA 588
                                                                                                                                                                                                                                                                                                                  737 LVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSP 796
                                                                                                                                                                                                                                                                                                                                                       589 KFNELKO-----TRNOIQEFINTNK-----NNPN----YSELISOLTSKRDS-- 626
                                                                             561 NQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKE 620
                                                                                                                  490 KQALAKAN-----DNLAKS 509
                                                                                                                                                        621 CRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCV 680
                                                                                                                                                                                               510 IKEQLNNSVSN----TIQQAKTE 541
502 RFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHS-I 560
                                     ----INTUKNNPNYSELISQLTSKRDSKNSVTDSSNKSDIESANTEL 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 -KLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYF---GSIVVAKICSSRRIP 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 LVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKE----L 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 QQDEENFVRELSKEEKE------ILNELQME-ATEVEKLFGRALPIR------ 470
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                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97176447; PubMed-9023993; Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.; Imai J., Hirayama Y., Kikuchi K., Kakinuma isoforms from carp fast skeletal muscle and their gene expression associated with temperature
                                                                      Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprininae; Cyprinis.
                                                                                                                                                                                                                                Hirayama Y., Watabe S.; "Structural differences in the crossbridge head of temperature-associated myosin subfragment-1 isoforms from carp fast skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 2.1%; Score 156; DB 13; Length 1933; Local Similarity 17.0%; Pred. No. 2.1;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                 Eur. J. Biochem. 246:380-387(1997).
                                                                                                                                                                                                      TISSUE=FAST SKELETAL MUSCLE;
MEDLINE=97352533; PubMed=9208928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acclination.";
J. Exp. Biol. 200:27-34(1997).
BMBL: D89990; BAA22067.1;
EMBL: D504/4; BAA09067.1;
HSSP; P08799; ILVK.
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Pfam; PF00612; IQ; 1.
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5 B	983	FUGGEFTRSAVOREVUDPKYPGILKNHDNEYLLYQDDWYILSSKVENSPEDYIFVYKG 806
Qy Db	807	RNDAWDGYGGSVLYTRS
Qy Dp	844	DFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEI 883 : : : : : : : : : : : : : :
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QQ	1146	: : SERLEEAGGATAAQIEMNKKREAEFOKMRRDLEESTLQHEATAAALRKKQADSVAELGEQ 1205
Qy Db	905 1206	FKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHD 964
Oy d	965	RINGTFLLKILDPIQSADLRTTGGRSSRP 101
	1254	QLSEIKAKSDENSRQLNDMNAQRARLQTENGEFSRQLEEKEALVSQ 1299
<u> </u>	1013	LSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCAC 1072 :
ολ	1073	
qq	1321	:
ζō	1119	NSVVDEFNECAVSRKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDA 1178
Op QG	1376	TDAIQRTEELEESKKKLAGRLQDAEESIEAVNSKCASLEKTKQR 1419
		FFTRSAVQKFVQDPNQP
ි සු	1420	LQSEVEDLMIDGERANALAANIDKKQRNFDKVLADWKQKYEESQAEL 1466
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0y 1	1356 N	MTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEK 1400
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RA :	Klenk HP., Clayton R.A., Tomb JF., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Pererson J D.	
RA RA	A.R., Graham D.E., Kyrpides N.C. ash J., Lee N.H. Sutton G.G. Gi	
RA RA	bougherty B.A., McKenney K., Adams M.D., Loftus B.,	
RA	R., Gorgine J.D., McDonald L., U	
RA	Jerryys I., Artrach F., Kaine B.P., D'Andrea K.P., Bowman C., Fujii C., (
RA RA	1 T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese Car J.C.;	
RT	nome sequence of the hype	
RL	0(1997).	
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D C	38;	
DR	IPR003439;	
K.W.	Ptam; PF00470; RecF; 1. Hypothetical protein	
S	SEQUENCE 886 AA; 103633 MW; D35641D499AA8B58 CRC64;	
ō.	2.18; Score 155.5;	
Ä Ř	ocal Similarity 20.6%; Pred. No. 0.78; 8 137; Conservative 85; Wismatches 221, Tagaia 221	
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qq	152 EDYENAWKNLGAVIRMLEREKERLKEFLSQEEQIKRQKEEKKAEIE 197	
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a a	290SILEKLLSEINQALRDVEKREGDLTREAAGIQAQLKKAEE 329	
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QQ	594QSLRPFYNKWLELKDAESRLESELKRRE-KLEDEISEAIAKLEEANGKA 641	
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 RRITESATATVLKDYLGKKVSNKRDELRE-----LVEHFNIDVENPCVVMSQDKAGS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 ALYNHDNEFLHYQDDWYILSSQIEN--KPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 ESIIPNLQKAAK-----SVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 EEIAQRLQQLKKKLAWSWVYDVGRQ------LOEQTEKIVKLKERIPTCQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 AVEIEEEVEKEVEKVRDT------EMTLFQRLLEGFKE-----LQQD 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 SYI-----LECK-----GN-----SSSFLRNLLQ---QVNDLLQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 ALKTCACLLKECRIE-----LAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFEN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 SVVDQFNECAVSR----KKCVPRKSDVGEFPVPDRNAVVQNFNM------KDFSGK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 WYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 SIYEHLTKATAIVD-----ELENTIKPIEKEISELRGK------IKNMEQV 234
                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%; Score 151; DB 10; Length 1055; Similarity 19.3%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV COLUMBIA,
MEDLINE-99380167; PubMed=10449416;
Mendiste T., Revenkova E., Bechtold N., Paszkowski J.;
"An SMC-like protein is required for efficient homologous
recombination in arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1055 AA; 121349 MW; E9F0C0427FB602E4 CRC64;
                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                       PRT; 1055 AA
                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 18:4505-4512(1999).
EMBL; AF120933; AAD5470.1; -.
EMBL; AF120932; AAD54769.1; -.
INTERPIC; IPR003439; -.
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                 SMC-LIKE PROTEIN.
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        642 EEIR 645
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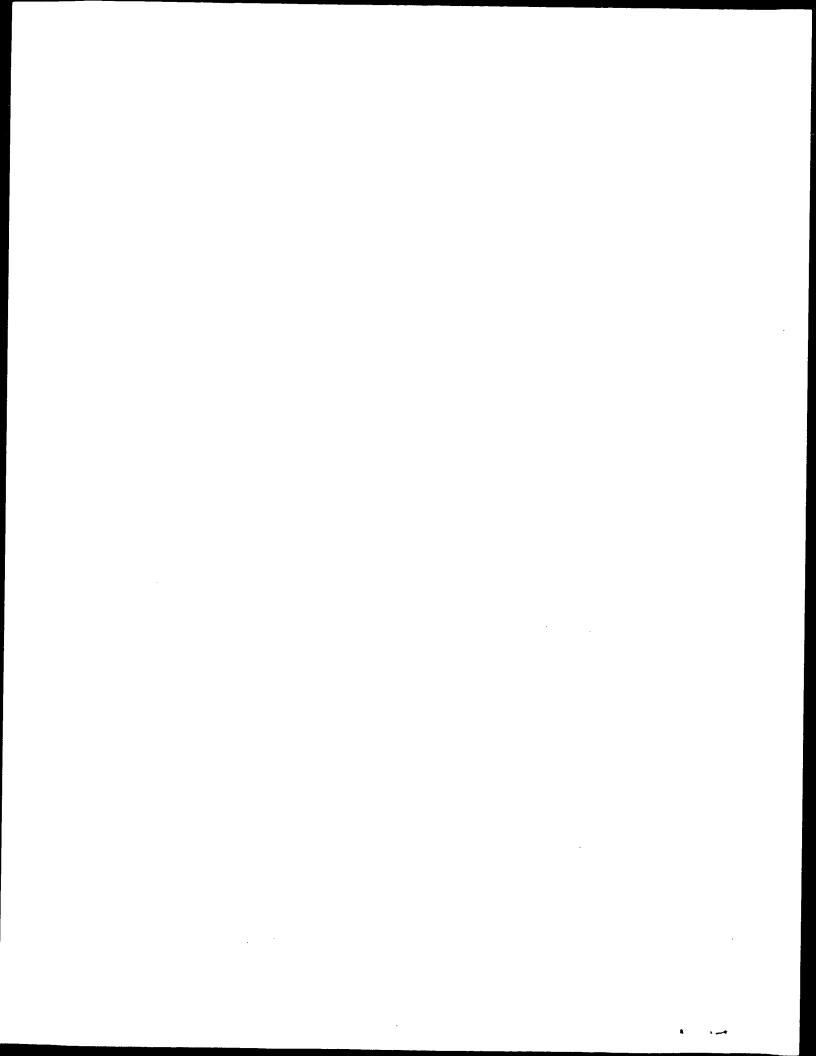
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         668 EFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQL 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 FVRE----LSKEEKEILNELQME----ATEVEKLFGRALPIRKLRMALAPHSNFLANHE 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 VKEYEVKIEELEKEL---KLEKEKQINKEYEKELNEKSEFIKROMELLKEKELNINLKEN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594 KRLSNLK-EVYTLDGYKMFFRGPVQTTLPPLSRRPSRLCASFDDQI----KDLBIEASKEQ 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDN 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650 NE----INQCMRRKREAEENLEELELKVROLKKHRSQAEKVLTTKELEMHDLK-----N 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    854 TCGPEPPLVERL-EKKVEEGERTIIKEVEEIEEE---VEKVRD--KEVTL----FSKLFE 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 189; Conservative 167; Mismatches 299; Indels 422; Gaps
                                                           630 SNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVS-RKKCVPRKSDVGD 688
                                                                                                                                                                                              689 FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTF-----DAFDCQLHEFHTEENKLV--- 738
                                                                                                                                                                                                                                                             555 FSVIDSD----------NPTFLNVLVDQSGVERQVLAENYEEGKAVAFG 593
                                                                                                                                                                                                                                                                                                                                739 ---GNLSWRIRTPDG-GFFTRSAVQKFVQD-PKYPGILYNHDNEYLLYQDDWYILSSKVE 793
513
                                                                                                                       514 -----TLRGCANEANYRNLKI-----IIYDFSRPRLNIPRHMVPQTEHPTI 554
-----HVTLVNGNKWASSVEQALGT--LLNAFIVTDHKDSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%; Score 151; DB 5; Length 1939;
17.5%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Werner E.B., Taylor W.R., Holder A.A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U43145; AAC63403.1; -
SEQUENCE 1939 AA; 229001 MW; B36E462001C6F22F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ol-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          904 GFKELQRDE----ENFLRELSKEEMDVLDGLKMEATEVEKL 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757 NMRESAKGEIDAFEEAENELKKIEKD-----LQSAEAEKI 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1939 AA
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Query Match 2.0%; Score 150.5; DB 4; Length 1332;
Best Local Similarity 19.3%; Pred. No. 2.6;
Matches 255; Conservative 182; Mismatches 405; Indels 477; Gaps
                                                                               307 SSQIENKPDDYIFVYYRGRN------DAWDGYGGSVIYTRSPTLPESIIPNLQKA 355
                                                                                                                    83 SAEEENKEN----LYAGKNTKIKRIYKTVADSDESYMEKSLYQEN--LEAQVKPCLELS 135
                                                                                                                                                               356 AKS-VGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRD 414
                                                                                                                                                                                           415 -------NFVR 439
                                                                                                                                                                                                                                                                                 186 LKKKETKNQEDDVEQPFNDSGCLLVDKDLFETGLEDENNSPLEDEESLESTRAAVKNKVK 245
                                                                                                                                                                                                                                                                                                                          440 ELSKEEKEILNELQM--EATEVEKLFGRALPIRKLRMA--LAPHSNFLANHETIKYYVGS 495
                                                                                                                                                                                                                                                                                                                                                                246 KHKKKEPSLESGVHSFEEGSELSK--GTT---RKERKAARLSKEALKQLHSETORLIRES 300
                                                                                                                                                                                                                                                                                                                                                                                                       496 --KLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGL----QLFS 548
                                                                                                                                                                                                                                                                                                                                                                                                                                   343 HHKEIIDTANTTEMNSDHHSKGSE------QTTGAENEVETNA---LPVVVKETQI 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            995 PPIQSADLRTTGGRSSRPLS-AFRSGFSKGIF--DIVPLPSKN--ELKELTAPLLLKLVG 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549 HGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAV 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 ----ITGSDESCRKDLVK------ 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 ------QKQSDIRPSP-GDSSVLQQESNF-----LG 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              822 ------RSAVLPESIIP------BLQTAAQKVG-----RDF----- 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 766 -KYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYT--- 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        846 NTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGF 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        906 KELQRDEEN-----FLRELSKEEMDVLDGLKME-----ATEVEKLFGRALPIRKLMAVA 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666 EEBEEEERQNQETAREL--LSSEEIETKDEKEMDKENNDGSSEIGKAVGFLSVPKSLSSDS 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             955 THCFTSPCHDRIRF-----FSSDDGIGR------LGITRKRINGTFLL--KIL 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           724 TLLLFKDSSSKMGYSPTEEKSETDENSGKQPSKLDEDDSCSLLTKESSHNSSFELIGSTI 783
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Query Match
Best Local Similarity
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Search completed: November 6, 2001, 05:13:20 Job time: 574 sec



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November 6, 2001, 03:04:01; Search time 6769.47 Seconds (without alignments) 3553.062 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                               2688314
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_htg_other:*
em_htg_rod:*
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em_fun:*
em_htgo_hum:*
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em_htg_hum1:*
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em_htg_hum5:*
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em_htg_hum7:*
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1555
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Maximum DB seq length: 2000000000
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9D_bal:

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9D_inl:

9D_inl:

9D_om:

9D_ow:

9D_pal:

9D_pal:

9D_pl:

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Perfect score:
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9b_htg9: *
9b_htg10: *
9b_htg110: *
9b_htg12: *
9b_htg12: *
9b_htg14: *
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gb_pr7:
em_ov:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

) ; ; ;	bidopsis	enomic s	bidopsis	otiana t	tuca sat	pinacia	ryza sat	enomic a
Description	U44133 Arabidopsis	AC003981 G	U39452 Ara	U34817 Nic	U31462 Lac	AJ250433 S	AF288196 O	2 6690004
QΙ	ATU44133	AC003981	ATU39452	NTU34817	LSU31462	SOL250433	AF288196	20006032
DB	14	12	14	14	14	15	13	1
Query Match Length DB ID	•	133843	2884	1589	1760	1686	1173	90770
Query Match	100.0	61.6	59.3	40.1	39.3	38.7	28.6	21.2
Score	1555	958	922	624.2	611.8	601.4	444.8	230 4
Result No.		7	3	4	S	9	7	a

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AC083812 Homo sapi
AC000667 Homo sapi
AC073799 Mus muscu
AC073799 Mus muscu
AC079627 Homo sapi
AC079627 Homo sapi
AC079627 Homo sapi
AC078629 Homo sapi
AC084849 Homo sapi
AC025669 Mus muscu
AC084849 Homo sapi
AC02668 Drosophil
AC026881 Mus muscu
AL58987 Homo sapi
AC026881 Mus muscu
AL589876 Mus muscu
AL589876 Homo sapi
AC016487 Homo sapi
AC010647 Homo sapi
AC010647 Homo sapi
AC010647 Homo sapi
                                                                                                                                                                                                                                                                            Continuation (2 of
Continuation (3 of
AL359205 Human DNA
AC023198 Homo sapi
AC090530 Homo sapi
AL137122 Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 1555)
Bugos, R.C., Hieber, A.D. and Yamamoto, H.Y.
Xanthophyll cycle enzymes are members of the lipocalin family, the first identified from plants
                                                      Oenothera o
                                                                                                                                                                                                                                                            AL589701 Mus muscu
AC087556 Mus muscu
Continuation (2 of
         AJ009612 Homo sapi
AC009601 Leishmani
AC005804 Leishmani
                                   AC023131 Homo sapi
AC021529 Homo sapi
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Arabidopsis thaliana violaxanthin de-epoxidase precursor (AVDE1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JAN-1996) Robert C. Bugos, Plant Molecular
Physiology, University of Hawaii, 3190 Maile Way, Honolulu, HI
96822, USA
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    .1555
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1. .1555

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AL359205
      HSAJ9612
AC009601
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CHOOORFS
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.6 147243
.6 39987
                                  3.5 162896
3.5 178617
3.5 12813
3.5 100000
3.5 103908
3.5 166335
3.4 200000
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Direct Submission
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TITLE
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iive 0; Mismatches
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Matches 1555; Conservative
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Ecker.J.R.

Direct Submission

L Submitted (29-JUL-2000) Arabidopsis thaliana Genome Center,
Direct Submission

E Submitted (29-JUL-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

E (basses 1 to 13843)

C heuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
                                                   1 (Gases, L. G. 129.43)
Khan, S., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Kim, C., Shinn, P., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howng, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Tralumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Genomic sequence for Arabidopsis thaliana BAC F22013 from
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Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
9 (bases 1 to 133843)
Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C.,
Khan,S., Kim,C., Altafi,H., Bei,B., Chin,C., Chiou,J., Choi,E.,
Conn,L., Conway,A., Gonzalez,A., Hansen,N., Howing,B., Koo,T.,
Lam,B., Lee,J., Liu,J., Liu,S., Liu,S.,
Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano, H., Schwartz,J.,
Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R.,
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Submitted (18-APR-1998) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
Chases I to 13843)
Chases I to 13843)
Chasen Hopson, C., Khan, S., Kim, C., Altafi, H., Bel, B., Chin, C.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bel, B., Chin, C.,
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Howing, B., Koo, T., Lam, B., Lee, J., Lancz, C., Li, J., Liu, A.,
Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Toriuml, M., Vaysberg, M.,
Vu, G. Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-JAN-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3 (bases 1 to 133843) Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-7AN-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA Ecker, J.R.
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Direct Submission
Brassicales; Brassicaceae; Arabidopsis.
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Ecker, J.R.
                                        (bases 1 to 133843)
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ELSSLETILIGANGFWGEIPEFEGKLTRLQYLLDAVONLTGQTPSSLGOLKQLTVYL
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SSAQELVDSLTNAGDKLYVVDFFSPGCGGCKALHPRICQFAEMNPDVQFLQVNYEEHK
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             FTVTGEHANDEMIEKIITDNAGGEEFLTRAIOEHGKGKVLETVVEIODRYDAAKEIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(13219. .13280,13397. .13477,13866. .13932,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAIPRLFFLFYYIGFALFPFVSSETFQNSEQEILLAFKSDLFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNNLQDWKRPENATTFSELVHCHWTGVHCDANGYVAKLLLSNMNLSGNVSDQIQSFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQALDLSNNAFESSLPKSLSNLTSLKVIDVSVNSFFGTFPYGLGMATGLTHVNASSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141]3. .14274))
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/codon_start=1
                                                                                                                       /note="similar to thioredoxin-like |
gb|AAD35005.1|AF144387_1; similar to ESTs gb|T46281.1,
db||AV442467.1, and db||AV549179.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to receptor protein kinase-like protein emb|CAB66905.1; similar to ESTs dbj|AV522839.1, dbj|AV528375.1, and dbj|AV541093.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5403 TIGTITICACTICACCTIGICATGACCGIATICGATITITICICAAGIGATGATGGTATIGG 5462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5583 CAGGICAGGATTCTCTAAGGTAATCAATCATACTAGTCTTGTGTTTCAATACAAAATTTG 5642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5523 AATCCAAAGTGCTGATCTCAGAACAACTGGTGGGAGATCCTCACGTCCTTTATCTGCATT 5582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ttgtttcacttcaccttgtcatgaccgtattcgatttttctcaagtgatgatggtattgg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 taggettggcattacaagaaagaggatcaatggcactttettgetcaagattttacetec 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 aatccaaaagtgetgatctcagaacaactggtgggagatcctcacgtcetttatctgcatt 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels 537; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 cacgeoficeggeittggigiggggaagaitagaitagaiggigaagaaiggeagtageiaeea 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 133843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 958; DB 12;
Pred. No. 2.2e-218;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16782. .19871
/note="similar to receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental/product="F22013.6"
                                                                                                                                                                                                                                                                  /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 caggicaggaticicia------
                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.6%;
73.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.6 Best Local Similarity 73.8 Matches 1541; Conservative
                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MGRAATSFAKLADTARKELPSTLAAVRLSGMEISDLTLELSDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDITDGINKSAKAVQAAEAGIKQIGTLAQQQTLSMIEERANLPEISLQPVVAGAAEKT
SHAIGSATKRLMNIITGGNKDED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MSSCLLPQFKCPPDSFSIHFRTSFCAPKHNKGSVFFQPQCAVST
SPALLTSMANDALLEDARANTYTRPDGFSTERKYLEALASETLITS
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GILGHLAVSDNGIVSDKITASASNKESIGDLESERQEEVELLEEQPSVSLAVRSTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERKARRAKGLEKTASGIPSVKTGSSPKKRLVAQEVDHNDPLRYLRMTTSSSKLLTYR
EEHELSAGIQDLLKLERLQTELTERSGROPTFAQWASAAGVDQKSLRQRIHHGTLCKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMIKSNIRLVISIAKNYQGAGMNLQDLVQEGCRGLVRGAEKFDATKGFRESTYAHWWI
KQAVRKSLSDQSRMIRLPFHMVEATYRVKEARKQLYSETGKHPKNEEIAEATGLSMKR
LMAVLLSPKPPRSLDQKIGMNQNLKPSEVIADPEAVTSEDILIKEFMRQDLDKVLDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPIOSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLA
CAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ
IKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFFAPDPSVLVQNFNISDFNGKWYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDDNQPG
TLYNBINDETHAQDDWTILSSKIENRPEDYIPVYRGKNDAMDGYGGAVTTRSSVLP
VSIIPELEKAAKIGORFSFPFTFTRDWTGPEPALVERIEKTVEEGERIIVKEVEETEE
EVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTREKOVIRWRFGMEDGRMKTLQEIGEMMGVSRERVRQIESSAFRKLKNKKRNNHLQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(1385. .1463,2004...2185,2419. .3015,3461. .3691,3803. .3643,4030. .4230,4333. .4620)
/note="similar to sigma factor 2 gb|AAB69385.1; similar to EST db|JAAS57315...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(5386. .5601,5679. .5845,6111. .6207,6312. .6706,
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// Acte="similar to s-syntaxin-like protein
gplack0648.118c009540_25; similar to ESTs
dbjjav556140.1, dbjjlav566414.1, and dbjjlav55627.1"
Federspiel, N., Theologis, A. and Ecker, J.
Direct Submission
Submitted (05-JAN-2001) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
On Jul 26, 2000 this sequence version replaced gi:3063438.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to viiolaxanthin de-epoxidase
emb|CAB59211.1; similar to ESTs gb|AI994713.1,
db|AV440942.1, and db||AV521985.1"
                                                                                                                                                                                                                                                                                                                                                                                      join(189. .319,505. .605,731. .876)
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                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                               /clone="F22013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                             1. .133843
                                                                                                                                                                                                                                    source
                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                                   FEATURES
                                    TITLE
                                                                                                                                                              COMMENT
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οy	285	catcaaagaatgaqctgaaagaqctgaccgctccgctgttgctaaaactcgtgggt
Dp	5703	CGTGGGTGT
Qy Db	345	ttagcttgcgcgttccttattgttccatctgcagatgcagttgatgcacttaaaacttgt 404
Qγ	405	catgcttattgaagg
Dp	5823	GCTTATTGAAGGGATG
Qγ	426	425
QQ	5883	CCCCCCACCAAAACCGGTTTTATTTTCATTGTGATTGTGATGCTATAAGTGTTTTGAATT 5942
δy	426	425
QQ	5943	GTATAGCTCCATACTCTTCAATTGTTGAGAATGTTAAAGCTAGATGAAGTTACTGTGTCT 6002
δý	426	425
QQ	6003	GICTATGATAGAGCTGAAATCAGTTGATGATATCTTTCTGATTTTTTGCCGTCAATTTA 6062
δý	426	aggatagaactcgc 439
qq	6909	CTTGTCTGACCATATGGAAGCCCCAATTATCTGTTAGGATAGAACTCG
oy Op	440	aaagtgcattgccaacctgcctgtgcagccaatgtcgcgtgccttcagacctgcaataa 499
ò	200	gtccagatgaaacc
op O	6183	AGGTTATAATTTATTTTG
οy	522	521
QQ	6243	AGAGATATTGCTTGCTTATGAAAGAGACCAATGATTTTGTTTATAATTATGTGCTTATA 6302
οy	522	gattaaatgtggggatctgtttgagaacagtgttgttgatgattc
gg	6303	4
δ d	57	tgtgctgtgtcgagaaaaagtgtgttc
Q D	٥	TGTGCTGTGTCGGGAAAAAGTGTGCTTCCTAGAAAATCTGATCTCGGAGAATTTCCTGCC 04.2
Qy Db	636	ccagacccttctgttcttgtacagaacttcaacatctcggactttaacgggaagtggtac 695
Qγ	969	attacaagtggcttgaatccaacctttgatgccttcgactgccagctgcatgattc
q	6483	ATTACAAGTGGCTTGAATCCAACCTTGATGCCTTCGACTGCCAGCTGCATGAGTTCCAC 65
oy Og	756	acagaaggtgacaacaagcttgttggaaacatctcttggagaataaagaccctagacagt 815
ò	816	ggattetttaetaggteageegtaeaaaattegtgeaagateetaaeeaaee
QQ	6603	
Qy	876	ctctacaatcatgacaacgagtaccttcactatcaagat
q	6999	CTCTACAATCATGACAACGAGTACCTTCACTATCAAGATG
ò	919	918
QQ	6723	TCCACCCACGAGGAGGTCTTGATAGTGCTGCTATTCTTTTGGCCTAACAAGCTTTC 6782
οy	919	ggtatatcctgtcatcaaagatagagaataaacctgaagactatat 964

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Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Burasicales; Brassicales; Carbidopsis.

1 (bases 1 to 2296)
Lukowitz,W., Mayer,U. and Jurgens,G.
Cytokinesis in the Arabidopsis embryo involves the syntaxin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (26-OCT-1995) Wolfgang Lukowitz, Lehrstuhl fuer
Entwicklungsgenetik, Universitaet Tuebingen, Spemannstrasse 37-39,
D-72076 Tuebingen, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana syntaxin-related knolle mRNA, complete cds. 039452 U39452.1 GI:1184166
                                                                                                                                                                                                                                                                                                                                                                    7202
                                                                                                                                                                                                                                                                                                                                                                                                                            7262
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1264
                                                                                                                                                                                                                                                                                                           7142
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6783 ATATGATTTTGCAGTATATCCTGTCATCAAGATAGAGATAAAACCTGAAGACTATAT 6842
                                                                                                  cataggcagagacttcagcacattcattagaacggataacacatgtggtcctgaacctgc 1144
                                                                                                                                                                                                                   gctcgtggagagaattgagaagacagtggaagaaggtgaaaggataatcgtaaaagaggt 1204
                                                                                                                                                                                                                                                                                                                                      cttgttccagagattggctgaaggatttaatgaactgaagcaagacgaggagaatttcgt 1324
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                                                                                                                                                                                                                                                                                                                                                                                                 6963 CATAGGCAGAGACTTCAGCACATTAGAACGGATAACACATGTGGTCCTGAACCTGC
                                                                                                                                                                                                                                                                                tgaagagatagaagaagaggtagaggaaggaagtggagaaggtcggtaggactgagatgac
                                                                                                                                                                                                                                                                                               7023 GCTCCTGGAGAGAATTGAGAAGACAGTGGAAGAAGGTGAAAGGATAATCGTAAAAGGGT
                                                                                                                                                                                                                                                                                                                                                       7383 TGTACACAGTCATCATCATTCCATAACAATTGGATACAGAAACACAA 7430

    2884
/organism="Arabidopsis thaliana"

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/db_xref="taxon:3702"
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LSSFLEEAEYVKAEMGLISETLARIEQYHEESKGVHKAESSVKSLRNKISNEIVSGLRK
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YDAAKEIEKSLLELHQVFLDMAVMVESQGEQMDEIEHHVINASHYVADGANELKTAKS
HQRNSRKWMCIGIIVLLIILIVVIPIITSFSSS"
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                                                                        /codon_start=1
/protein_id="AAC49163.1"
/db_xref="G1:1184167"
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              /gene="knolle"
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnodlophyta; endicotyledons; core eudicots; Asteridae; euasterids 1: Solanales; Solanaceae; Nicotiana. 1 (basea 1 to 1589)
Bugos, R.C., Hieber, A.D. and Yamamoto, H.Y.
Kanthophyll cycle enzymes are members of the lipocalin family, the first identified from plants
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KLSSRRIPHYFRKSPRICCCLLDSRGIACHNLSPAHSINDNPKGNSGCRFPK
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CAANVACLQTCNNFPDFFECQIKCGDLFENSVYDEFNECAVSRKKCVPRKSDVGDFPV
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GRFFTRSAVOKFVQDBNYFGLIXNHDNRYLLYDDWYILSSNYENSBPBZIFYYKGR
NDAWDGYGGSYLYTRSAVLEBIIPELGTAAQKVGRDFNTFIKTDNTGGPEPLYBEL
EKKVBEGERTIIKEVVEEIEEEVEKVRDKEVTLFSKLFBGFKELQRDEENFLREISKEE
                                                                                                                                                                                                      1331 gttaagtaaaggaagagtggagtttttggatgagatcaaaatggaagcaagtgaggttga 1390
                                                                                                                                                  2005 CCAGAGATTGGCTGAAGGATTTAATGAACTGAAGCAAGACGAGGAGAATTTCGTGAGAGA 1946
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1211 gatagaagaagaggtagagaaggaagtggagaaggtcggtaggactgagatgaccttgtt
                           2065 GATAGAAGAAGAGGAAAGAAGGAAGTGGAGAAGGGTGGGTAGGACTGAGATGACCTTGTT
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/db_xref="GI:1463123"
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                                                                                                                                          Score 624.2; DB 14; Length 1589;
Pred. No. 8.2e-139;
0; Mismatches 268; Indels 15;
                                                                   /product="violaxanthin de-epoxidase"
a 262 c 366 g 461 t
MDVLDGLKMEATEVEKLFGRALPIRKLR"
              42. .443
/gene="TVDE1"
444. .1475
/gene="TVDE1"
                                                                                                                                          Query Match 40.1%;
Best Local Similarity 74.3%;
Matches 820; Conservative C
              transit_peptide
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactucae.; Lactucae. 1 (bases I to 1760). Bugos, R.C. and Yamamoto, H.Y. Molecular cloning of violaxanthin de-epoxidase from romaine lettuce and expression in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTFYODPDLEGALYHIDNEFLHYODDWYILSSOIENRPDDYIFYYYRGRNDAWDGYGG
SVIYTRSPTLPESIIPNLQRAAKSYGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEK
LLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILN
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SNOFYNERFERFYSYRSPOSSHCKNRSQICSIDFSFEEDGREDKRGMILLERG
WROFIQLAIVLVFTYVTVPRYDAYDALKTCACLIKEORIELARCIANDSCAMVACLO
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                        1429 AGGTAGAAAAACTTTTTGGGCGTGCTTTACCAATAAGGAAATTAAGGTAAGTATTTTAA 1488
ccttgttccagagattggctgaaggatttaatgaactgaagcaagacgaggagaatttcg 1323
                                                                                   tgagagagttaagtaaagaagagatggagtttttggatgagatcaaaatggaagcaagtg 1383
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Submitted (12-JUL-1995) Plant Molecular Physiology, University
Hawaii, 3190 Maile Way, Honolulu, HI 96822, USA
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96270536
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/organism="Lactuca sativa"
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                                                                            324 ttgctaaaactcgtgggtgttttagcttgcgcgttccttattgttccatctgcagatgca 383
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                                       3; Gaps
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

1 (bases 1 to 186)
Emanuelsson, A.K., Eskling, M. and Akerlund, H.E.
Cloning and sequencing of Spinacia olercea violaxanthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MALVARSICVSYYEIAGICNNVSHRNFKKWVQWKNPFLFQDDAR
NNFRNDRKLSCYRFICASERLGHSKSPRSGLISCGWFWNSSKVVSWAYIPKKWWLLK
IKVVRPYTATYACTFFWSSAQAVDAIKTCTCLIKECRFELAKCIANFSCAANYACLQT
CNNRPDFFECQIKCGDLFANKVVDEFNECAVSRKKCVPQKSDVGEFPVPDPSVLVKSF
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KFAQDPSQPGMLYNHDNAYLHYQDDWYILSSKIENQPDDYVFVYYRGRNDAWDGYGGA
FLYTRSATVPENIVPELNRAAQSVGKDFNKFIRTDNTCGPEPPLVERLEKTVEEGERT
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                                                                                                                                                                                                                                                                SOL250433 1686 bp mRNA PLN 21-OCT-1999
Spinacia oleracea mRNA for violaxanthin de-epoxidase (sydel gene).
AJ250433
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Submitted (20-OCT-1999) Emanuelsson A.K., Dept. of Plant
Biochemistry, Lund University, Chemistry Center, POB 117, 221
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svdel gene; violaxanthin de-epoxidase.
                                                                                       1404 aaagetttgecaateaggaaggteaggtaga 1434
                                                                                                                                             1627 CGCGCGTTACCGATTAGGAAACTTAGATAAA 1657
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/db_xref="G1:6103243"
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Emanuelsson, A.K.
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                                                  367 CAAGCTGTTGATGCTCTTAAAACTTGTACCTGTTTGCTGAAGGAATGCAGAATTGAACTC
                                                                                                                      aaccgtccagatgaaaccgagtgccagattaaatgtgggggatctgtttgagaacagtgtt
                                                                                                                                                      487 AATAGACCTGATGAAACCGAATGCCAAATCAAATGTGGGGACTTGTTCGCCAACAAGTT
                                                                                                                                                                                          gttgatgagttcaacgagtgtgctgtgtcgagaaaaagtgtgttcctagaaaatctgat
                                                                                                                                                                                                                          547 GIIGACGAGIICAACGAGIGIGCAGICICICGAAAGAAATGCGIGCCICAGAAGICIGAI
                                                                                                                                                                                                                                                                                                                               tttaacgggaagtggtacattacaagtggcttgaatccaacctttgatgccttcgactgc
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PESIVPBLERAAKSVGRDFSTFITDNTCGFBFPLURBIEKTVEGGERTIIRVQEIE
GEIEGEVKELEBEEEVTIFKRLTDGLMEVKQDIAMFFGGISKEEMELLDQMNMEATEVE
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                                                                                                                                                                              Oryza sativa subsp. indica
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3...(bases 1 to 1173)
Lin,R.-C., Xu,C.-C., Li,L.-B. and Kuang,T.-Y.
Direct Submission
Submitted (18-SEP-2000) Photosynthesis Research Center, Institute
of Botany, Chinese Academy of Sciences, Xiangshan, Beijing 100093,
                                                                                                                                                                                                                                                                           1 (bases 1 to 1173) Lin, E.-B. and Kuang, T.-Y. Lin, R.-C., Xu, C.-C., Li, Li-B. and Kuang, T.-Y. Molecular cloning and expression of rice violaxanthin de-epoxidase
              AF288196 1173 bp mRNA PLN 18-SEP-2000
Oryza sativa subsp. indica violaxanthin de-epoxidase mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                           Lin,R.-C., Xu,C.-C., Li,L.-B. and Kuang,T.-Y.
Direct Submission
Submitted (18-JUL-2000) Photosynthesis Research Center, Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Botany, Chinese Academy of Sciences, Xiangshan, Beijing 100093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 ggagaatttcctgccccagacccttctgttcttgtacagaacttcaacatctcggacttt 680
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On Sep 18, 2000 this sequence version replaced gi:9716690.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa subsp. indica"
/cultivar="Zhenhui-249"
/sub_species="indica"
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/product="violaxanthin de-epoxidase"
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/db_xref="G1:10181228"
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Local Similarity 69.9%;
hes 615; Conservative
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/translation="MNFYFHLCSLTLQRKATTSGKQLDAKTLRRLAQNREAARKSRLR
              Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
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/db_xref="taxon:3702"
/chromosome="1"
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/evidence=not_experimental
/product="T27G7.1"
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/product="T27G7.2"
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/db_xref="GI:6664302"
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                                  3 (bases 1 to 89479)
Ecker, J.R.
Direct Submission
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Ekkaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Ekkaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassicaceae; Arabidopsis.

I (bases 1 to 89479)
Shinn, P., Brooks, S., Buehler, E., Chao, O., Johnson-Hopson, C.,
Khan, S., Kim, C., Altafi, H., Bei, O., Chin, C., Chiou, J., Choi, E.,
Conn, L., Conway, A., Gonzales, H., Hansen, N., Howing, B., Koo, T.,
Inan, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S.,
Mukharsky, N., Nquyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J.,
Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G.,
Federspiel, N.A., Theologis, A. and Ecker, J.R.
Genomic sequence for Arabidopsis thaliana BAC T27G7 from chromosome
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Genomic sequence for Arabidopsis thaliana BAC 72767 from chromosome
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                                                                                                                                                                                                                                                          981 gggcgaaacgatgcttgggatggatatggtggtgcagttgtatacacgagaagttctgta 1040
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                                                                                                                  298 GCACAACCCGCGATCCTCTATAACCATGACAACGAGTTCCTGCACTATCAAGATGACTGG 357
                                                                                                                                                                921 tatatcctgtcatcaaagatagagaatagaactgaagactatatatttgtatactaccgt 980
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238 CGCACCCCGACTCTGGCTTCTTCACCAGAACAGCCATACAGCGGTTTGTGCAGGACCCA 297
                                                                        861 aaccaacctggtgttctctacaatcatgacaacgagtaccttcactatcaagatgactgg 920
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Ecker, J.R.
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Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lan, B., Lee, J., Len, Z., Liu, J., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Theologis, A. and Ecker, J. Bourited (03-JAN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA

7 (bases 1 to 89479) University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA

8 Chao, O. Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Conway, A., Gonzalez, A., Hansen, W., Howing, B., Koo, T., Lan, B., Lee, J., Lenz, C., Li, J., Liu, S., Mukharsky, N., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J., Liu, S., Wakharsky, N., Theologis, A. and Ecker, J., Cann, C., Chin, C., Davis, R., Choi, E., Chon, L., Choi, E., Choi, S., Cho
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LINYHEIPQGGHLIYHYDGICDTILRALLIKEEQGKLYKIN"
complement(join(1334. 22261,3126. 3288,4062. 4283,
4505. 4776,4882. 4930,5090. 5167,5499. 5558,5719. 5796))
/hote="similar to basic leucine zipper protein gi|2865394;
similar to ESTs gb|H76000, gb|AA651460"
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YRWPSLPKKLIKKDYRTGIIKWGLRISKYAPGLLHWWIIQKLFASTSSVLESNPEKLR
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-OCT-1999) Arabidopsis thaliana Genome Center, bepartment of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 89479)
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/note="unknown protein gb|AAD21437.1; similar to EST
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Submitted (11-02T-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, Pa 19104-6018, USA
On Nov 25, 1999 this sequence version replaced gi:6143825.
Location/Qualifiers
Submitted (20-MAY-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Str. Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 89479)
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RILSAYSKVNQKPKASSSKSEFEELEAKPTMAVMDGPLEPSSTARDAPDDPAFYNFFS
SYMLGNTASAGSASGSATENQPROPHOFTAPPVAAAAPPQIQSSPPLQSSSPL
MILENDNNEWISSNSNIHTDLWTPSFFGPPRWAQPHLIPGYSMFTAPPLNNNASHO
ORSYGTPVLQPFPPPTPPPSLAPAPTGPVISRDKVKEALLSLLQBDEFIDKITFLQN
                                                                                                                                                                                                                                                                                                                                        EFNIELSQWSRKDVEGSLFVVKRLLLSIFNYVYLIFNRLLKSDWILFFVSFRSTQPRF
QFIVMNRRNTDNLVENLLGDFEYEVQGPYLLYRNASQEVNGIWFYNKRECEEVATLFN
                                                                                                                                                                                                                                                                                                     /translation="MSQNGKIIPNLDQNSTRLLNLTVLQRIDPYIEEILITAAHVTFY
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26545. .26839))
/note="similar to inerleukin-1 beta convertase homolog A
20295. .20409,20600. .21079,21145. .21201)
/note="similar to yeast dcpl gli3169719; similar to ESTs gplH37036, emb|Z27040, gblR90173, gblA1999440.1"
/codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88259 CTCAGGTATTGCTTGGTGTGGGGAAGATTAGATAGTGTGAAGAATGGCAGTAGCTACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taggcttggcattacaagaaagagatcaatggcactttcttgctcaagattttacctcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88379 TAGGCTTGGCATTACAAGAAAGAGGATCAATGGCACTTTCTTGCTCAAGATTTTACCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---aggggatatttgacattgtgccatta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 89479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 330.4; DB 12; LCL2-
Pred. No. 2.5e-68;
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                                                                                                                                                        /evidence=not_experimental
/product="T27G7.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/product="T27G7.8"
/protein_id="AAF22903.1"
/db_xref="G1:6664321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Sequence 14 from patent US 5670367.
                                                                                                                                                                                                                       /protein_id="AAF22887.1"
                                                                                                                                                                                                                                                              /db_xref="GI:6664305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor sp|P55865"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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83.5%;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSKLQSEAVREAITTITCKSEAKKRNFVETIELQIGLKNYDPOK
DKRFSGSVKLPHIPRPKMK.CMLGDAQHVEEAEKMGLENMDVESLKKLNKNKKLVKKL
AKKYHAFLASESSVIKQIPRLLGPGLNKAGKFWLQLIFHFGNLSMEEKQIFQNVOMSVN
FLVSTLKKNWQNVRCLIKASYMGPPQRIF"
join(19189. .19347,19428. .19605,19741. .19885,20087. .20143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAQFLLTVLQVLLALTFWIGIGSGSSNHYNAGDHVPLFVNKVGP
LINPSETYOYYDLPPCRRGFVIEKOBTLGFVLNGDRLMSSIJKLKRFREDKTHFVLCRK
RLTSSDIARFEDIIAQDYYFOMYYDDLPWGFVGKVEGDYFGQGEKHTKYYIFSHLKF
NVLYNADKVLEINSFSDPSYMYDISRYTEIDVOFTYSSVSWLITSERSETRAMKYSRAS
FHPISQKIHFFSFLNSITVVVLLIGLISFLFMRHLKNELRSYSIGDEEBRKEAGWKLV
                                                                                                     OSLIDTLAASPVIDGMOOMAVALĞKISNLEĞFIRQADNLROÇTVÜQLRRILIYEVGAAR
CELVIGEYYGEKRALSSIMLERPROSVSEQTRAAALAELKLISKQDPDSRLIIADAĞA
IPVLAETLYSSHSOSIMLERPROSVSEQTRAAALAELKLISKQDPDSRLIIADAĞA
AVQSSAATIYSLLIAEESYRPIIGSKRDIIFSLIHIIRYDDSHPSIROSLKALFAIA
                                                                                                                                                                                                                                                      LYPMNRSTMISLGAIPALFSLIVKDSRCGIVEDATAVWAQVACCEDSEDGMRRVSGAN
VLADLLDPCTGSSLRIKENSVGALLNLARCGGAAARSEVAAAVASGADEGAMEGIVYV
AENGSLKGRKKAVDLLKLVVSGNGGGDSRFDYLFNENPNSRSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mnrDrpLHLINCQVLASPLTAIKLIEKGGEKERVMMNHKGFFTY
YRENNNHERSTRIKFDFTRELENGVLELLEVLHQVAUTERBANNHRMSEATNHNHNH
HLPYSLIHGLINNNHPSGFFINDDGSSEPDFGELEAIVLQVGG
GATTLEMFPSWPIRTHQTLPTESSKSGGESSDSGSANFSGKAESQQPESPMSSKHHLM
                           DDNRHÄSEIRTGLQAHLSDNDLRLIVDGYIAHFDEIFRLKAVAAKADVFHLIIGTWAS
PAERCFIWWAGFRPSDLIKILVSQMDLLTEQQLMGIYSLQHSSQQAEEALSQGLEQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MOHILIMPASGPYSFGLLDCSNGFARGEIERLRKLGKSELWWFG
GSTSSVGRYVLELARCFSTAEVEDNDRPAMDIGGPTNIRHVAHVTFDRFDGFLGLPSE
FEPDVPRKAPSARFHIIILEVFGSATVFGVSTESMQLSYDSRGNCVPVILLLLQSRLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGVLDPLPSEQVMQCESDEDFVKVVRLLPQTEASLLNWAI NLMADVIQFEHVNKMNSR
NLALVFAPNMSQMADPLTALMYAVQVMKLLKSLTEKTVREREASSSVVDRRCSKEAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSEFECSSAPDSKGDMCVVQPPICSSNR" complement(join(14188 . 14733,14829 . 14985,15122 . 15253, 15357 . 15945,16043 . 16083,16294 . 16439))
//note="putative multispanning membrane protein gb|AAD20090"
   KKAYVQQLESSRIKLSQLEQELQRARSQGLFMGGCGPPGPNITSGAAIFDMEYGRWLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQGGLQAEGVFRITGENSEEFFVREQLNKGIIPDGIDVHCLAGLIKVLVVIAWFRELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEKEKDNEEEEEDEEEEEEEEDEDEDEEEEGDGVYIIKEEEASEIIKVVADEHKSGSI
                                                                                                                                                                                                                                                                                                                                                                       complement(join(6389. .6646,7024. .7106,7608. .7702,8179. .8287,8565. .8654,8797. .8890,9113. .9184))
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/product="T27G7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/product="T27G7.4"
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/product="T27G7.5"
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/product="T27G7.6"
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/db_xref="G1:6664304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAF22905.1"
/db_xref="GI:6664323"
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/db_xref="GI:6664303"
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/db_xref="G1:6664322"
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contig 01
contig 02
contig 03
contig 04
contig 05
contig 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-JUL-1998) MPIMG, Abt.Lehrach, Max Planck Institut fuer Molekulare Genefik, Thnestrasse 73, Berlin, 14195, Germany on Jul 15, 2000 this sequence version replaced gi:8248731. HTGS_phase1: Unordered fragments separated by 100 N nucleotides
                                                                                                                                                                                                                                                                                                                                 1176 gaaggtgaaaggataatcgtaaaagaggttgaagagatagaagaagaaggtagagaaggaa 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1236 gtggagaaggtcggtaggactgagatgaccttgttccagagattggctgaaggatttaat 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1296 gaactgaagcaagacgaggagaatttcgtgagagagttaagtaaagaagaagatggagttt 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1356 ttggatgagatcaaaatggaagcaagtgaggttgaaaattgtttgggaaagctttgcca 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases I to 147243)
Radelof,U., Hennig,S., Ramser,J., Francis,F., Steffens,C.,
Unpublished
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-2000
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                   Score 92.4; DB 10; Length 7218; Pred. No. 1.4e-11;
                                                                                                                                                                                                      368 others
                                                                                                                                                                                                                                                                                                  12; Conservative 255; Mismatches 121; Indels
                                                                                          1 (bases 1 to 7218)
Dorner,F., Scheifflinger,F. and Falkner,F.Gunter.
Recombinant fowloox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1416 atcaggaaggtcaggtagaaacaagaac 1443
                                                                                                                                                                                    /organism="unknown"
1491 c 1486 g
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                   Query Match 5.9%;
Best Local Similarity 3.1%;
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 I66494
I66494.1 GI:2724471
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                                                                             Unclassified.
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Clone received from the Resource Centre of the Human Genome Project
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                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                    at the Max-Planck-Institute for Molecular Genetics.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.6%; Score 56; DB 84; Length 147243;
Best Local Similarity 54.5%; Pred. No. 0.011;
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37994 64306: contig of 26313 bp in length
64307 64406: gap of 100 bp
916407 91739: gap of 100 bp
91640 91739: gap of 100 bp
91740 94000: contig of 2221 bp in length
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64407. .91639
91740. .94000
94101. .134454
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                                                                                                                                                                                                                                                                                    NLGK ITLDVLPRRLLRSSQSSIPLLESGSSTAATDGAQAAAGDDDGYAWTHHVETSDV
VERYPDHMRDVLQSLKGPLHHDGVPRRHQAPSVKNLDSPSDCTVISRKKGPISRVTAF
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DALARATARIETETHVAATARDRELELEALRARWIETETRVYTSGSSWULKPPEASSAQPP
EGVSSATARFAEALAYEKTVQALNNELALLHENNAALSRATTREVDMLKRHWAEDQ
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VIVSSCMSTPVFNITAASFQSPSPSCVASNELIIPSVTFRGSPNPALEMLSMVTQSIP
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IIFNKAELSNEDSNRAIQEYYERNGAFALFTSARRCWRDVVEAVQRFTTHILPPLPYK
                                                                                                                                                                                   TVAHVGLVVGMPNVGKSTLINSLRLAHEYQFHREDFRRSRSPETVSITPGTTRGMKLV
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Prosite profile Prokar_Lipoprotein and Prosite pattern
Prokaryotic membrane protein, contains Pfam Glycos Transf
I Glycosyl transferase"
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/note="predicted using Glimmer, Testcode and CodonUsage"
14801. .>15382
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methyltransferase domain,has Blastp similarity to
hypothetical protein W02B12.10 from Caenorhabditis
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                                                                          AC009601 39987 bp DNA INV 20-JUN-2000
Leishmania major chromosome 35 clone L165 strain Friedlin, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myler, P.J., Sisk, E., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M., Cawthra, J., Marsolini, F., Sunkin, S. and Stuart, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nickerson Street, Seattle, WA 98109-1651, USA
2 (bases 1 to 3988)
Myler, P.J., Sisk, E., Cawthra, J., Handley, F., Vogt, C., Robertson, L.,
McDonagh, P., Ivens, A., Nguyen, D., Munden, H., Sunkin, S.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-JUN-2000) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA On Jun 20, 2000 this sequence version replaced gi:6001967. Location/Qualifiers
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/strain="Friedlin"
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/protein_id="AAF77208.1"
/db_xref="G1:8573035"
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/db_xref="GI:8573034"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:5664"
/chromosome="35"
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/gene="611.8"
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\/\dxxxef="G1:8573041"
/\translation="WSYRSSBARKEEFRKYLESTQWVDALTRVLVNLYEEEEKPEDPV
DYIKRVLGGASSADYEALQQENARLRAEVELLKKQLSGQAQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETGAQKTKLVAHDKDVYDIAFASAHTFASCGADGSVRFFDLRNMDHCTILYETQGLSP
LLRLAWNQFDPYFIATFGIDSPDAVVIDMRYPTVPASQLSQLHQLPINNLTWSPQNAQ
NICTAGEDGLVCVWEARAEKGRSILWCDCEVPINNVAWRRAQNEDWMAITTSKGAQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISPAQQLVMKQYSGRIPPMHPIGQPLMYDSWSELVELHKPDNEYQLLPRRARNNNAYA
VMSALCCSAGSPFEMDHRLEPVDFKLVFKSQADQDARTAFUNKHTDKVPQTIFLDGLM
PERKASALLYSFHNILTPAHVNNLAGTEQFLREWCRAPADGDRHRQLKLCFSSELEKQT
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27619. .27753
                       /translation="MLMCECTFASLCGNPCLPDPRWLGALYCLRLMGYACVRDPARPS VEVARRVPRRADDQQPARKACFLSFCGWGSARGLDSVATPLQVVSCVAAQTHRLDSLD
                                                                             TMATPPPPSFRTSLAHLSSIPRYFVSSHQHRRGTHAGAVYMTTGCRVIRMLTFTVLVL
                                                                                                       AALALLCHCRKRAYARNTVGFLHAAAGGGGGFRVLWVALDGLQHADAARGVKRQYVL
FTNEYKPADRLSAESSDQHLLSLVEKQFSIRLLRPVRFIYLRPALTRWLSGDAYPRLT
                                                                                                                                                                LLLQTFWGGAALFYEVAVANAVTPIVVETVGVPFAYPLLRLLAGCMVISYTHYPIVSS
AMTQRVRSGEVSHTNSPTVAMNPMLRCAKVVYYGVFSLLYRCMGFFPNVVLTNSSWTQ
                                                                                                                                                                                                                        NHVQSIFWPRACIRLYPPCDVAGFAAGSQPPALRNNRIVSVGGFRPEKNHMLQLVAFH
AAMPRLPRDAKLVWIGGARNADDRKRAEQLHVRAKELGIEEQVELLVNATVAEVQAEL
                                                                                                                                                                                                                                                                                   GKCVIGLHTMRDEHFGIVLLEYLAAGCIPLGHRSGGVELDILNSPDLGFLAVTAEEYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSLLNSTLQTLVVRLRDMSGNVTQQKLHNRVFDAYEAKSLVFQA
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23148. .>23402
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                                                                                                                                                                                                                                                                                                        AAMVEICEMRLRDPDRYVQFQKRGSEHVKSFDDSSFRTRFVELVSEYVYAC'
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Pred. No. 0.011;
0; Mismatches 139; Indels
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/db_xref="G1:8573042"
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/db_xref="G1:8573043"
/db_xref="GI:8573040"
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/gene="L165.2"
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/gene="L165.3"
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/gene="L165.3"
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/gene="L165.4"
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/gene="L165.4"
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Matches 139; Conservative
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Submitted (09-ocr-1998) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA (bases I to 42160) Myler, P.J., Sisk, E., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M., Cawthra, J., Marsolini, F., McDonagh, P., Stuart, K.D., Cunningham, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-OCT-1999) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA dibases 1 to 42160) Myler, P.J., Sisk, E., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M., Cawthra, J., Marsolini, F., McDonagh, P., Stuart, K.D., Cunningham, M.
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FIYRIRELLDGYVNAKGALEKESLKEYARSMRRTEWFPSVDCTVHESTTNVLYFHKTL
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YLASHPPNHYGTEIEARTEMQLQQIVRISEDFVKSAFINAVQRSKVSPSGASADGSTG
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TDACACLQRYVLTPLEDDYAVADIPSELATVVFELVYRRAIKVIQLDTSFFRADPTKLF
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SCEGASARKDTAAPPPDPPLSQLFDMLNSERERYVEAFGASWHKCFPSIKGQSDLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myler,P.J., Sisk,E., Hixson,G., Kiser,P., Rickel,E., Hassebrock,M.,
Cawthra,J., Marsolini,F., McDonagh,P., Stuart,K.D., Cunningham,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAGGSLSVAPRMDSALTAPTANRLIRNEAALQGVDQIVQRLGENFNRTDILRKDVRKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (31 MAY-2000) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA On Oct 2, 1999 this sequence version replaced gi:3723957.
1293 aatgaactgaagcaagacgaggagaatttcgtgagagagttaagtaaagaagagatggag 1352
                                        AC005804 42160 bp DNA INV 31-MAY-2000 Leishmania major chromosome 35 clone 6.1.1 strain Friedlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains a Proline-rich region (PRO_RICH), contains recA family and SURF1 domains (Pfam)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                               1353 tttttggatgagatcaaaatggaagcaagtgaggttga 1390
                                                                                                                                                                      2473 GAGGAGGAAGAGGAGGAAGAGGAAGAGGAAGAGGA 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Leishmania major"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Also known as 611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAF73077.1"
/db_xref="G1:8122319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:5664"
/chromosome="35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Friedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535. .>2694
/gene="511.9"
535. .>2694
/gene="511.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                AC005804.2 GI:6006841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="6.1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania.
1 (bases 1 to 42160)
Myler,P.J., Sisk,E., 1
                                                                                                                                                                                                                                                                                                                                                                              complete sequence.
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania major.
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/translation="MLLMRSSSPAATVQATHQRVQSAQERHVRREYASDVNTPRALSV
RSSRGGSFAFAPQVQEKYNTMNILVLGAPQVGKSLFINSYRAAITNTTRWPAAPVGIS
GFYGTTTVAPFPNHARQPTWLCIDTPGSLYTEKHAVLLEKLTEGMPWKTKLKGPNALT
                                                                                                                                                                                                                                                                                                                                            LRQIKDISPIAANKAHQCIIVVPATDLIEDDGLINTLLWRNRYRPAGGVADIIFYLKG
LISSLRTLMDDASPFVVVTKMDKVGGARNSSACAALVSILGQCVPVNHVYFTAAVENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLTLEWMEGQVGLFLLRGSVWSVTCGVPARNVSFAAVQALVLAAATCRCNVSGDELVM
STATCSNLVDTRHPYYCTVVLVGCLSATAFLAFLAFLAFLRANSTSYRFGVLDGPISWRRL
CKGNVLLSPAAVLLPPCACWLSWYETAGSTYPTLSSVWRPRADLLARPEWPHYRSDA
LIGAFVATLVTDALFYPIATMATRRFMSDLYKPQRPPSFGRSLYAGSYRYRLLSNLVIL
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SDSVSLDVASSFCGTPYYLAPELWERKRYSKRADMWSLGVILYELLTLHRPFKGPSQR
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LVRHSETISPNDRAEILKQLQESGERAPLPSSIRYGVMTSQVTHGGYLYKYGSDCRWK
KRYFYIGDGQLRISLSENPENDGVAPKSVNLETVGDVFPVPEVYSQKHPNQLVLWFNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mSAEHDSPSLAHVRSGDVLFWNRKCLAMKDPLGMLLCGLSKTEN
RFDHVGMFLKISEEELRKYPEARKRIAVLSPSGTYVLETNMRGITLYAAEGRVSRTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEVASRSVNVGDTEKQQEAQEAFLEQMETMYSTPYENEVFHLIPSICSPPDKMDRVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHKFNTLRLEVAALTEMANTHPSQAEVYRAVAHKYQHAQSFLLSTYFPHLASTSPTDA
LAVNWITGHYWIDGVNNADKMYCSELICNLWHRVGLTVGYVPASSIRPFDFLENBRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVSPASELGEIVPIRISKPYARYWKAPSGGAPATTRSAKATQAAMTEDQRLKFYNDVF
TSSGRPPVGSLRAAAASSEPLPSRWVVQSNTRSDVIPNLWFRVFSSGVLFAVCAVPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MPAKEVEHGSASTELLNQYAKYFPHVLFTSQEAFEKHAATLDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYKTCVDLPEGEESPESNPREHMYVLTTLVGRNPTTAAFVATRGSDPSEKVVAKFVML
NDDRQATYARSELHCLAACKHFGIVKHFDDFKSDDKLLLIMFYGSGGDLNKQIKQRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /hote="611.6; ORFdelta; predicted using Glimmer, Testcode and CodonUsage, Glimmer predicts second ATG as start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains Zinc finger domain, contains similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted using Glimmer, Testcode and CodonUsage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ORFgamma; predicted using Glimmer, Testcode and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1113 agaacggataacacatgtggtcctgaacctgcgctcgtggagaagaattgagaagacagtg 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="has similarity to nrk kinase, contains kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                /note="contains similarity to GTP binding proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Leishmania NIMA-related Kinase 1"
/protein_id="AAF73084.1"
/db_xref="GI:8122326"
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                                                                                                                                                                                                                                                                                                                                                                                                         ALLATGRIMVLESSTKQNLVRLHEDICLAVQWRNQVDAM"
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                                                                                                                                                                                       /protein_id="AAF73082.1"
/db_xref="GI:8122324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAF73083.1"
/db_xref="GI:8122325"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="611.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                /codon_start=1
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/gene="LNK1"
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/gene="611.3"
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                                   14694. .15641
/gene="611.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16520. .18433
/gene="611.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26724. .27497
/gene="611.8"
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         CodonUsage'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CodonUsage
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                                                                                                                                                                                                                                                                                                                                                               RAAEGSTDVIPVARVKAKSSLTRPVHATPTS IPSTRELLHWYEGSSVLNODVGHASAALT
HLSDCVAQBRRLKVEWEAARLAKIRALRAVKKVFMOSFIDRGSFARSTSVGGKVMSDT
LAVARCSVITWILVGTVQNFWRARFRSRRLCAARGPVSGLQLFVNIAGQESDRFTLSLY
SSAEGGAESSVNESYVSPHISVSDVLEEEEVSRIKQLYFDYFDCEAVSISSAVASGSD
MSIFAYSAASSISRPSSPVSRGGDHSSFSHCASTTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRSFHPKVULAICIORLFEKGLADGLMRLSIQPMLFGRYGLTGAMYQRLSTLYTLGM
ALNAFITWADTFALEGYTKRWYCWSAVGGSVFALLYGLLPAKESSAKPAALMFLT
ALFASNIDVFAVALYSEOTRRPAAGPALVSWWWGTALIGIMISSVILGPLSDNGLAH
FGVYTTAAILLLGGLEVFULPEERRNRAARLEDAMTEFLQKTKSASSESTAGSPPSP
HKLDGHLTIDNRVEEEDDNVDEQEAAAMDAQGFVRRPMDTYLCGAVEMNRDYLLKNWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /traislation="MHYEWFWOYAMYEAALKACLRAYPTVI.SKDGATRILHWGCGNS
DFCDHVEGILSDLHPVPSSSSRASEVLNVDICESIVAHLALHFPSRLYAVGNCCDLHV
SSSPSMPFSSNAAWYSRDPALKLRKVLQSSVDVVFDKGTADALLSSFAGEYNPNMEAY
MGEALKVLRFGGLLFLISINSEDVLSPYALSADDGLKSFHLAYTDVIELGAHDLRHLR
EPNSTMELRKSQRMAVKQWHRRVNDALLKKIYYCKAEAVMDAKSRTQLFDVSVAAVR
                                                                                                                                                                                                                                                                                                     /translation-"MERNPAHPLDATAKLPVRQKEVTFDSLCVNADDRFVEGLSGKSE
ERRGFRPNTKLYAANAARTRGRTGGASDLGFTESLPTLNEVIGEEKISHLGRLRARPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNAILYLSLPGVLNTFYVAKPSCLPDGPHFSYTFYNAMNGFLGNIAGIGGTIVFTHLF
PHHSYRFVMGLSAVLLPAASMFDVLILKRWNLAIGIPDHAMYIFGDTIIYEVCNMLLN
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ALWLVITGHIVTPVFILPLAYILLPSARISDHIDHTGRKVMEVALPETRTEEAEEPIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MALFCLILTLGVIANSLVSILGTWWDIMYVCIVLAAVLCVSSFFTLPLAIAKAVVFMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAAGFAQEHAQLFSVVTQFHAERIPLVLFLAGPERCGKTTLAHLLAARINCSTVINAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPGRYRVPSAPESPPPQGAKYVHPVSAHVLRAAPFLGYIPVFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLRDISASIDDSLPLFAVPETSSPDSTPSMLRGAEVSAVVAAEVDKAVREGRAIIVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains similarity to T.brucei ESAG10, contains transporter motifs and multiple transmembrane domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains SAM-dependent methyltransferase domain"
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                             DGFERMEVLLNGRTWSSQPQKWMSFTPTEWEDQIRQAF"
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/protein_id="AAF73080.1"
/db_xref="G1:8122322"
                                                                                                                                                                                                                                           /protein_id="AAF73078.1"
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/db_xref="G1:8122321"
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                                                      3675. .>4784
/gene="511.10"
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/gene="511.11"
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/gene="611.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Jul 15, 2000 this sequence version replaced gi:7344118.
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 2 clone RP11-41806, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162896)
25092 AGGAAGGAAAACAAAAGTGCACGCGTTTGCAGGGCGGAGGAACGAAGCGGCGGGATGTGG 25033
                                                                   1233 gaagtggagaaggtcggtaggactgagatgaccttgttccagagattggctgaaggattt 1292
                                                                                                                                                                            1293 aatgaactgaagccaagacgaggagaaatttcgtgagagagttaagtaaagaagagagatggag 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center
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                                                                                                                                                                                                                                                                                24852 GAGGAGGAAGAGGAAGAGAGAAGAGAAGAGGA 24815
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The sequence of Homo sapiens clone
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
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                                                                                                                                                                                      41167: contig of 12889 bp in length
41267: gap of unknown length
63710: contig of 22443 bp in length
63810: gap of unknown length
86811: contig of 23001 bp in length
86811: gap of unknown length
86911: gap of unknown length
113896: contig of 26985 bp in length
113996: gap of unknown length
s: contig of 2419 bp in length
s: gap of unknown length
t: contig of 4201 bp in length
s: contig of 7739 bp in length
s: contig of 7739 bp in length
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/note-"assembly_name:Contig8"
41268. 63710
/note-"assembly_name:Contig9"
63811. 86811
/note-"assembly_name:Contig10"
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/note="assembly_name:Contig12"
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/note="assembly_name:Contig11"
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/note="assembly_name:Contig6"
16754. .28378
/note="assembly_name:Contig7"
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2095. .4513
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/note="assembly_name:Contig5"
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/note="assembly_name:Contig4
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Erown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Forlins, S., Collymore, A., Cooke, P., Perreira, P., Fitzhugh, M., Forrest, C., Gage, D., Galagan, J., Ferreira, P., Fitzhugh, M., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Haeford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, D., Marquis, M., McEwan, P., McGurk, A., Wckernan, K., McHeeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dirnert, S., and Gody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dirnert, S., and Gody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dirnert, S., and Gody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dirnert, S., Anderson, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dirnert, S., Willey, R., Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 15, 2001 this sequence version replaced gi:11323390.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatWasker.html
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 178617)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo, sapiens chromosome 8, clone RP11-363G16
             Homo sapiens chromosome 8 clone RP11-363G16 map 8, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 363_G_16

Center clone name: 363_G_16

Sequencing vector: M13, M77815, 0% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 174502 bases at least Q40

Consensus quality: 1776097 bases at least Q30

Consensus quality: 177098 bases at least Q20

Insert size: 181000; agarose-fp

Insert size: 177917; sum-of-contigs

Quality coverage: 9.1 in Q20 bases; agarose-fp
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        873: contig of 873 bp in length
                                               SEQUENCE, 8 unordered pieces.
                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                  AC021529.4 GI:12229514
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                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
DEFINITION
                                                                                                                                                                                                                                                        ORGANISM
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JOURNAL
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JOURNAL
                                                                                                                         VERSION
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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Oenothera odorata chloroplast ORF80 and ORF2280 DNA.
X64616.555421
X64616.1 G1:14334
ORF 2280; ORF80.
                                   4719 4818; gap of 100 bp 4819 13584; contig of 8766 bp in length 13585 13684; gap of 100 bp 13685 29992; contig of 16308 bp in length 30093 178617; contig of 148525 bp in length. Location/Qualifiers
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5: gap of 100 bp
4718: contig of 1132 bp in length
                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11 Human Male BAC"
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51158 a 36845 c 38717 g 51192 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
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/note="assembly_fragment"
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                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                               /clone="RP11-363G16"
                                                                                                                                                                                                                                                                                                                                                                                                  vector_side:left"
974. .1610
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YKWYFELGTSMKKLTILLYLLTCSAGSIAQDLLSPPGPDEQNLITSYGLVENDSDLVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHEEBEBEBEBEBEBEBDELQENDSEFFRVKPIIPRHRWIFRKKKDVFEVLSYPEEAT
EISKELLKLLNPKTKRDAPKRPRQRWWTKKKQDKHYELLLDRQRWLITKRSLSKSNGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEVEGTEDEEVEGTEKDSSQFDNDRYTLLLRPKPRNPLDIQRLIYQHQKYESELEEDD
DDDEDVFAPQKMLEDLFSELVWSPRIWHPWDFLLDCEAEIPAEEIPEEEDELPEDALE
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1 (bases 1 to 2813)
Nimzyk, R., Schondorf, T. and Hachtel, W.
In frame length mutations associated with short tandem repeats are
located in unassigned open reading frames of Oenothera chloroplast
                                                                                                                                                                                           Hachtel, W.
Direct Submission
Submitsed (18-FEB-1992) W. Hachtel, Botanisches Institut der Uni
Bonn, Kirschalle 1, 5300 Bonn 1, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1140 cctgcgctcgtggagagaattgagaagacagtggaagaaggtgaaaggataaaggataatcgtaaaa 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1200 gaggttgaagagatagaagaagaagaggtagagaaggaagtggagaaggtcggtaggactgag 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
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Pred. No. 0.012;
0; Mismatches 162; Indels 2;
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                                                                                                                            Curr. Genet. 23 (3), 265-270 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3951"
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50.0%;
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/number=2
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2705. .280
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Best Local Similarity 50.09
Matches 164; Conservative
                                                                                                                                                       93169690
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6, 2001, 02:55:53 ; Search time 313.48 Seconds (without alignments) 3114.671 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                 Description
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                     730101 seqs, 313950809 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  sw model
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1555
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Maximum DB seq length: 200000000
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U I	12	102.8	9.0	936	22	AAF58257	Oligonucleotide D1
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ט ט		102.8	9.9	938	22	AAF58255	Oligonucleotide D1
		50.2	3.2	49999	50	AAZ23891	. Murine LOBO genomi
		50.2	3.2	49999	50	AAZ23896	Murine LOBO homolo
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	ო •	46.4	۰ د د	3901	198	AAT89345	Human p160 cDNA 16
	er Kr	4.4 0.1.4	, c	70307	7 0	AAC44224 AAV15422	Mouse noly Id rece
	n 40	44.4	9.0	7215	202	AAX13039	Enterococcus faeca
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	0,	43.6	8 6	2277	5.5	AAV13834	Homo sapiens ambig
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ی د	4 m	43.2	9.0	137507	9 6	AAV19941	KSHV long unique c
)	4	42.6	2.7	,	18	AAT51756	DAX-1 gene promote
	ı.	42.4	2.7	5935	21	AAA28818	Murine T cell indu
	9	42.4	2.7	6888	21	AAA59599	DNA encoding a cyt
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	œ	42.2	2.7	3717	21	AAA64660	
υ	σ.	42	2.7	1607	17	AAT35277	Chemokine receptor
ပ	0,	4.2	2.7	1677	27	AAA58872	DNA encoding a num
U	⊣ c	7 4 7	,,	1324	77	AAC30308	Arabidoneis thalia
	7 ~	41.0	, ,	1835	700	AAX91242	T. gondii immunoge
	. 4	41.2	2.6	1559	18	AAT91855	DUB-1 enhancer/pro
	ιn.	41	2.6	4677	21	AAA70259	Plasmodium falcipa
						ALIGNMENTS	
RES	RESULT	₽					
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AC *	AAT662	56243;					
Y E	28-3	-JUL-1997	(first	st entry)	<u> </u>		
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DE	Arak	Arabidopsis	viola	violaxanthin	ф	-epoxidase cDNA.	
YY	10,10	44444	0.00	9000		abt. photogen	
K K K	y 101 phot xant	Violaxanchin de-epoxidase; photoprotection; transgeni xanthophyll; lettuce; ss.	ion; lett	transge trensge	0	vos, ilync, phocosensicivity plant; zeaxanthin; antherax	antheraxanthin;
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OS A	Arak	Arabidopsis	thaliana	C	. col	columbia.	
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(CALJ) CALGENE INC.

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AAT66243

1553.4 624.2 608.6

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                                                                                                                                                                                              A cDNA clone (AAT66243) codes for Arabidopsis violaxanthin de-epoxidase (VDE) (AAW09976), an enzyme that catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. VDE nucleic acids (see also AAT66241-42), in sense or antisense plastid translocation sequence, to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                              modify the
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                                                                                                        DNA encoding plant violaxanthin de-epoxidase
                   Yamamoto HY;
                                                                                                                                                               Disclosure; Fig 3; 41pp; English.
                                                                                                                             sensitivity of a plant to light
                   ъ,
                   Rockholm
                                                   WPI; 1997-281036/25
                                                                      P-PSDB; AAW09876.
                   RC,
                   Bugos
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Sequence 1555 BP; 485 A; 286 C; 375 G; 409 T; 0 other;

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                                                                                                                           121 gtaggettggeattacaagaaagagatcaatggeaetttettgeteaagattttaeete 180
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Query Match 99.9%; Score 1553.4; DB 18; Length 1555; Best Local Similarity 99.9%; Pred. No. 0; Matches 1554; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.1%; Score 624.2; DB 18; Length 1589; 74.3%; Pred. No. 1.7e-162; Live 0; Mismatches 268; Indels 15;
photoprotection; transgenic plant; zeaxanthin; antheraxanthin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1589 BP; 500 A; 261 C; 367 G; 461 T; 0 other;
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                                                           Location/Qualifiers
42..1478
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                                    Nicotiana tabacum L. cv. xanthi
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Matches 820; Conservative
           xanthophyll; lettuce; ss.
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                                                                                                                                                                                                                                                                                                           gcataggcagagacttcagcacattcattagaacggataacacatgtggtcctgaacctg 1143
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                                                      aattogtgcaagatcctaaccaacctggtgttctctacaatcatgacaacgagtaccttc 903
                                                                                                                                          atttatcttggagaatacgtacacctgatggaggatttttttactcgatcagcggtgcaaa 900
                                                                                                                                                                                                                                                                                                                        acacgagaagttctgtattacccaatagcattataccagaactcgaaaaagcagcaaaaa
                                                                                                                                                                                                                                                                                                                                                         cgctcgtggaggaattgagaagacagtggaagaaggtgaaaggttaaatcgtaaaagagg
                                                                                                                                                                                                                                                                                                                                                                                                    ttgaagagatagaagaagatagagaaggaagtggagagaggtcggtaggactgagatga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccttgttccagagattggctgaaggatttaatgaactgaagcaagacgaggagaatttcg
tcaacatctoggactttaacgggaagtggtacattacaagtggcttgaatccaacctttg
          atgeettegaetgeeagetgeatgagtteeacacagaaggtgacaacaagettgttggaa
                                                                                      acatctcttggagaataaagaccctagacagtggattctttactaggtcagccgtacaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; lettuce; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Romaine lettuce violaxanthin de-epoxidase cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT66241 standard; cDNA; 1981
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gttgatgcacttaaaaacttgtgcatgcttattgaagggatgcaggatagaactcgcaaag 443

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A cDNA clone (AAT66241) codes for the 55 kDa violaxanthin de-epoxidase (VDE) (AAM09874) of romaine lettuce. VDE was purified from romaine lettuce chloroplasts and 2 tryptic peptides were used to develop primers (see also AAT6624445), which amplified a partial VDE sequence. The amplified sequence was then used to screen a lettuce CDNA library, and the 1981 bp DNA sequence was identified. VDE nucleic acids (see also AAT6624-43), in sense or antisense orientation, can be used in genetic constructs, pref. also contg. a plastid translocation sequence, to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases photosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding plant violaxanthin de-epoxidase - used to modify the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                                  /*tag= c
/note= "bases 105-110 are illegible in Fig 1"
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/note= "bases 147-149 are illegible in Fig 1"
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/note= "bases 186-189 are illegible in Fig 1"
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/note= "bases 226-227 are illegible in Fig 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto HY;
 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sensitivity of a plant to light
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                                                        misc_difference 66..72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CALJ ) CALGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-281036/25.
                                                                                                                                            misc_difference 147
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             misc_difference 26.
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                                                                                                                                                                                                                                                                                                                                                                            W09717447-A2
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                                                                                                                                                                                                                                                                                                                                   mat_peptide
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970 catgagtttcatatggaaaatg---ataaacttgttgggaacttaacatggcgcataaaa 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgaaacgatgcttgggatggatatggtggtgcagttgtatacacgagaagttctgtatta 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1147 atattatetteeeaaategaaaaeaaaeegaeegattaeaaeattegtataetaeegaggt 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cccaatagcattataccagaactcgaaaaagcagcaaaaagcataggcagagacttcagc 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtagaagaaaggaagtggagaaggtcggtaggactgagatgaccttgttccagagattggct 1283
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                                                                                            730 cctgacgagaccgaatgtcagataaaatgtggtgacttgttcgaaaacagtgtggtggac 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               864 caacctggtgttctctacaatcatgacaacgagtaccttcactatcaagatgactggtat 923
       tgtatagcaaacccatcttgtgcggcaaacgttgcctgtctacagacttgcaacaatcgt 729
                                                    ccagatgaaaccgagtgccagattaaatgtggggatctgtttgagaacagtgttgttgat 563
                                                                                                                                                                                    790 caattcaacgagtgtgcggtttcccgaaagaaatgtgtccccggaaatcggatgtgggt 849
                                                                                                                                                                                                                               624 gaatttoctgococagaccettetgttettgtacagaaettcaacateteggaetttaae 683
                                                                                                                                                                                                                                                                                                                                                                910 gggaagtggtatataacaagtggtttaaatcccacatttgatgcatttgattgtcaactt 969
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39.1%; Score 608.6; DB 18; Length 1981; 72.4%; Pred. No. 3.9e-158; Live 0; Mismatches 304; Indels 3;

Matches 804; Conservative

• QY

Best Local Similarity

Query Match

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AAF58254;
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                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022 atacacgagaagttctgtattacccaatagcattataccagaactcgaaaaagcagcaaa 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             782 aaacatctcttggagaataaagaccctagacagtggattctttactaggtcagccgtaca 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    842 aaaattogtgcaagatoctaaccaacctggtgttctctacaatcatgacaacgagtacct 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%; Score 104; DB 22; Length 936; 0.6%; Pred. No. 6.8e-19; lve 467; Mismatches 302; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                               ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 127; 159pp; English
                                                                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 467;
                        AAF58252 standard; DNA; 936 BP
                                                                                                                                                                                                                                                 26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                            99US-0145695
                                                                                                                                                                                                                                                                                       17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monitoring gene expression.
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                                                                             (first entry)
                                                                                                                               Electron-transfer group;
                                                                                                    Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-159728/16
                                                                                                                                           gene expression; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                           a single surface
                                                                                                                                                                                              WO200107665-A2
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                                                                             24-APR-2001
                                                                                                                                                                     Synthetic.
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                                                   AAF58252;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1382 tgaggttgaaaaattgtttgggaaagctttgccaatcaggaaggtcaggtagaaacaaga 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accaccattgttgtacaaactatatatacatactgtgttcggttcatataaagtaatat 1501
tgcgctcgtggagagaattgagaagacagtggaagaaggtgaaaggataatcgtaaaaga 1201
                                                                                                               ggttgaagagatagaagaagaggtagaaggaaggaagtggagaaggtcggtaggactgagat 1261
                                                                                                                                                                                                                              1262 gaccttgttccagagattggctgaaggatttaatgaactgaagcaagacgaggagaattt 1321
                                                                                                                                                                                                                                                                                                                                                                                                   1322 cgtgagagagttaagtaaagaagagatggagtttttggatgagatcaaaatggaagcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Electron-transfer group; ETM; mismatch; genotyping;
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Best Local Similarity 0.6%; Pred. No. 6.8e-19;
Matches 5; Conservative 467; Mismatches 302; Indels (
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17-MAR-2000; 2000US-0190259.
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic

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detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                               Ouery Match 6.6%; Score 102.8; DB 22; Length 936; Best Local Similarity 1.0%; Pred. No. 1.5e-18; Matches 8; Conservative 472; Mismatches 314; Indels 0;
                                                      Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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                                            Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
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                                                                                                                                                                         (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                             26-JUL-2000; 2000WO-US20476.
                                                                                                                                                        17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                  monitoring gene expression.
       (first entry)
                          Oligonucleotide D1875
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                                                     gene expression; ss
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                                                       The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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17-MAR-2000; 2000US-0190259.
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AAF58257/c
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Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

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Query Match
Best Local Similarity 1.0%; Pred. No. 1.5e-18;
Matches 8; Conservative 472; Mismatches 314;
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AAF58259 standard; DNA; 936 BP
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24-APR-2001 (first entry)

AAF58259

Oligonucleotide D2004

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Electron-transfer group; ETM; mismatch; genotyping;
gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
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                                                                  1362 gagatcaaaatggaagcaagtgaggttgaaaattgtttgggaaagctttgccaatcagg 1421
                                                                                                        1482 cggttcatataaagtaatatttttgtacacagtcatcatcattccataacaattggataa 1541
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                               The present invention relates to a composition comprising two nucleic
                                                                                                                                                          acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
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                                                                                                                                                                                                                                                                                                                               Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                   AAF58262 standard; DNA; 936 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-2000; 2000US-0190259
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Query Match
6.6%; Score 102.8; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 1.5e-18;
Matches 8; Conservative 472; Mismatches 314; Indels 0;

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942 gagaataaacctgaagactatatttgtatactaccgtgggcgaaacgatgcttgggat 1001
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                                                                                                                                                                   ggtgacaacaagcttgttggaaacatctcttggagaataaagaccctagacagtggattc 821
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                     The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 938;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                            Example 6; Page 127; 159pp; English
                                                                                                                                        (CLIN-) CLINICAL MICRO SENSORS INC.
                                                          26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                        monitoring gene expression.
                                                                                           99US-0145695
                                                                                                        17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                   WPI; 2001-159728/16
                                                                                                                                                                                                                                                               single surface
WO200107665-A2
                                                                                           26-JUL-1999;
                              01-FEB-2001
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                                                                                                                                                                                                                                                                               762 ggtgacaacaagcttgttggaaacatctcttggagaataaagaccctagacagtggattc 821
                                                                                                                       Query Match
6.6%; Score 102.8; DB 22; Length
Best Local Similarity 1.0%; Pred. No. 1.5e-18;
Matches 8; Conservative 472; Mismatches 314; Indels
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Search completed: November 6, 2001, 02:56:07 Job time: 11226 sec

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: CDNA to mRNA US-08-747-574-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         US-08-747-574-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
STATE:
November 6, 2001, 02:51:40 ; Search time 166.68 Seconds (without alignments) 2112.871 Million cell updates/sec
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Sequence 2, Appli
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                                                                                                                                                                Sequence 6, Al
Sequence 17, A
Sequence 17, A
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                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_NA:*
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    /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
    /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-770-379-20
US-08-757-669A-20
US-09-178-973B-17
US-08-875-573-19
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US-08-574-959A-8
US-09-357-014-8
US-08-574-959A-6
US-09-007-005-17
US-09-244-796-17
US-08-676-97-2
US-08-676-97-2
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US-09-676-97-2
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US-08-323-170B-1
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                                                                                                                                                                                                                               351203 seqs, 113238999 residues
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                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 209, Applisequence 3, Applisequence 3, Applisequence 6, Applisequence 16, Applsequence 8, Applisequence 5, Applisequence 101, Appleaquence 101, Appleaquence 3, Applisequence 1, Applisequence 2, Applisequence 1, Applisequence 2, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 4, Applise
                                   Sequence
                       US-07-915-246-1
US-08-741-891-209
US-08-741-891-209
US-09-244-796-3
US-09-244-796-3
US-09-078-294-6
US-09-078-294-6
US-09-018-584A-8
US-09-018-584A-8
US-08-13-934A-5
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US-08-742-185-101
US-09-272-032-8
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TITLE OF INVENTION: PELANT VDE GENES AND
TITLE OF INVENTION: METHODS RELATED THERETO
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STRREST: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-864-004B-3
US-08-251-937A-3
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SOFWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,574
FILING DATE: No. 6015939ember 7, 1996
CLEATOATION DATA:
APPLICATION NUMBER: 60/006,315
FILING DATE: NO. 601593ember 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: CATI J. SCHWEGIER
REGISTRATION NUMBER: 34,719
NAME: CATI J. SCHWEGIER
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 36,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/08747574
; Patent No. 6015939
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MEDIUM TYPE: Diskette
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	1141	1201	Db 1201 AGGTTGAAGAGATAGAAGAAG Qy 1261 tgaccttgttccagagattgg	1261	1321	1381		Oy 1501 tttttgracacagtcatcatcatcatcatcatcatcatcatcatcatcatcat	RESULT 2 US-08-747-574-2 ; Sequence 2, Application US/08	; Patent No. 5019939 ; GENERAL INFORMATION: ; APPLICANT: CALGENE, INC. ; TITLE OF INVENTION: PLANT	; TITLE OF INVENTION: METHOR ; NUMBER OF SEQUENCES: 3 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Calgene, Inc.	; STREET: 1920 Fifth Stree; CATY: CATY: CA ; STATE: CA ; COUNTRY: USA	ZIP: 95616 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette, 3 ; COMPUTER: Apple Macintos			; FILING DATE: August 6, 1; PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/C; FILING DATE: No. 6015939		
Query Best I Matche	1 CCACGCG 61 attgttt 	Db 61 ATTGTTCACTTCACCTTGTCATGACCGTATTTGTCTCAAGTGATGATGATTG 120 Qy 121 gtaggcttggcattacaagaaagagatcaatggcactttcttgctcaagatttacctc 180	GGCATTACAAGAAAGAGGATCAATGGCACTTTCTTGCTCAAGATTTTACCTC antactaatatcaagaactataatataaacaaaatataataataataataataat		Oy 241 tcaggtcaggattctctaaggggatatttgacattgtgccattaccatcaaagaatgagc 300 	Qy 301 tgaaagagctgaccgctccgctgttgctaaaactcgtgggtgttttagcttgcgcgttcc 360 	Oy 361 ttattgttccatctgcagatgcagttgatgcacttaaaacttgtgcatgcttattgaagg 420 Db 361 TTATTGTTCCATCTGCAGATGCAGTTGATGCACTTAAAACTTGTGCATGCTTATTGAAGG 420	Oy 421 gatgcaggatagaactcgcaaagtgcattgccaacctgcctg	Oy 481 gccttcagacctgcaataaccgtccagatgaaaccgagtgccagattaaatgtggggatc 540 	Qy 541 tgtttgagaacagtgttgttgatgatgattcaacgagtgtgctgtgtcgagaaaaagtgtg 600 	Oy 601 ttcctagaaaatctgatctcggagaatttcctgcccagacccttctgttcttgtacaga 660 	Oy 661 acttcaacatctcggactttaacgggaagtggtacattacaagtggcttgaatccaacct 720 	Oy 721 ttgatgccttcgactgccagctgcatgagttccacacagaaggtgacaacaagcttgttg 780°	Oy 781 gaaacatctcttggagaataaagaccctagacagtggattctttactaggccagccgtac 840 	Qy 841 aaaaattogtgcaagatcctaaccaacctggtgttctctacaatcatgacaacgagtacc 900 	Oy '901 ttcactatcaagatgactggtatatcctgtcatcaaagatagagaataaacctgaagact 960 	<pre>Qy 961 atatatttgtatactaccgtgggcgaaacgatgcttgggatggat</pre>	Oy 1021 tatacacgagaagttctgtattacccaatagcattataccagaactcgaaaaagcagcaa 1080
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                                                                                                                                                           Length 1589;
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                                                                                                                                                       Query Match 40.1%; Score 624.2; DB 3; Best Local Similarity 74.3%; Pred. No. 2.4e-171; Matches 820; Conservative 0; Mismatches 268;
TELECOMMUNICATION INFORMATION:
        TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARATERISTICS:
LENGTH: 1589
                                                                                                       MOLECULE TYPE: CDNA to mRNA
                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                        1589
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.40 MB
COMPUTER: Apple Macintosh
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,574
FILING DATE: No. 6015939ember 7, 1996
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/023,502
FILING DATE: August 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,315
FILING DATE: No. 6015939ember 7, 1995
ATYONEY/ABONT INFORMATION:
NAME: Donna E. SCHAFER
REGISTRATION NUMBER: 34,719
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REFERENCE/DOCKET NUMBER: 119-2
                                                                                                                                                                                                                                                                                                                                                                            1489 AACTATCAACATATATACTACAT 1511
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1920 Fifth Street
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TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 36
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39.3%; Score 611.8; DB 3; Length 1981; 72.5%; Pred. No. 1.1e-167;

Query Match Best Local Similarity

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1567 GAGAAGGAAATTCTGAATGAACTTCAAATGGAAGCGACTGAAGTTGAAAAGCTTTTTGGG 1626
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                                       324 ttgctaaaactcgtgggtgttttagcttgcgcgttccttattgttccatctgcagatgca 383
                                                             384 gitgaigcacitaaaaacitgigcaigcitaitgaagggaigcaggaiagaacicgcaaag 443
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                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                               APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
IITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                           1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                   Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,768
                                                                                                                                                                                                       Foley & Lardner
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                APPLICANT: DORNER, F. APPLICANT: SCHEIFLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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                                                                                                                                                                                                                                                Alexandria
                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22313-0299
                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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US-08-232-463-14/C
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1296 gaactgaagcaagacgaggagaatttcgtgagagagttaagtaaagaagaagatggagttt 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger.
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TELEPHONE: (617)227-7400

TELEPHONE: (617)227-5941

INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 3211 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                         1091 RRRRRRRRRRRRRRRRRRRATC 1064
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STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08574959A Patent No. 5962224
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Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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US-08-574-959A-8
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                                                                                                                                                 1275 agattggctgaaggatttaatgaactgaagcaagacgaggagaatttcgtgagagatta 1334
                                                                                                                                                                                                                                                                                                                                                                                                              RELATED POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                    AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/574,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                Sequence 8, Application US/09357014 Patent No. 6291645 GENERAL INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
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439..3157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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Matches 126; Conserv
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1335 agtaaagaagagatggagtttttggatgagatcaaaatggaagcaagtgaggttgaaaaa 1394
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                                                                                                                                                                                                             APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger.

APPLICANT: and Jack L. Strominger

TITLE OF INVENTION: pc2 POLYPEPTIDES, RELATED POLYPEPTIDES

TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%; Score 46.4; DB 2; Length 39(52.5%; Pred. No. 0.0013;
ive 0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
                                                                                                                                                                                                                                                                                                                                              E: LAHIVE & COCKFIELD
60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/574,959A FILING DATE: 19-DEC-95 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: DFN-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                ; Sequence 6, Application US/08574959A; Patent No. 5962224; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
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Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2; CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                             Massachusetts
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                              US-08-574-959A-6
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1155 agaattgagaagacagtggaagaaggtgaaaggataaatcgtaaaagaggttgaagagata 1214
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                                                                                                                      and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.0%; Score 46.4; DB 4; Length 3901; 52.5%; Pred. No. 0.0013; tive 0; Mismatches 111; Indels 3
                                                                                                 APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-041-1999
PRIOR FAPFILCATION DATA:
APPLICATION NUMBER: 08/574,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 439..3847
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 17, Application US/09007005B
; Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                       Sequence 6, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                     NUMBER OF SEQUENCES: 22
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Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                        Boston
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US-09-007-005-17
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US-09-357-014-6
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                                                                                                                                                                                                                                   DB 4; Length 289;
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                                                                                                                                                                                                                              Query Match 2.8%; Score 43.8; DB 4; Length 2 Best Local Similarity 6.2%; Pred. No. 0.0019; Matches 14; Conservative 103; Mismatches 110; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARTENTINE Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Science & Technology Law Group
268 Bush Street, Suite 3200
                        FEATURE: OTHER INFORMATION: Translation template
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VENTION: Human Telomerase
                                                                   FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(289)

OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08676967; Patent No. 5747317; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUNDMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-676-967-2
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Sequence 17, Application US/09244796

Patent No. 628134

GENERAL INFORMATION:

APPLICANT: SZOSTEK, Jack W.

APPLICANT: SZOSTEK, Jack W.

APPLICANT: SZOSTEK, Jack W.

APPLICANT: ROBERTS, RICHAID W.

APPLICANT: INFORMATION: SELECTION OF PROTEINS USING RNA-PROTEIN

TITLE OF INVENTION: FUSIONS

FILE REFERENCE: 10786/350007

CURRENT APPLICATION NUMBER: 08/095,963

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER FILING DATE: 1997-01-27

BARLIER FILING DATE: 1997-01-27

SERLIER FILING DATE: 1997-11-06

EARLIER FILING DATE: 1998-01-14
GENERAL INFORMATION:

A PPLICANT: SZOSLAK, Jack W.

APPLICANT: ROBERTS, Richard W.

TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: EVISIONS; FILE REFERENCE: 00786/35003; CURRENT APPLICATION NUMBER: 05/09/007,005B; CURRENT APPLICATION NUMBER: 05/095,963

EARLIER APPLICATION NUMBER: 06/005,963

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-11-06

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PASSEQ for Windows Version 4.0

EENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%; Score 43.8; DB 4; Length 289; Best Local Similarity 6.2%; Pred. No. 0.0019; Matches 14; Conservative 103; Mismatches 110; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A.T.C or
015-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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LENGTH: 289
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LENGTH:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   466 TIYGGNTIYGTNCARTIYAARAAYYINYINGARGCNGGNAARGCNYINAARGGNAIGAAY 525
                                                                756 acagaaggtgacaacaagcttgttggaaacatctcttggagaataaagaccctagacagt 815
                                                                                                    226 ACNGTNGCNAARAARAARYTNMGNAAYAARACNAARGARAARGGNAARAAYGARAAYWSN 285
                                                                                                                                                876 ctctacaatcatgacaacgagtaccttcactatcaagatgactggtatatcctgtcatca 935
                                                                                                                                                                                                                                                                         346 YINATHATHMGNAAYYINWSNTIYAARTGYWSNGARGAYGAYYTNAARACNGTNTTYGCN 405
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                                                                                                                                                                                           286 GARTGYCCNAARAARGARCCNAARGCNAARACCNAARGTNGCNGAYAARAARGCNMGN 345
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                           Gaps
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Best Local Similarity 25.9%; Pred. No. 0.0064;
Matches 138; Conservative 86; Mismatches 308; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science & Technology Law Group
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08676974
Patent No. 5770422
GENERAL INFORMATION:
APPLICANT: COLLINS: KATHLEEN
TITLE OF INVENTION: Human Telome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415)343-4341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415)343-4342
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94104
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                                                                                                                                                                   2.8%; Score 43.6; DB 1; Length 2277; 25.9%; Pred. No. 0.0064; Live 86; Mismatches 308; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Science & Technology Law Group
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: COLLINS, Kathleen
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5917025
                                                                                                                                                                                                                 Matches 138; Conservative
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                    ; MOLECULE TYPE: CDNA
US-08-676-974-2
                                                                                                                                                                                            Similarity
                                                linear
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.8%; Score 43.6; DB 2; Length 2277; Best Local Similarity 25.9%; Pred. No. 0.0064; Matches 138; Conservative 86; Mismatches 308; Indels 0.
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                                                                           UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08728323A Patent No. 5948676
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                                                                REFERENCE/DOCKET NUMBER: UCB9
TELECOMMUNICATION INFORMATION:
TELERAN: (415)343-4341
TELERAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                       LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: CDNA
US-09-098-487-2
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Sequence 20 Application US/08770379
Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bolenaky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Moore, Patrick S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 112-278-0400
                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 138;
                   1185 Avenue of the Americas
                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Cooper & Dunham LLP
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
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                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                     New York
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                                                New York
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                                                                                           COUNTRY:
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CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,379

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 52342

FREERENCE/DOCKET NUMBER: 52342

TELEPHONE: (212) 276-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 20:

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 20:

LEMGTH: 32207 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

STRANDEDNESS: double

STRANDEDNESS: double

STRANDEDNESS: linear

MOLECULE TYPE: DNA (genomic)
                           ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CORRESPONDENCE ADDRESS:
                                              STREET: 1185 Aven
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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Gaps Ouery Match
2.8%; Score 43.2; DB 2; Length 32207;
Best Local Similarity 47.7%; Pred. No. 0.033;
Matches 126; Conservative 0; Mismatches 138; Indels 0;

20903 ACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGATGACGAGGATG 20844 1258 agatgaccttgttccagagattggctgaaggatttaatgaactgaagcaagacgaggaga 1317 d ò g

1318 atttcgtgagagagttaagtaaagaagagatggagtttttggatgagatcaaaatggaag 1377 g δ

20783 ATGACGATGATGAGGACAATGAGGACGAGGAGGACGAGGAGGAGAGAAGAAGAGGG 20724 οy

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1438 aagaaccaccattgttgtacaaac 1461 οy

20663 AGGAGCCACAACAGCAGGAGCCAC 20640

Search completed: November 6, 2001, 02:52:34 Job time: 11033 sec

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November 6, 2001, 00:54:09; search time 3841.92 Seconds (without alignments) 3826.000 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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190: qb_estil0:*

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193: em_qss_fun:*

194: em_qss_fun:*

195: em_qss_huml:*

196: em_qss_huml:*

197: em_qss_huml:*

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197: em_qss_huml:*

198: em_qss_huml:*

199: em_qss_huml:*

200: em_qss_
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TITLE JOURNA COMMENT		FEATURES			FEATURES			FEATURES			FEATURES sou		FEATURES		FEATURES		FEATURES		FEATURES		FEATURES				BASE COU			Best L			Db 1	Qy 48	Db 7	Qy 54	Db 13	Qy 60	Db 19	Qy 66	Db 25	Qy 72	Db 31	0у 78	Db 37	Qy 84	OY 84 DD 43 RESULT AV440942, LOCUS DEFINITI ACCESSION VERSION KEYWORDS SOURCE		ORGANI
Description	AI994713 701499353	AV442545 AV442545 AV442545 AV442545	AV521985 AV521985 N37612 18839 Lambd	BF069291 st45b12.y	B28051 T2/G/TFB TA B08217 T27M8-T7.1	B13003 T27G7-T7.1	AV410579 AV410579	B13009 T27M8-T7 TA BE018838 EM1 2 E01	A1668224 605018D09	AZ126934 OSJNBD007 AZ126249 OSJNBD007	AQ858812 nbeb0002N	BE191198 sn93d05.y	AW398615 EST309115 BE595698 PI1 55 E1	BG123331 EST468977	BE440946 sp30a05.y	BF623692 HVSMEa000 AL060767 Drosophil	BG157169 Sab23304.	AW929268 EST338056	AL08773 Drosophil AL108773 Drosophil	ALUS6019 Drosophil	BF641377 NF061G021 AL108415 Drosophil	ALU/2006 Drosophil		AL108618 Drosophil AL108811 Drosophil		ממ				EST 08-SEP-1999 set Arabidopsis thaliana		ambryophyta; Tracheophyta;	spermatophyta; magnoilophyta; euolcocyledons; core euolcots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 483)	Carroon,B., Gilliland,D., Doyle,M., Brzoska,P., ttoua,M., Nguyen,D., Tan,R.													
SUMMARIES	AI994713	AV442545	AV521985 N37612	BF069291	B08217	B13003	AV410579	B13009 BE918838	A1668224	AZ126934 AZ126249	AQ858812	BE191198	AW398615 BE595698	BG123331	BE440946	BF623692 CNS005TE	BG157169	AW929268						CNSO182P CNSO182P			SENEMBLIA	CINTERIOR		State clone	ilkina sequelice.	tae; Streptophyta; E	iopnyta; eudicotyled Brassicales; Brassi	. Chan, E., Mooney, M., Carroon, B., Gillila Guegler, K., Kim, C., Doyle, M., Brzoska, P . Griffin, J., Mouanoutoua, M., Nguyen, D.,													
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Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and Hanson,D. Arabidopsis thallana Gene Expression MicroArray Unpublished (1999)
Contact: David Smoller, Ph.D. Genome Systems, Inc., a wholly owned subsidiary of Incyte
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Pred. No. 6.3e-113;
0; Mismatches 4; Indels 0;
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Asia World Parkway Circle, St. Louis, MO 63134, USA Tel: 877-577-2733
Fax: 314-427-3324
                                                                                                                                                                                                                                                           Email: service@genomesystems.com
Location/Qualifiers
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Local Similarity 99.1%;
es 466; Conservative
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 424)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size—selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="APZ16c07_r"
/clone_lib="Arabidopsis thaliana above-ground organ two to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="aboveground organs"
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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0; Mismatches 4
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(bases 1 to 400).

Asamizu, E., Nakamura,Y., Sato,S. and Tabata,S.
Alarge scale analysis of cDNA in Arabidopsis thatgo scale analysis of cDNA in Arabidopsis thatlana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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/clone="Ap216c07_f"
/clone_lib="Arabidopsis thaliana above-ground organ two to
                                                                                                                                                                                                                     The First Laboratory for Plant Gene Research
Kasusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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/dev_stage="two to six-week old"
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/clone_lib="Lambda-PRL2"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_l: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) steade plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
ollog off primed cDNA.

97 c 102 g 114 t 17 others
                       Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
                                                                                        Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/strdin="var columbia"
                                                                                                                                                                                     Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                          MSU-Local Lansing, Mi

Lansing, Mi

Tel: 517-353-0854

Fax: 517-353-9168

Email: 22313tcn@ibm.cl.msu.edu

Seg primer: 77 dye primer.

Location/Qualifiers
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/clone="207C23T7"
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1 (bases I to 335)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Alarge scale analysis of conn. In Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected conn.
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu(ekazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone_lib="Arabidopsis thaliana aboveground organs two to
six-week old"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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18839 Lambda-PRL2 Arabidopsis thaliana cDNA clone 207C23T7, mRNA
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/strain="Columbia"
/db_xref="taxon:3702"
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XhoI; The CDNA library was constructed from mRNA isolated
from germinating shocts of 3 day old seedling for the
cultivar Williams 82. The seedlings were germinated in a
growth chamber using germination paper in a solution
containing 100ppm auxin. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT) sequence
with a XhoI restriction site. EcoRI adapters were ligated
to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). This library was constructed
in the laboratory of Dr. Randy Shoemaker."
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/clone_lib="Gm-c1067"
/tissue_type="Germinating shoot, 3 day old seedling, auxin
treatment"
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BF069291 17-CCT-2000 EST 17-CCT-2000 EST 545BiL2 Y Gm-cliof Glycine max cDNn clone GENOME SYSTEMS CLONE ID: Gm-cliof7-1991 5' similar to TR:040593 040593 VIOLAXANTHIN DE-EPOXIDASE PRECURSOR. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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High quality sequence stop: 421.
Location/Qualifiers
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Public Soybean EST Project
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                                                                                                                                                                                                                                              BF069291.1 GI:10846383
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314 286 1810
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62 ATTGTATACTACCGAGGCAGAAATGATGCATGGATGCTTATGGAGGTGCTGTTATATA 121

905 ctatcaagatgactggtatatcctgtcatcaaagatagagaataaacctgaagactatat 964

2 CTATCAAGATGACTGGTATATTTTGTCATCAAGATTGAGAATAAGCCAGATGACGT 61

0; Mismatches 142; Indels 12; Gaps

Conservative

Local Similarity

Matches 371: Query Match

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DB 144; Length 515;

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/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII; Produced by Rod Wing" 130 c 111 g 163 t
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Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
1025 cacgagaagttctgtattacccaatagcattataccagaactcgaaaaagcagcaaaag 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1265 cttgttccagagattggctgaaggatttaatgaactgaagcaagacgaggagaatttcgt 1324
                                                                                                                                     1085 cataggcagagacttcagcacattcattagaacggataacacatgtggtcctgaacctgc 1144
                                                                                                                                                                                                                                                                   .145 gctcgtggagagaattgagaagacagtggaagaaggtgaaaggtgaaaggataatcgtaaaagaggt 1204
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                                                                                                                                                                182 TGTGGGAAGACATTTAGCACGTTCATCAGGACAGATAACACATGCGGGCCAGAGCCTTC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 TGAACAGTTAGAAGAAGAGG------GTGGAGAAGGTGGGGAAAACGGAGGCCAC 349
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                                                                122 CACAAGAAGTGCCAGTTTTGCCTGAATCTATAGTTCCTGAACTTGAAAAAGCAGCTAAGAG 181
                                                                                                                                                                                                                                                                                                                             410 AAGAAGGTTATCAAAACAAGAAATGGAAATTCTTTATAGGCTCAAAATGGAAACCCAGTG 469
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T27G7TFB TAMU Arabidopsis thaliana genomic clone T27G7, DNA
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Location/Qualifiers
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Seg primer: M13-21
Class: BAC ends
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Contact: Steve Rounsley
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/sex="hermaphrodite"
//note="Vector: BeloBACII, Site_1: HindIII, Site_2: HindIII
//note="Vector: BeloBACII, Site_1: HindIII, Froduced by Rod Wing"
3 372 c 198 g 319 t 9 others
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Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.
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Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
                                                                                                                              260 GTGTCGAGAAAAAAGTGTGTTCCTAGAAAATCTGATCTCGGAGAATTTCCTGCCCCAGAC 201
                                                                                                                                                                                   642 cettetgttettgtacagaaettcaacateteggaetttaaegggaagtggtacattaca 701
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T27G7-T7.1 TAMU Arabidopsis thaliana genomic clone T27G7, DNA
                               200 CCTTCTGTTCTTGTACAGAACTTCAACATCTCGGACTTTAACGGGAAGTGGTACATTAAA
                                                                                                                                                                                                                                                                               582 gigicgagaaaaagigigitcciagaaaatcigaicicggagaaiiiccigccccagac
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Unpublished (1997)
Other_GSSs: T27G7-Sp6, T27G7-T7, T27G7-Sp6.1
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Seg primer: T7
Class: BAC ends
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/clone="T27G7"
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B13003.1 GI:2094j35
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Fax: 215-898-8780
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/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII
: Produced by Rod Wing"
366 c 195 g 357 t 25 others
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                                                                                       Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
                                                                                                                                                                                                                                          642 ccttctgttcttgtacagaacttcaacatctcggactttaacgggaagtggtacattaca 701
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T27M8-T7.1 TAMU Arabidopsis thaliana genomic clone T27M8, DNA
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Pred. No. 2.2e-54;
0; Mismatches 5; Indels 0; (
                 Length 599;
                                                    Indels
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Other_GSSs: T27M8-Sp6.1, T27M8-Sp6, T27M8-T7
             Score 256; DB 256;
Pred. No. 1.7e-57;
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16.5%; Scor.
100.0%; Pred. No. 1...
'-. 0; Mismatches
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Seq primer: T7
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High quality sequence stop: 594.
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/clone="T27M8"
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98.0%;
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Arabidopsis thaliana
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Best Local Similarity 98.03
Matches 247; Conservative
                                                  Matches 256; Conservative
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  DB 256; Length 1147;
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Query Match 15.6%; Score 243; DB 256; Best Local Similarity 96.1%; Pred. No. 6e-54; Matches 249; Conservative 0; Mismatches 10;
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0; Gaps

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/sex="hermaphrodite"
/note="Vector: BelobACII; Site_1: HindIII; Site_2: HindIII
/ Produced by Rod Wing"
/ 293 c 132 g 262 t 52 others
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                      527 taaatgtggggatctgtttgagaacagtgttgttgatgattcaacgagtgtgctgtgtc 586
                                      582 gtgtcgagaaaaagtgtgttcctagaaaatctgatctcggagaatttcctgccccagac 641
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320 CAGATTAAATGTGGGGATCTGTTTGAGAACAGTGTTGTTGATGAGTTCAACGAGTGTGCT 261
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727G7-T7 TAMU Arabidopsis thaliana genomic clone T27G7, DNA
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Pred. No. 1.8e-52;
0; Mismatches 10; Indels
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Unpublished (1997)
Other_GSSs: T27G7-Sp6, T27G7-T7.1, T27G7-Sp6.1
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Seq primer: T7
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Arabidopsis Thaliana Genome Center
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96.0%;
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Yana 1532-3, Kisarazu. Chiba 292-0812, Japan
Email: yaakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotus.
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/dev_stage="young plants (two-week old)"
/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
a 85 c 102 g 128 t
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
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                      279 GAGAAAAAAGTGTGTTCCTAGAAAATCTGATTTCGGAGATTTTCNTGCCCCAGACCCTTC 220
                                                                     647 tgttcttgtacagaacttcaacatctcggactttaacgggaagtggtacattacaagtgg 706
                                                                                                                 219 TGTTCTTGTACAGCACTTCCACATCTCGGACTTTAACGGGAAGTGGTACATTACAAGTGG 160
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AV410579 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MWL074g05_r 5', mRNA sequence.
0;
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Kazusa DNA Research Institute
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/db_xref="taxon:34305"
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DNA Res. 7 (2), 127-130 (2000)
2027479
Contact: Yasukazu Nakamura
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AV410579.1 GI:7723433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lotus japonicus
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/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII; Produced by Rod Wing" 75 others
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Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 GGGATCTGTTTGAGAACAGTGTTGTTGATGAGTTCAACGAGTGTGCTGTGTCGAGAAAA 282
                                                                                                                                                   Dept. of Biology, University of Pennsylvania, Philadelphia, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 gggatctgtttgagaacagtgttgttgatgagttcaacgagtgtgctgtgtcgagaaaaa 594
                                                                         596 gigigitectagaaaatetgateteggagaattteetgeeeeagaeeettetgitettgt 655
536 ggatctgtttgagaacagtgttgttgatgagttcaacgagtgtgctgtgtcgagaaaaa 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                   242 GGACCTGTTTGAAAACAGTGTGGTTGATCAATTTAATGAGTGTGCAGTCTCCCGGAAGAA 301
                                                                                                               302 ATGTGTACCTAAGAAATCTGACGTGGGAGAGTTTCCTGCTCCAAATCCTGATGTCCTTGT 361
                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                      T27M8-T7 TAMU Arabidopsis thaliana genomic clone T27M8, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 256; Length 985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.9%; Score 231.2; DB 256; Lengt 95.9%; Pred. No. 8.2e-51; tive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC End Sequences at ATGC
Unpublished (1997)
Other_GSSs: T27M8-T7.1, T27M8-Sp6.1, T27M8-Sp6
Contact: Ecker J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: jecker@atgenome.bio.upenn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis Thaliana Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 350
High quality sequence stop: 477.
Location/Qualifiers
1. 985
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                                                                                                                                                                                                                                                                                                                                                                    985 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 215-898-9384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T7
Class: BAC ends
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/clone_lib="Floral-induced Meristem 1 (FM1)"
/clone_lib="Floral-induced meristems; Vector:
/note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_l: XhOI; Site_2:
ECORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/Fearly May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda ZAP II. clones to be sequenced were prepared by
mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 549)
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sorghum propinguum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                               29-SEP-2000
                                                                                                                                                                                                                                                                                                                             BE918838 549 bp mRNA EST 29-SEP-2
FM1_2_F01.91_A003 Floral-Induced Meristem 1 (FM1) Sorghum
propinguum cDNA, mRNA sequence.
BE918838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An EST database from Sorghum: floral-induced meristems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sorghum propinguum"
/db_xref="taxon:132711"
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High quality sequence start: 89
High quality sequence stop: 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                      BE918838.1 GI:10422122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Botany
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Matches 271; Conserv
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Alb68224 602 bp mRNA EST 02-FEB-2000 605018D09.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays Alg68224
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/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="nucellar, post-pollination"
/lab_host="DH5(alpha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; 2ea.
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1177 aaggtgaaaggataatcgtaaaagaggttgaagagatagaagaagaggtagagaaggaag 1236
                                                                                                                                                                                                                     1297 aactgaagcaagacgaggagaatttcgtgagagagttaagtaaagaagaagatggagtttt 1356
                                                                                                                                               1237 tggagaaggtcggtaggactgagatgaccttgttccagagatttgctgaaggatttaatg 1296
                                                                                                                                                                                                                                                                                           1357 tggatgagatcaaaatggaagcaagtgaggttgaaaaattgtttgggaaagctttgccaa 1416
                                                                                                                                                                                                                                                        229 AGGIGAAACAGGATTIGATGAACTICTIGCAGGGCTGAGCAAGGAGGAGATGGAGCTGI 288
                     181 AGAAGGAG------GAGGCATCATTGTTTCAAAAGCTGGCAGAAGGTCTCATGG 228
                                                                                                                                                                                                                                                                                                                  Walbet, V. Malze ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                   1417 tcaggaaggtcaggtagaaacaagaaccaccattgttgtacaaacta 1463
                                                                                                                                                                                                                                                                                                                                                                                                      855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 728 8221
Email: walbot@stanford.edu
Plate: 605018 row: D column: 09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays.
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10.6%; Score 164.8; DB 23; Length 602; 66.6%; Pred. No. 3.8e-33; tive 0; Mismatches 117; Indels 12; Gaps

Best Local Similarity 66.6 Matches 257; Conservative

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Query Match

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/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBACIndigo; Site_1: ECORI; Site_2: ECORI;
/note="Vector: pBACIndigo; Site_1: ECORI; Site_2: ECORI;
/note="Vector: pBACIndigo; Site_1: ECORI; Site_2: ECORI;
/note="Vector: pBACIndigo; Site_1: ECORI;
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/note="Vector: pBACIndigo; Site_1: ECORI;
/note="Vector: pBACIndigo; Site_1: ECORI;
/note="Vector: pBACING: PBACING:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ126934 411 bp DNA GSS 02-JUN-2000 OSJNBb0079L12r CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone OSJNBb0079L12r, DNA sequence.
                                                                                    1113 agaacggataacacatgtggtcctgaacctgcgctcgtggagagaattgagaagacagtg 1172
                                                                                                                                                                                                                                                             1173 gaagaaggtgaaaggataatcgtaaaagaggttgaagagatagaagaagaggtagagaag 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                1233 gaagtggagaaggtcggtaggactgagatgaccttgttccagagattggctgaaggattt 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1293 aatgaactgaagcaagacgaggagaatttcgtgagagattaagtaaagaagagatggag 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1353 tttttggatgagatcaaaatggaagcaagtgaggttgaaaaattgtttgggaaagctttg 1412
                                                                                                                                   476 GTGGAAGGAGAAGAACCATCGTCAGGGAGGTGAAGGAGTCAGGAGGAGGAGGAGGAGGAG 417
596 ATAATACCGGAGCTGGAAAGAGCTGCAAAGAGCGTAGGTCGGGACTTCTCGACGTTCATC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 CIGGAGAAGGAG------GAGGCGTCACTGTTTCAGAAGCTGGAAGGTCTC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 ATGGAGGTGAAACAGGATTTCATGAACTTCTTGCAGGGGCTGAGCAAGGAGGAGATGGAG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 411)
Mupy,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="OSJNBb0079L12r"
/clone_lib="CUGI Rice BAC Library (ECORI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
Clemson University
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/organism="Oryza sativa"
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High quality sequence stop: 374.
Location/Qualifiers
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Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1413 ccaatcaggaaggtcaggtagaaaca 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 CCGTTGAGGAAGCTAAGGTAGCTGCA 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ126934.1 GI:8202199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
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times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Gryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
```

108

BASE COUNT ORIGIN

0; Gaps Query Match 9.7%; Score 151; DB 238; Length 411; Best Local Similarity 75.7%; Pred. No. 1.7e-29; Matches 187; Conservative 0; Mismatches 60; Indels 0;

;; 0

523 agattaaatgtggggatctgtttgagaacagtgttgttgatgagttcaacgagtgtgctg 582 g ŏ

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763 gtgacaa 769

30 GAGACAA 24

Search completed: November 6, 2001, 00:54:15 Job time: 4104 sec

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November 6, 2001, 04:59:38; search time 93.61 Seconds (without alignments) 914.444 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-075-375A-6
7495
1 MALSLHTVFLCKEEALNLYA......MEASEVEKLFGKALPIRKVR 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | SIDSI//GGGdata/geneseq/Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antisey-Antis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412676
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412676 seqs, 60623988 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                        Run on:
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	Description	Tobacco violaxanth	Romaine lettuce vi	Arabidopsis violax	Arabidopsis thalia	P. falciparum live						
	ID	1	AAW09874	AAW09876	AAG49996	AAG49997	AAG06331	AAG06330	AAG49998	AAG06332	AAY44787	AAW24790
	DB	18	18	18	21	21	21	21	21	21	21	18
	Duery Match Length DB	478	473	462	525	522	522	526	428	428	1055	1786
æ	Query Match	34.1	33,3	32.2	2.8	2.8	2.8	2.8	2.8	2.7	2.0	2.0
	Score	2554	2498	2417	212.5	210	209	209	207	206	151	147.5
	Result No.	1	7	m	4	S	9	7	œ	6	10	11

ALIGNMENTS

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Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; tobacco.
                                                                                                                                                                                                                                                                                                   /note= "conserved Cys residue"
Misc-difference 155
                                                                                                                                                                                                                                                                                          'note= "conserved Cys residue"
                                                                                                                                                                                                                      135.206
/label- Cys-rich_domain
385.478
/label- Highly-charged_domain
                                                                                                                                                                                                                                                                      note= "conserved Cys residue"
                                                                                                                                                                        /label= Transit_peptide
                                                                                                                                                                                 135..478
/label= Mat_protein
                                                                                                                                                      Location/Qualifiers
                  AAW09875 standard; Protein; 478 AA
                                                                         Tobacco violaxanthin de-epoxidase.
                                                                                                                                                                                                             "Claim 8"
                                                                                                                                   Nicotiana tabacum cv. xanthi.
                                                       (first entry)
                                                                                                                                                                                                    135..147
                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                 Misc-difference 143
                                                                                                                                                                                                                                                             Misc-difference 141
                                                      28-JUL-1997
                                     AAW09875;
                                                                                                                                                               Peptide
                                                                                                                                                                                   Protein
                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                         Domain
          AAW09875
RESULT
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654 QIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT 713

δ g ò g ŏ q ŏ g à

121 vaifilsvaskadavdalktctcllkecrlelakcisnpacaanvaclqtcnnrpdetec 180

RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773

714 241 774 HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 833

894 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 950

AAW09874 standard; Protein; 473 AA.

AAW09874

AAW09874;

834 LQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDK 893

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acid sequence of the VDE was deduced from an isolated CDNA clone (AAT66242). VDE nucleic acids (see also AAT66241, AAT66243), in sense or antisense orientation, can be used in genetic constructs to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The 55 kDa violaxanthin de-epoxidase (VDE) (AAW09875) of tobacco catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. This system, termed energy dependent non-radiative energy dissipation or non-photochemical fluorescence quenching, reduces the quantum efficiency of photosystem II (PSII), helping to prevent PSII over-reduction and photoinhibitory damage. The amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding plant violaxanthin de-epoxidase - used to modify the
 /note= "conserved Cys residue"
                               'note= "conserved Cys residue"
                                                           note= "conserved Cys residue"
                                                                                                                           /note= "conserved Cys residue"
                                                                                                                                                          'note= "conserved Cys residue"
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                                                                                           'note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rockholm DC, Yamamoto HY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sensitivity of a plant to light
                                                                                                                                                                                                                                                                                                                                                                                 96WO-US18291.
                                                                                                                                                                                                                                                                                                                                                                                                               96US-0023502
                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0006315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-281036/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CALJ ) CALGENE INC.
                                                                                                                                                                         Misc-difference 190
                                                                                                                                                                                                       Misc-difference 206
                Misc-difference 161
                                            Misc-difference 167
                                                                                                          Misc-difference 180
                                                                                                                                          Misc-difference 184
                                                                                                                                                                                                                                     Misc-difference 252
                                                                                                                                                                                                                                                                     Misc-difference 382
                                                                          Misc-difference 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT66242
                                                                                                                                                                                                                                                                                                                  WO9717447-A2
                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                               36-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                            37-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                15-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bugos RC,
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Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin; xanthophyll; lettuce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "conserved Cys residue"
Misc-difference 171
                                                                                                                                                                                                                                                                                                                                                                      'note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                             'note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "conserved Cys residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                 /label= Highly-charged_domain
                                                                                                                                                                                                                                                           /label= Lipocalin_signature
                                                                                                                                                                                                                                                                                                                                                 /label= Tryptic_peptide-15
                                                     Romaine lettuce violaxanthin de-epoxidase.
                                                                                                                                                                                                                                                                                                    /label= Tryptic_peptide-11
                                                                                                                                                                                                                                                                                                                             /label= Tryptic_peptide-21
                                                                                                                                                                                                                                     /label= Cys-rich_domain
                                                                                                                                                                    'label= Transit_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "conserved Cys
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                         'label= Mat_protein
                                                                                                                                                                                                               "Claim 8"
                                                                                                                        Lactuca sativa L. cv. romaine.
                                (first entry)
                                                                                                                                                                             ..473
                                                                                                                                                                                                                                               .231
                                                                                                                                                                                                                                                                                                                                      .353
                                                                                                                                                                                                    126..138
                                                                                                                                                                                                                        .197
                                                                                                                                                                                                                                                                                                                 .289
                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                            Misc-difference 132
                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 134
                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 139
                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 162
                                28-JUL-1997
                                                                                                                                                        Peptide
                                                                                                                                                                              Protein
                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                     Domain
                                                                                                                                              Key
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 RICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAI 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 VAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETEC 653
                                                                                                                                                                                                                                                                                                                                                                                                              474 MALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSP 533
                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                   34.1%; Score 2554; DB 18; Length 478; 99.8%; Pred. No. 3.9e-191; Live 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                         Matches 476; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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Query Match

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RESULT
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                                                                                                                                                                                                                                                                                                                                  The 55 kDa violaxanthin de-epoxidase (VDE) (AAW09874) of romaine lettuce catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. This system, termed energy dependent concradiative energy dissipation or non-photochemical fluorescence quenching, reduces the quantum efficiency of photosystem II (PSII) helping to prevent PSII over-reduction and photosinhibitory damage. The amino acid sequence of the VDE was deduced from an isolated con an an acid sequence of the VDE was deduced from an isolated con a contisens orientation, can be used in genetic constructs to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of photosensitivity of a range of crops, trees and ornamentals can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWYITSGLNPTFDA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 FDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPGALYNHDNEFLHYQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQFIQLAIVLVCTFVIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MALSLHTVFLCKEEALNLYARSPCNERFHRSGQPPTNIIMMKIRSNNGYFNSFRLFTSYK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                    DNA encoding plant violaxanthin de-epoxidase - used to modify the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2498; DB 18;
Pred. No. 9.2e-187;
); Mismatches 2;
                    /note= "conserved Cys residue"
                                                                              'note= "conserved Cys residue"
 "conserved Cys residue"
                                        residue"
                                                                                                  /note= "conserved Cys residue"
                                                    /note= "conserved Cys
Misc-difference 243
                                        /note= "conserved Cys
                                                                                                                                                                                                                                   Yamamoto HY;
                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                                               sensitivity of a plant to light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.3%;
99.6%;
                                                                                                                                                            96WO-US18291
                                                                                                                                                                                96US-0023502
95US-0006315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                  Bugos RC, Rockholm DC,
/note=
Misc-difference 175
                                                                                                                                                                                                                                                       WPI; 1997-281036/25.
                                                                                                                                                                                                               (CALJ ) CALGENE INC
                             Misc-difference 190
                                                                                          Misc-difference 373
                                                   Misc-difference 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 AA;
                                                                                                                                                                                                                                                                 N-PSDB; AAT66241
                                                                                                                       WO9717447-A2
                                                                                                                                                              07-NOV-1996;
                                                                                                                                                                                  06-AUG-1996;
                                                                                                                                                                                           07-NOV-1995;
                                                                                                                                           15-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Best Local S
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DDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVG 360
                                                                   RDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Violaxanthin de-epoxidase; VDE; light; photosensitivity; photoprotection; transgenic plant; zeaxanthin; antheraxanthin;
                                                                                                                                                                                        QRLLEGFKELQQDEENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLR 473
                                                                                                                                                                                                        /note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "conserved Cys residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "conserved Cys residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364..462
/label= Highly-charged_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l..113
/label= Transit_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Cys-rich_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "conserved Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "conserved Cys
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                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis violaxanthin de-epoxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana var. columbia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Claim 8"
                                                                                                                                                                                                                                                                                                                 AAW09876 standard; Protein; 462
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114..185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114..462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xanthophyll
                                                                                                                                                                                                                                                                                                                                                       AAW09876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                         301
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                                                                                                                                                                                                                                                                                                                       The violaxanthin de-epoxidase (VDE) (AAW09876) of Arabidopsis catalyses the de-epoxidation of violaxanthin to zeaxanthin and antheraxanthin. This system, termed energy dependent non-radiative energy dissipation or non-photochemical fluorescence quenching, reduces the quantum efficiency of photosystem II (PSII), helping to prevent PSII over-reduction and photoinhibitory damage. The amino cid sequence of the VDE was deduced from an isolated cDNA clone (AAT66243). VDE nucleic acids (see also AAT66241-42), in sense or antisense orientation, can be used in genetic constructs to modify VDE levels in plants. Increased levels result in the plant being tolerant of increased light and therefore more productive and/or more resistant to disease. Underexpression of VDE increases photosynthetic efficiency under low light. The photosensitivity of a range of crops, trees and ornamentals can be modified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1011 RPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1191 DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1251 NKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSYLPNSIIPELEKAAKSIGRDFSTFIRTDN 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEVEKVGRTEMTLFORLAEGFNELK 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                    {\tt DNA} encoding plant violaxanthin de-epoxidase - used to modify the sensitivity of a plant to light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.2%; Score 2417; DB 18; Length 462; 99.8%; Pred. No. 1.9e-180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1371 QDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 1412
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                                                                                                                                            Bugos RC, Rockholm DC, Yamamoto HY;
                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 41pp; English
                   96WO-US18291.
                                                   96US-0023502.
95US-0006315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                          (CALJ ) CALGENE INC.
                                                                                                                                                                              WPI; 1997-281036/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 AA;
                                                                                                                                                                                                     N-PSDB; AAT66243.
                 07-NOV-1996;
                                                     06-AUG-1996;
                                                                        07-NOV-1995;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 63310.
               AAG49996 standard; Protein; 525 AA.
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99US-0131449.
99US-0132048.
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990S-0132486.
990S-0132487.
990S-0132863.
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99US-0134219.
99US-0134221.
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990S-0135124.
990S-0135529.
990S-0136629.
990S-0136392.
990S-0136782.
                                                                                                                                                    25-FEB-2000; 2000EP-0301439
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99US-0134768.
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                                             (first entry)
                                                                                          termination sequence.
                                                                                                         Arabidopsis thaliana.
                                                                                                                        EP1033405-A2
                                             18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-1999;
16-JUN-1999;
                                                                                                                                                                                                                             08-APR-1999;
16-APR-1999;
                                                                                                                                                                                                                                                                                                              06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                            14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                           6661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1999
                              AAG49996;
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18-MAY-19
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16-JUN-1
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RESULT
AAG49996
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US-0139459 US-0139460 US-0139461 US-0139462 US-0139750 US-0139763 US-01398917 US-01398917 US-0140353 US-014069353 US-014069353 US-0141842 US-0141842 US-0141842	9905-014203. 9905-014203. 9905-014203. 9905-014202. 9905-0143624. 9905-0144005. 9905-0144085. 9905-0144332. 9905-0144333. 9905-0144333. 9905-0144333. 9905-0144333. 9905-0146384. 9905-0146384. 9905-0146384. 9905-0146384. 9905-0146387.	905 - 0145276 905 - 0145913 905 - 0145913 905 - 0145919 905 - 0146386 905 - 0146386 905 - 0147302 905 - 0148317 905 - 014936 905 - 014936
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330 DGYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDFNNFITTDNSC---GPEPPLVERLEKT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 AEEGEKLLIKEAVEIBEEVEKEVEKVRDTEMTLFQRLLEGFKELQOBEENFVRELSKEEK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 FFTRSAVQTFVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAM 329
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36;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                        507 WEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPK 566
                                                         155 wiqtnsknyknmic-----fesspnlmnrlgg------tdvgsvnkd--- 190
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                                                                                                                                           447 EILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWG 506
                   128 ramn-ltgelngtdilvvva------n 154
                                                                                                   611 LKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFN 670
                                                                                                                                                                        671 ECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK-----------709
                                                                                                                                                                                                                                     753 FTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVENSPEDYIFVYYK 805
                                                                                                                                                                                                                                                                           806 GRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKTDNTCGPEPPLVE 863
                                                                                                                                                                                                                                                                                                                      WFITRGLNPTFDAFDCQLHEFH-------TEENKLVGNLSWRIRTPDGGF 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 63311,
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                                                                                                                                                                                                                                                                                                                                                                501 ----gipggsrlhsrisiieepdseek 523
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990S-0137724

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30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 qnlrsk----gfstlscmvkncgpqilnclldpncrkalqclnqcs--pvdqvcsyrci 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659 DLFENSVYDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK----- 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        710 -----TEENKLVGN 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | || :| || || 33 lfvgwlgelewswrvvagqnpayddfpcqyqlfyrgkgkssfwyepvfqvrtleeklv-- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     741 LSWRIRTPDGGFFTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVE 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%; Score 210; DB 21; Length 522;
21.1%; Pred. No. 7.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                555 SPAHSINQNVPKGNSGCKFPKDVALMV-----WEKWG----QFAKTAIVAIFILSV--- 601
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17-OCT-2000 (first entry)

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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AAG06330 standard; Protein; 526 AA
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                             333 lfvgwlgelewswrvvaggnpaydqfpcqyqlfyrgkgkssfwyepvfqvrtlegklvwr 392
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Best Local Similarity 21.2%; Pred. No. 8.5e-08;
Matches 122; Conservative 76; Mismatches 191; Indels 186; Gaps
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AAG06332;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Wengiste T, Paszkowski J;
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                                                        884 EE 885
                                                                       425 ek 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 yrgkgkssfwyepvfqvrtlegklvwrrr----rysvkr----gkipatfrfsvld 319
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99US-0161993
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The present sequence is a MIM protein from Arabidopsis thaliana, which contributes to recombination repair of DNA damage in plant cells. The protein was tracked down with the help of a T-DNA tagged Arabidopsis mutant showing hypersensitivity to methyl methanesulphonate (MMS). It shows homology to a member of SMC (Structural Maintenance of Chromosomes) protein family and confers hypersensitivity to treatment with MMS, X-rays, UV light or mitomycin C. The present sequence is useful for DNA repair in plant cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM: recombination; plant; DNA repair; hypersensitivity; SMC protein family; Structural Maintenance of Chromosomes; MIM; methyl methanesulphonate; irradiation; mitomycin C.
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AAW24790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDN 853
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                                                                                                                                                                                                                                                                                                                                                                                     eeiagrlgglkkklawswvydvgrg------1qegtekivklkeriptcg 278
                                                                                                                                                                                                                                                                                                                                                                                                                    ---EMTLFORLLEGFKE-----LQQD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EENFVRELSKEEKEILNELQMEATEVEKLFGRALP 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FLANHETIKYYVGSKLPGHKRFSWGWEDY 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 FGSIVVAKICSS-RRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNS 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570 GCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCI 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTF-----DAFDCQLHFFHTEENKLV--- 738
                                                                                                        128 ALKTCACLLKECRIE-----LAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFEN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVS-RKKCVPRKSDVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----tlrgcaneanyrnlki----ilydfsrprlniprhmvpqtehpti
                                                                                                                                                                                                                               WYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPG
                                                                                                                                                                                                                                                                                         288 ALYNHDNEFLHYQDDWYILSSQIEN - - KPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLP
                                                                                                                                                                                                                                                                                                                        siyehltkataivd-----iknmeqv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fggdrvinllqaiernhrrfrkpp-------igpigs-----
                                           2.0%; Score 151; DB 21; Length 1055; 19.3%; Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 fnhkcnyvqkikdrvrrlerqvgdineqtmkntqaeqseieeklkylerevek-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                904 GFKELQRDE----ENFLRELSKEEMDVLDGLKMEATEVEKL 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nmresakgeidafeeaenelkkiekd-----lqsaeaeki 791
                                                                          Conservative 119; Mismatches 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     AVEI EEEVEK EVEKVRDT - - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 IRKLRMALAPHSN-
 1055 AA;
                                                           Similarity
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                                                             Best Local Sim
Matches 182;
 Sequence
                                              Query Match
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pre-erythrocytic liver stage antigen. 3 (LSA-3) protein. The encoding gene sequence was isolated by screening a P. falciparum strain T9/96 library with serum from a missionary treated by prophylaxis (for strain T9/96 library with serum from a missionary treated by prophylaxis (for strain T9/96 see F84010286). Of 20 clones isolated, clone 7928 was used to screen a library generated from Thai strain Kl. One clone contained a comprises a 1.8 kb region encoding 3 major blocks of tetrapeptide comprises a 1.8 kb region encoding 3 major blocks of tetrapeptide cropeats (especially the amino acid sequence VEES, VEEN, VEEI, VAPT, etc.) and a 3' hydrophobic region corresponding to a glycosyl-phosphatidyl- inositol membrane anchoring sequence. The cromation relates to new polypeptides of at least 10 amino acids derived from the LSA-3 protein with the exception of the peptides AMW24/91-4.

The LSA-3 peptides can be used to raise antibodies and as vaccines for immunotherapy of malaria.
                                                                                                                                                                                                                                                               Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum; prophylaxis; Thai strain; gene organisation; exon; intron; hydrophobic; glycosyl-phosphatidylinositol membrane anchoring sequence; antibody; vaccine; Immunotherapy; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 EKLLIKEAVEIEEEVEKEV----EKVRDTEMTLFQRLLEGFKELQQD----EENFVREL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               858 tilenveettaesvttfsnileeigentitndti---eekleelhenvlsaalentgsee 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum poly:peptide(s) and related nucleic acids - derived from the liver stage antigen-3, useful for malaria vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence corresponds to a Plasmodium falciparum strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18;
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1537..1576
/note= "repeat region
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                                                                                                                                                                                                       P. falciparum liver stage antigen-3.
AAW24790 standard; Protein; 1786 AA
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N-PSDB; AAT78868.
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                                                                                                                                        08-0CT-1997
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                                                                  AAW24790;
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6 6	1	ALKTCIC 616 1109
QY	Qy 617 LLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECA	DEFNECA 673
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οy	QY 674 VSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIIRGLNPIFDAFDCQLHEFH	20гнЕFH 731
g	1164ekedltdkmidaveesieiss-dskeet	 esi 1193
QY Dp	QY 732 TEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSK :: : : : : : : : : : : Db 1194 kdkekdyslyveeydddmdesyeky]e knmeee]mkdayajadiditsk	VXILSSK 791 :: inditsk 1242
δy	792	
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δλ	849 IKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEETEEFRVEKVRD	- 1
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δy	946	FLLKIL 994
Ор	Db 1390 sleveeekkleevhelkeevehiisgdahikg	1421
δy	995 PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLP	GVLACA 1054
QQ	Db 1422leeddleevddlkgsildmlkgdmelgdmdkesledvttkl	1462
δy	1055 FLIVPSADAVDALKTCACLLK	TECQIK 1112
qq	Db 1463gerveslkdvlssalgmdeegmktrkkagrpkleevllk	: eevllk 1501
δy	QY 1113 CGDLFENSVVDEFNECAVSRKKCYPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGL	WITSGL 1172
QQ	Db 1502vrfdikkvrfdikd	k 1524
QY	1173 NPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAV	VLYNHD 1232
qq	Db 1525 epkdeivevemkdedieedveedieed	1
δy	1233 NEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLF	IIPELE 1292
QQ	1552ieedkvedidedigedkdevid	: : livgke 1583
δy	1293 KAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEE	-IEEEVE 1345
qq	Db 1584 kriekvkakkkklekkveegvsglkkhvdevmkyvqkidkevd	:: : idkevd 1626
οy	1346 KEVEKVGRTEMTLFQRLAEGFNEL	KMEASE 1397
qq	1627 kevskalesknd	
δy	Qy 1398 VEKLF 1402	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An anti-mitosin antibody, antibody fragment or a phosphorylated mitosin mutein ( or nucleic acid encoding it) can also be used to inhibit cell division which is particularly useful for the study of the cell cycle. A further use is to control hyperproliferative cells, and so control diseases such as psoriasis and breast cancer. It can also be used to block gametogenesis of an immature gamete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 2.0%; Score 147; DB 16; Length 2482; Best Local Similarity 18.4%; Pred. No. 0.064; Matches 240; Conservative 188; Mismatches 443; Indels 434; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | | : | | | : | | | | 315 lsetlslekkemssiislnkreieeltqengtlkeinasInqekmnliqk-sesfanyid 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purified mammalian protein mitosin and agents that bind it and inhibit its action – used to promote cell growth or to inhibit cell division and/or proliferation
                                                                                                                                                                                                                                                                                                                      Cell cycle; M phase; mitosin; retinoblastome; mitosis; cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1480.1659
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                              AAR72826 standard; Protein; 2482 AA.
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                                                                                                                                                                                                                                                      Human mitosin.
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                                                                                                                                                                                                                                                                                                                                                        inhibition.
                                                                                                      AAR72826;
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AAR72826
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qq	544	eamlrnkelklqe
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qq	597	kekeciqhelqtirgdletsnlqdmqsqeisglkdceidaeekyisgphelstsqndnah 656
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Οy	827	PESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGE 873
Dp	869	: :: : : :: :
δy	874	RTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKE 922
QQ	929	::
٥y	923	EMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHCFTS 960
Dp	985	tlemesklaaekkqteqlslelevarlqlqqldlsrsllgidtedaiqgrnescdiske 1044
οy	961	PCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADL 1002
qq	1045	htsettertpkhd-vhgicdkdaggdlnldiekitetgalkptgecsgegspdtnye 1100
Qy	1003	RTTGGRS SRPLSAFRSGFSKGIFDIVPLPSK 1033
g	1101	: : ppgedktggsseciselsfsgpnalvpmdflgngedihnlglrvketsnen1r11hvied 1160
φ	1034	IVPSADAVDALKTCACLLKGCR
qq	1161	: : : : rdrkvesllnemkeldsklhlqevqlmtkieacieleki 1199
٥y	1085	ANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVS
QQ	1200	: vkkensdlse 1212
ΟŊ	1144	EFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGN 1197
QQ	1213	sdle
οy	1198	
QQ	1259	dswkerfldvenelsrirsekasiehealyleadlevvqteklclekdnenk 1310

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1253 P-----EDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFI 1306
            1307 RTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEE---VEKEVEKVGRTEMTLFQRLA 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence for mitosin, a phosphoprotein necessary for the cell to ente mitosis. The protein's degradation is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated mitosin protein and gene - useful for, e.g. developing products for therapy and diagnosis of hyper-proliferative disorders such as cancers or psoriasis
                                                                                                                                                                                                                                                     Mitosin; phosphoprotein; mitotic cell cycle; antibody; analogue; inhibition; M phase; Antagonist; hyperproliferative cell; cancer; leukaemia; lymphoma; chromosome segregation.
                                                                                                 1364 EGFNELKQDEENFVRE-----LSKEEMEFLDEIK-MEASEVEK 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= "Bipartite targeting motif"
/note= "Optionally C or G"
2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= "Bipartite targeting motif"
/note= "optinally A or T"
                                                                                                                                                                                                                                                                                                                                               /note= "leucine heptad repaet"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "leucine heptad repeat"
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                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
258..280
                                                                                                                                                                  AAW23996 standard; Protein; 2482 AA
                                                                                                                                                                                                                                  Human mitosin amino acid sequence.
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93US-0141239.
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564..593
1387..1443
1885..1962
2146..2188
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Misc-difference 2300
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Misc-difference 2301
Misc-difference 2303
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N-PSDB; AAV09076.
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                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-1994;
22-OCT-1993;
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                                                                                                                                                                                        AAW23996;
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Domain
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Domain
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                                                                                                                                              RESULT 13
                                                                                                                                                         AAW23996
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The mitosin protein, can be used to control the growth of cells. An anticosin protein, can be used to control the growth of cells. An anticosin antibody, a mutant or a non-functional analogue of mitosin can inhibit the mitotic cell cycle by preventing the cells from entering the M phase, and over expression of mitosin or its functional equivalent, would inhibit the cycle by preventing cells from leaving the M phase. Antagonists to this protein can be used to control hyperproliferative cells in, (e.g. thyroid hyperplasia, Grave's disease, psoriasis, benign prostatic hypertrophy, il-Fraumeni syndrome, breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer and various leukaemias and lymphomas). Reintroduction or supplementation of lost mitosin function by introduction of the protein or nucleic acid encoding the protein into a cell can restore defective chromosome segregation, which is a marker of progressing malignancy. Malignant proliferation of cells can then be halted. The protein can also be used for the detection and diagnosis of hyperproliferative 60; 379 LVERLEKTAEEGEKLLIKEAVEIEEEVE----KEVE-KVRDTEMTLFQRLLEGFKELQQ 432 315 lsetlslekkemssiislnkreieeltgengtlkeinaslngekmnligk-sesfanyid 373 450 ---NELQMEATEVEKLFGRALP--IRKLRMALAPHSNFLANHETIKYYVGSKLPGH---- 500 434 nrknele----qlkeafakehqefltklafaeernqnlmleletvqqalrsemtdnqnns 489 374 ereksiselsdgykgeklillgrceetgnayedlsgkykaageknsklecllnectslce 433 490 kseagglkgeimtlkeegnkmgkevndllgeneglmkvmktkhecgnlesepir---- 543 544 -----nsvkereserng-cnfkpgmdlevkeisldsynaglvgleamlrnkelklgese 596 Gaps 501 KRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRI------CCGLDSRGLQLFSHGK 551 552 HNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDAL 611 -----LKECRLEL-AKCISNP-----ACAAN 637 597 kekeciqhelqtirgdletsnlqdmqsqeisglkdceidaeekyisgphelstsqndnah 656 638 VAC-LQTCNNRPDETE--CQIKCGDLFENSVVDEFNECAVSRKKCV--PRK--SDVGDF- 689 -TFDAFDC 725 726 QLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQD-- 783 769 qmhfaelqek-------flslqsehkilhdqhcq--msskmselqtyvdsl 810 784 -- DWYILSSKVENSPEDYIFVYYKGRND--------AWDGYGGSVLYTRSAVL 826 827 PE----SIIPELQTAAQ----KVGRDFNTFIKTDNTCGPEPPL----VERLEKKVEEGE 873 869 eqtgdmsllsnlegavsangcsvdevfcsslgeenltrketpsapakgveeleslcevyr 928 RTIIKEVEEIEEEVEK---VRDKEVTLFSKLFEG-----FKELQRDEENFLRELSKE 922 Query Match 2.0%; Score 147; DB 19; Length 2482; Best Local Similarity 18.4%; Pred. No. 0.064; Matches 240; Conservative 188; Mismatches 443; Indels 434; 690 ----PVPDPSVLVQKFDMKDFSGKWFITRGLNP----433 DEENFVRELS---KEEKEIL------2482 AA; 612 KTCTCL-----Sequence 셤 ð q g Op qq g Οý ōλ ò Dp ŏ g g Op 원 g δ ò δ ò ò

-----PCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPI-----QSADL--- 1002 1045 htsettertpkhd-vhqicdkdaqqdlnldiekitetgalk---ptgecsgegspdtnye 1100 1101 ppgedktqgsseciselsfsgpnalvpmdflgnqedihnlqlrvketsnenlr1lhvied 1160 1085 IANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLG- 1143 1259 dswkerfld----venelsrirsekasiehealyleadlevvqteklclekdnenk 1310 985 tlemesklaaekkgteglslelevarlglggldlssrsllgidtedaiggrnescdiske 1044 -----NELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKC 1084 1161 rdrkvesllnemkeldsklhlqevqlmt-------kieac----ieleki 1199 ------kk---ensdise 1212 1144 -- EFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTE----GDNKLVGN 1197 1213 kleyfscdhgellgrvetse----glns----dlemhadkssredigdnvakvn 1258 1198 ISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLH-----YQDDWYILSSKIENK 1252 1253 P-----EDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFI 1306 1311 gkvivcleeelsvvtserngl---rgeldtmskkttaldglsekmkektgeleshgsecl 1367 1307 RTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEE---VEKEVEKVGRTEMTLFQRLA 1363 1368 hciqvaeaevkektellqtlssdvsellkdkthlgeklgslekdsgalsltkcelengia 1427 923 EMDVLDGLKMEATEVEKLF------GRALPIRKLMAVATH------CFTS-- 960 Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide. Plasmodium falciparum chromosome 2 related protein SEQ ID NO:182 1364 EGFNELKQDEENFVRE-----LSKEEMEFLDEIK-MEASEVEK 1400 -----RTTGGRS-----SRPLSAFRSGFSKGIFDIVPLPSK-----Venter JC; AAB18324 standard; Protein; 1558 AA. Gardner M, 99WO-US26796. 98US-0107131. (first entry) Hoffman S, Carucci D, 1200 v----Plasmodium falciparum CARUCCI D.
GARDNER M.
VENTER J C. WPI; 2000-365347/31 WO200025728-A2. 05-NOV-1998; 07-NOV-2000 05-NOV-1999; 1-MAY-2000 AAB18324; (HOFF/) (VENT/) (GARD/) (CARU/) 1034 1428 1003 AAB18324 g ò g ŏ g δ qq à a a g à ŏ

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The present invention describes proteins and their fragments (1) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described arre: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are riffins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in the cube control of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insectioides have led to a resistance to drugs and many control of the parasite in many and provide new targets for the parasite in the control of many and provide new targets for the parasite have led to a resistance to drugs and many control of the parasite in many and provides a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAAB1814 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| : | : | : | : | 1011 lieetge-----sedskei 1046
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Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 1558;
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Matches 206; Conservative 153; Mismatches 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 SIIPNLQK-AAKSVGRDFN-----NFITTDNSCGPEPPLVE-
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17.9%; Pred. No. 0.059
                                                                                                                                                                                                                                          Disclosure; Page 410-414; 577pp; English
                                                                                                                                 diagnosis of P.falciparum infection -
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                                                           evkeikeleseiledykelktietdileekkeiekdhfekfeeeaeeikdleadilkevs 1157
                                                                                                                                                        995 PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACA 1054
1047 idakd-----dtlekvieeehditttldevvelkdveedkiekvsdlkdleedilk 1097
                                EV----TLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRAL---- 945
                                                                                            -----PIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL 994
                                                                                                                                                                          1190 --ieeddleevddlkgsildmlkgdmelgdmd-----kesledvtakl-----
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1320 -----ieedkvedidedid------
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24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 RLEKTAEEGE----KLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENF 437
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                                            Human tumour suppressor gene RAD50 - useful to detect predisposition to, decrease risk of and treat cancer, also Septin-2
                                                                                                                                                                                                                                                              Claim 5; Page 82-86; 195pp; English
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663 NSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDA 722

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723 FDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQ 782

701 ----lgsklrlapdklksteselkkkekrrdemlglypmrqsiidlkekeipelrnklg 755

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840 KVGRDFNTFIKTD-------879 -----VEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENF-----LRELSKEE 923 815 klggidldrtvggvngekgekghkldtvsskielnrkligdggegighlksttnelksek 874

783 DDWYILSSKVENSPEDYIFV--YYKGRNDAWDGYGGSVLYTRSAV-LPESIIPELQTAAQ 839

Search completed: November 6, 2001, 04:59:49 Job time: 7633 sec

924 MDVLDGLKME-----ATEVEKLF 941

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Sequence 4, Appli
Sequence 184, App
Sequence 19, Appl
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Sequence 51, Appl
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                                                                                                                                                                                                                                                                                    1 MALSLHTVFLCKEEALNLYA.......MEASEVEKLFGKALPIRKVR 1412
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Sequence 2,
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-687-080-51
US-08-08-01-60-2
US-08-08-08-849B-2
US-08-08-08-849B-2
US-08-08-68-88-56A-2
US-08-476-900A-28
US-08-476-900A-6
US-08-476-900A-6
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US-08-37-014-9
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Maximum Match 100%
Listing first 45 summaries
                                                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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7495
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Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Patent No. 5444158 Sequence 16, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli	STAGE POLYPEPTIDE MOLECULES	DB 4; Length 1786; s 374; Indels 409; Gaps 50; PEPPLVE
US-08-366-4 US-08-353-700-1 US-08-353-700-1 US-08-923-992A-4 5444188-2 US-08-755-87-16 US-08-603-753D-4 US-08-923-992A-6 US-08-923-992A-6 US-08-923-992A-6 US-08-923-992A-6 US-08-923-992A-6 US-08-923-992A-6 US-08-923-992A-8 US-08-923-992A-8 US-08-923-992A-8 US-08-923-992A-8 US-08-923-992A-8 US-08-923-992A-8 US-08-93-992A-8 US-08-93-992A-8 US-08-93-992A-8 US-08-93-992A-8 US-08-93-992A-8 US-08-93-992A-8 US-08-93-953-9		DB .0031; s 37.37 p EPPL
114 1.5 523 4 112.5 1.5 3248 1 111.5 1.5 1.04 4 111.5 1.5 1130 6 111.5 1.5 2328 1 111.5 1.5 3418 2 111.5 1.5 3418 4 111.5 1.5 3418 4 110.5 1.5 1128 4 110.5 1.5 1164 4 110 1.5 1098 4 110 1.5 689 4 110 1.5 689 4 110 1.5 689 4 110 1.5 1098 4 109.5 1.5 1098 4	62-8 8, Applicat 8, Applicat 10, 6191270 11 DRULLHE, 12 DRUBERSI 13 INVENTION: 14 INVENTION: 15 INVENTION: 16 APPLICATION 16 APPLICATION 17 ING DATE 16 APPLICATION 18 APPLICATION 18 APPLICATION 19 BAPPLICATION 19 BAPPLICATION 10 BAPPLICATION 10 BAPPLICATION 11 BAPPLICATION 12 BAPPLICATION 12 BAPPLICATION 13 BAPPLICATION 14 BAPPLICATION 15 BAPPLICATION 15 BAPPLICATION 15 BAPPLICATION 15 BAPPLICATION 15 BAPPLICATION 16 BAPPLICAT	2 - 2 - 2 - 2 - 2 - 2 - 3 - 3 - 3 - 3 -
80001000000000000000000000000000000000	SULT -08-975 Sequent Sevent Sevent Sevent APPLIC TITLE TITLE CURRE CORRE CORRE TYPE CORRE	-08-973- Ouery Ma Best Loc Matches 347 858- 391 915 442 972 502
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558 HSINQNVPKG-NSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTC 616

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US-08-487-826B-4 US-08-755-587-184 US-08-482-728A-19

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1110 -LKEMFFNLEDVFKS---ESDVITVEEIKDEPVQKEVEKETVSIIEEMEENIVDVLEE-- 1163
                                                                                                                                                                                                1243 LIEETQE----LSEDSKEI 1278
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                                                                                                                 995 PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACA 1054
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617 LLKECRLELAKCISNPACAANVACLQTCNNRPDETECQ---IKCGDLFENSVVDEFNECA 673
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                                                                                      674 VSRKKCVPRKSDVGD--FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH 731
                                                                                                                                                                        732 TEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSK 791
                                                                                                                                                                                                                                                      792 -VENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESI--IPELQTAAQKVGRDFNTF 848
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Patent No. 5710022
GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022e1 Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCE: 8
CORRESPONDENCE ADDRESS:
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STREET: 4370 La Jolla Village Drive, Suite 700
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379 LVERLEKTAEEGEKLLIKEAVEIEEEVE----KEVE-KVRDTEMTLFQRLLEGFKELQQ 432
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                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                  COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                            Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2482 amino acids
                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-328-254-6
                                                                                         COMPUTER READABLE FORM:
                STATE: California COUNTRY: USA
                                                                                                                                                      OPERATING SYSTEM:
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CITY: San Diego
                                                                                                             MEDIUM TYPE:
                                                                 92122
                                                                                                                                                                                SOFTWARE:
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1259 DSWKERFLD------VENELSRIRSEKASIEHEALYLEADLEVVQTEKLCLEKDNENK 1310
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                                                                                                                                                                                                                                                                                                                                                                -----PCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPI-----QSADL--- 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RTTGGRS-----SRPLSAFRSGFSKGIFDIVPLPSK------1033
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                                                                      827 PE----SIIPELQTAAQ----KVGRDFNTFIKTDNTCGPEPPL----VERLEKKVEEGE 873
                                                                                                  RTIIKEVEEIEEEVEK---VRDKEVTLFSKLFEG-----FKELQRDEENFLRELSKE 922
                                                                                                                                                                                                             929 OSL----EKLEEKMESQGIMKNKEIQELEQLLSSERQELDCLRKQYLSENEQWQQKLTSV 984
                                                                                                                                                                                                                                                                923 EMDVLDGLKMEATEVEKLF-----GRALPIRKLMAVATH------CFTS-- 960
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
SOFERATING SYSTEM: PC-DOS/MS-DOS
SOFERATING SYSTEM: PC-DOS/MS-DOS
SOFEWARRE: PatentIn Release #1.0, Version #1.25
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STREET: 350 Cambridge Avenue, Suite 250
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Patent No. 5821091
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US-08-592-126-148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----HTTTRIQMEMLIKDKADKDEQIRKIKSRHSDELTSLLGYF----PNKKQLEDWL 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 YVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGK 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 1.8%; Score 135.5; DB 2; Length 1312; Local Similarity 19.7%; Pred. No. 0.02; nes 124; Conservative 95; Mismatches 218; Indels 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: Rad50.pro-translation of SEQ ID NO:54
                                                                                                                    NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
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                     APPLICATION NUMBER: US/08/592,126
                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            840 KVGRDFNTFIKTD--
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                   FILING DATE
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E: Needle & Rosenberg, P.C. 133 Carnegie Way, Suite 400
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APPLICATION NUMBER: US/08/021,601
FILING DATE: 19930212
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Nichols, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                           639 ESDLDRLKE---
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US-08-021-601-2
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1.8%; Score 135.5; DB 2; Length 1312;
Best Local Similarity 19.7%; Pred. No. 0.02;
Matches 124; Conservative 95; Mismatches 218; Indels 191; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 KTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIK------CGDLFE 662
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                                                                                                             Human RAD50 Gene and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: TRANS. OF RAD50 cDNA (SEQ. 54), NT. INDIVIDUAL ISOLATE: 389 TO 4324
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                          3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4600-0111.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    ; Sequence 51, Application US/08687080
; Patent No. 5965427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                            GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RA
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                                                                                                                                NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                            STREET: 350 Camb
CITY: Palo Alto
                                                                                                                                                                                                                                                                  USA
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US-08-687-080-51
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669 FITQL----TDENOSCCPVCORV-----FOTEAELQEVISD------700
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----EIEKSSKORAMLAGATAVYSO 668
                                                                     723 FDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQ 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               880 -----VEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENF-----LRELSKEE 923
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APPLICANT: Singh, Yogendra
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: RELATED METHODS
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
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1223 NQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTR--S 1280
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733 EENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHD---NEYLLYQDDWY--I 787
                                  177 IKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLY 236
                                                                                                                                                                                                                                                                                                                                                                                  237 APEAFNYMDKFNEQEINLSLEELKDQRMLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LQRDEENFLRELSKEEMDVLDGLKMEATEV----EKLFGRALPI-------RKL 950
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                                                                                                             788 LSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNT
                                                                                                                                                               129 L---VIQSSEDYVENTEKALN------VYYEIGKILSRDILSKINQPYQKFLDVLNT
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APPLICANT: Leppla, Stephen H.
APPLICANT: Kiimpel, Kurt R.
APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anchrax Toxin Fusion Proteins and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GADLVDST-----
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                                                                                                                                                                                                                                                                                                                                 -----EVEEIEEEVEKVRDKEVTLFSKLFEGFKE---
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                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
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                                                                                                                                                                                                                        25-JUN-1993
                                                                                                                                                                                                                                                                                             FILING DATE: 25-JUN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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San Francisco
California
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                                                      COUNTRY:
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788 LSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNT 847
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; Patent No. 5863724
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; NUMBER OF SEQUENCES:
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                                                                               848 FIKTDNTCG--
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                                                     1223 NQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTR--S 1280
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                                                                                         534 ----IIKQSEKEYIRI-DAKVVPKSKIDTKIQE----AQLNINQEWNKALGLPKYTKLIT 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Steuart Street Tower, 20th Floor, One Market STREET: Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Arora, Naven
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
NUMBER OF SEQUENCES: 31
TOWNSEND and TOWNSEND KHOURIE and CREW
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PatentIn Release #1.0, Version #1.25
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US94/01624
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9401624 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leppla, Stephen H. APPLICANT: Klimpel, Kurt R.
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FILING DATE: June 25, 1993
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weber, Kenneth A. REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                 511 AGYLENG------
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Best Local Similarity
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951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1165 KWYITSGLNPTFDAFDCQLHEFHTEGDNKLV--GNISWRIKTLDSGFFTRSAVQKFVQDP 1222
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                                                                                                                                                                               177 IKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                             908 ---LQRDEENFLRELSKEEMDVLDGLKMEATEV----EKLFGRALPI------RKL 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 GLIDSPSINLDVRKOYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATL----- 450
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129 L---VIQSSEDYVENTEKALN------VYYEIGKILSRDILSKINQPYQKFLDVLNT 176
                                                                                                                                                                                                                                                                                                                                                     237 APEAFNYMDKFNEQEINLSLEELKDQRMLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKL 296
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STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
                                                                                       --PEPPLVERLEKKVEEGERTIIK-
                                                                                                                                                                                                                                                                  -----EVEEIEERVEKVRDKEVTLFSKLFEGFKE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.7%; Score 124; DB 2; Length 1498;
18.8%; Pred. No. 0.24;
tive 72; Mismatches 221; Indels 178;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                           US-08-476-900A-28; Sequence 28, Application US/08476900A; Patent No. 6031150; ERNERAL INFORMATION:
                                                                                                FILING DATE: 15-MR-1995
CLASSIFICATION: 435
ATORNEY AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFREENCE/DOCKET NUMBER: BYLR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
INFORMATION FOR SED ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1498 amino acids
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Best Local Similarity 18.8%
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
TITLE OF INVENTION: and Method of Detecting Persistent Hyperinsulinemic Hypogly
TITLE OF INVENTION: Infancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.7%; Score 124; DB 3; Length 1498; Best Local Similarity 18.8%; Pred. No. 0.24; Matches 109; Conservative 72; Mismatches 221; Indels 178; Gaps
                                                                                                                                                                                  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6031150ris
STREET: One Liberty Place 46th, Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/476,900A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYI
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TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-476-900A-28
                                                                                                                                      NUMBER OF SEQUENCES: 4:
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                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                            COUNTRY:
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34,293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                  1024 IFDIVPL----
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                                               1248 KIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIR 1307
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor Patent No. 6054313

NUMBER OF SEQUENCES: 49
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846 STPMIVFLDDPFSALDVHLSDHLMQAGILELLRDDKRTVVLVTHKLQYLPHA-DWIIAMK 904
                                                                                                   ----- ETVME 946
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18.8%; Pred. No. 0.24;
tive 72; Mismatches 221; Indels 178; Gaps
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                                                                                            905 DGTIQREGTLKDFQRSECQLFEHW------KTLMNRQDQELEK---
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ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSE: No. 6054313ris STREET: one Liberty Place 46th. Floor CITY: Philadelphia
                                                                                                                                           1308 TDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKE 1347
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYI
TELECOMMUNICATION:
TELEPHONE: 215-568-3100
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MOLECULE TYPE: protein
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                                                                                                                                                            ------RIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLF 1117
                                                                                                                                                                                                                                                                                                                             -----SVLVQNFNI-SDF 1162
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                                                                       637 KYQAVPLKVVNRKRPAREEVRDLLGPLQ------RLTPSTDG-DADNFCVQIIGG 684
                                                                                                                                                                                                                                    685 FFTWTPDGIPTLSNITIRIPRGQLTMIVGQVGCGKSSLLLATLG-----EMQKVSGAVF 738
                                                                                                                                                                                                                                                                                                                                                                                                    739 WNSLPD-----SEGRRPQQPRAGDSGRFGCQEQRPCGYASQKPWLLNATVEENITFESPF 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             794 NKQRYKMVIEACSLQPDIDIL------PHGDQTQIGERGINLSTGGQRPDQCRPEPST 845
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STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                    1118 ENSVYDEFNECAVSRKKCVPRKSDLGEFPAPDP------
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FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
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Patent No. 5863724
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Sequence 6, Application US/08488546A
Patent No. 6054313
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
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                                                                                   BYLR-0027
                           NAME: Beardell, Lori Y. REGISTRATION NUMBER: 34,293
                                                                             REFERENCE/DOCKET NUMBER: BY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-310
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                1581 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 109; Conservative
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-476-900A-6
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NUMBER OF SEQUENCES:
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TITLE OF INVENTION: Infancy
NUMBER OF SEQUENCES: 49
                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1024 IFDIVPL-----PSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKG 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SVLVQNFNI-SDF 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LDSGF------FIRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSS 1247
                                                                                                                                                                                                                                                                                                                                                                ---SADLRTTGGRSSRPLSAFRSGFSKG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---RIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLF 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1163 NGKWY----ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKT------- 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1248 KIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIR 1307
                                                                                                                     868 KVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFK--ELQRDEENFLRELSKEEMD 925
                                                                                                                                                             926 VLDGLKMEA--TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDD-----GIGRL 978
                                                                                                                                                                                                                                                                                  : |: | | : | | 529 EMISLRAFAVYISIFMNTAIPIAAVLITFV-----GHVSFFKESDFSPSVAFASL 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            685 FFTWTPDGIPTLSNITIRIPRGQLTMIVGQVGCGKSSLLLATLG-----EMQKVSGAVF 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739 WNSLPD----SEGRRPQQPRAGDSGRFGCQEQRPCGYASQKPWLLNATVEENITFESPF 793
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                                                                Gaps
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   Query Match 1.7%; Score 124; DB 2; Length 1581; Best Local Similarity 18.8%; Pred. No. 0.26; Matches 109; Conservative 72; Mismatches 221; Indels 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          947 RK---APEPS--QGLPRAMSSRDGLLLDEDEEEEEAAESE 981
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ADDRESSEE: No. 6031150ris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/476,900A FILING DATE: 07-JUN-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                   ---KILPPIQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08476900A Patent No. 6031150
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IBM PC compatible
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905 DGTIQREGTLKDFQRSECQLFEHW------KTLMNRQDQELEK----
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Best Local Similarity 18.8%; Pred. No. 0.26;
Matches 109; Conservative 72; Mismatches 221; Indels 178; Gaps
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
E: No. 6054313ris
One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Beardell, LOTI Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
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APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
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TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TRNGTH: 1581 amino acids
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             STREET: One ____
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ADDRESSEE:
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1284 PNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERI------EKTVEEGERIIV 1334
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                                                                                                                                                                                                                                           APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.6%; Score 119; DB 2; Length 905;
Best Local Similarity 31.0%; Pred. No. 0.28;
Matches 39; Conservative 15; Mismatches 34; Indels
1308 TDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKE 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC 95
ATTORNEY/AGENT INFORMATION:
                            947 RK---APEPS--QGLPRAMSSRDGLLLDEDEEEEEAAESE 981
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                    Sequence 9, Application US/08574959A Patent No. 5962224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
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amino acid
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    714 EGELEE 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                  US-08-574-959A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-357-014-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                        RESULT 14
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us-09-075-375a-6.rai

Page 11

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1284 PNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERI------EKTVEEGERIIV 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1335 KEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKME 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.6%; Score 119; DB 4; Length 905;
Best Local Similarity 31.0%; Pred. No. 0.28;
Matches 39; Conservative 15; Mismatches 34; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
CONTRY: USA
ZIP: 02109-1875
COMPUTER: READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATE: 19-011-1999
PRIOR APPLICATION NUMBER: US/09/357,014
FILING DATE: (Unknown)
ATPORREY/AGENT INFORMATION:
NAME: MANDIAGEN: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
RECERPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (17)227-7400
TELEPHONE: (17)227-7400
TELEPHONE: (17)227-7400
TELEPHONE: (17)227-7400
TELEPHONE: (17)227-7400
SEQUENCE CHARACTERISTICS:
LENGTH: 906 amino acids
TYPE: anino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-357-014-9
AND USES THEREFOR CORRESPONDENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: November 6, 2001, 05:01:40 Job time: 7529 sec
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714 EGELEE 719
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

November 6, 2001, 05:03:18; search time 82.15 Seconds Run on:

(without alignments)
1309.294 Million cell updates/sec

US-09-075-375A-6 7495 Title:

.....MEASEVEKLFGKALPIRKVR 1412 1 MALSLHTVFLCKEEALNLYA.. Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

pir1:*
pir2:*
pir3:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		violaxanthin de-ep	hypothetical prote	rhoptry protein -	prote	hypothetical coile	lmpl protein - Myc	conserved hypothet	reticulocyte-bindi	hypothetical prote	repeat organellar	myosin heavy chain	myosin beta heavy	nuclear migration	DNA topoisomerase	hypothetical prote	RESA-H3 antigen PF	conserved hypothet	hypothetical prote	cag island protein	myosin beta heavy	hypothetical prote	nitrite reductase	surface-located me	hypothetical prote	probable membrane	hypothetical prote	myosin-like protei	phosphoprotein pho
	ΩI		T00708	A84606					: н69378	: A42771			<		ß					-						ÇZ,		2 T05113	S3	2 A40801
	Length DB										2469 2																	2712		1109 2
% Query	- 1	34.1	32.4	2.8		2.2		2.1	2.1	2.1	2.1			1.9	1.9	1.9	1.9	1.9			1.9	٠			1.9	•		1.9	1.8	1.8
	Score	2557	2430	210	194.5	167.5	158.5	156	155.5	155.5	155	151	148.5	146	146	144.5	144	143.5	142.5	142.5	142.5	142.5	142.5	141	140.5	140	139.5	139	137.5	137
Result	No.	7	7	33	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable centromer	hypothetical prote	ORF MSV156 hypothe	dystrophin, muscle	myosin heavy chain	conserved hypothet	major merozoite su	hypothetical prote	myosin heavy chain	hypothetical prote	hypothetical prote	chromosome assembl	anthrax toxin leth	hypothetical prote	chromosome segrega	major merozoite su
E71410	T18427	T28317	S02041	I38055	A70387	805603	T20978	148153	T25592	C71622	B70356	JQ0032	A72287	E69444	SAZQK1
7	7	~	Н	7	7	7	ď	7	7	7	7	Н	7	ď	-
9	74	27	09	37	7.8	39	61	34	54	ō	9	9	0	ي	31
1676	37.	11	36	19	6	16	22	19	16	197	115	80	117	115	16
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137 1.8 167	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.7	1.7

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violaxanthin de-epoxidase precursor - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000

C;Accession: T03750
R;Bugos, R.C.; Hieber, A.D.; Yamamoto, H.Y.
J. Biol. Chem. 273, 15321-15324, 1998
A;Title: Xanthophyll cycle enzymes are members of the lipocalin family, the first ide A;Reference number: 215054; MUID:98288256
A;Accession: T03750

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-478 <BUG>

A;Cross-references: EMBL:U34817; NID:g1463122; PIDN:AAC50031.1; PID:g1463123 A;Experimental source: strain Xanthi; tissue-type leaf C;Genetics:

A; Gene: TVDE1

A; Description: violaxanthin de-epoxidase and zeaxanthin epoxidase catalyze the additid in protecting the photosynthetic apparatus from excessive light A; Note: established as member of the lipocalin family F;1-134/Domain: transit peptide (plastid) **status predicted <TNP>F;1-134/Domain: transit peptide (plastid) **status predicted <TNP>F;135-478/Product: violaxanthin de-epoxidase **status predicted <MAT>

Gaps ; 0 Length 478; 0; Indels Query Match

34.1%; Score 2557; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.4e-142;
Matches 477; Conservative 0; Mismatches 0;

; 0

474 MALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSP 533 pp δλ

534 RICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAI 593 δλ

61 g

594 VAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETEC 653 ò

g

QIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT 713 654 δ

qq 714 RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773 Ω

qq

HDNEYLLYQDDWXILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 833 δλ

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A;Gene: At2g21860
A;Map position: 2
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                                                                                                                                                                                                                       C; Species: Arabidopsis thalland (mouse-ear cress)
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C; Accession: T00708
R; Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Consologis, A.; Ecker, J.R.
Submitted to the EMBL Data Library, April 1998
A; Description: Genomic sequence for Arabidopsis thaliana BAC F22013.
A; Reference number: 214200
                                                                                                                                                                                                                                                                                                                                                                                                                    A:Cross-references: EMBL:AC003981; NID:g3063438; PID:g3063441; GSPDB:GN00059; ATSP:F2201
A:Experimental source: cultivar Columbia
C:Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  951 MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSS 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1071 ACLLKGCRIELARCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDN 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1311 TCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKVEKVGRTEMTLFQRLAEGFNELK 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 360
                              834 LQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDK 893
                                                 Gaps
                                                                                             894 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 950
                                                                                                              ;
0
                                                                                                                                                                                                          violaxanthin de-epoxidase homolog F22013.3 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 QDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.4%; Score 2430; DB 2; L 100.0%; Pred. No. 1.1e-134; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     A; Accession: T00708
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-462 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
A; Introns: 72/3; 128/2; 160/3; 292/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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RESULT A84606

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hypothetical protein At2g21860 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 02-Peb-2001
C.Accession: A84606
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.M.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A.; Reference number: A84420; MUID:20083487
A.; Accession: A84606
A.; Accession: A84606
A.; Accession: A84606
A.; Accession: A84606
A.; Residues: 1-522 <STO>
A.; Residues: 1-524 <A.; Residues: 1-544 <A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T28677, C45527, C45217, C45521
#F;Reen, J.: Sinha, K.: Brown, K.: Holder, A.
Mol. Biochem. Parasitol. 65, 171-177, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 PEPPV--KLIALVGKGEVSPLK-STSWEEVMLHTARRLKWVD------EGYEMLVFDD 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555 SPAHSINQNVPKGNSGCKFPKDVALMV-----WEKWG----QFAKTAIVALFILSV--- 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TEENKLVGN 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             741 LSWRIRTPDGGFFTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVE 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 --WRRR-----WIIVD--VS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 DDLSWGLFHYHGAARVAGQSYTGAVLVTPDGSYPAEKDKERLQSALEKCGIKEWELF-AV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 SKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 QNLRSK-----GFSTLSCMVKNCGPQILNCLLDPNCRKALOCLNOCS--PVDOVCSYRCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659 DLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 210; DB 2; Length 522; Pred. No. 8.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8%; Score 210; DB 2; L 21.1%; Pred. No. 8.3e-05; tive 77; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 DNCSCENPPL-----GIPQGSRLHSRISIIEEPDSEEK 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         852 DNTCGPEPPLVERLEKKVEEGER----TIIKEVEEIEE 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                710 ------WFITRGLNPTFDAFDCQLHEFH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rhoptry protein - Plasmodium yoelii
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itle: }	• A:Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii. A:Reference number: 220508; MUID:95021522	QY	902 FEGF
essic tus:	nn: 1286// preliminary; translated from GB/EMBL/DDBJ + trans: DNA	Op	733 GNLF
idues	: LYPE: UNA 5: 1-2056 (KEE> Ferrance: PMD::177839: NIT: AA57145: DID: AA57146: DIDN: AAA271204 1	QŸ	956 HCFT
D , C	TETERICES, EMBELIZAÇIOSO, NED-9497149, FIDINAMIZAÇIOSET, PROPERTOR A.; HOLIGACIA A.; Playfatt, J.; Lockyer, M.; Lewis, A.	qq	792 HDDD
le:	identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple co	QY	1016 FRSG
erencessic	se number: A45521; MOID:91101660 n: C45521	qq	843 SQNH
tus: ecul(Preliminary type: DNA	Oy	1043 LLLK
ss-r(: 1111-1209 < KKZ> sferences: GB:M34283	qq	900 VIKK
ž	0 69. GOOD 104 F. GO O. 100000	Qy	1100 CNNR
t r	%; Pred. No. 0.0052;	qa	939 -NIL
cnes	VALLVE ZIS	Qy	1129
700		qa	998 KSHK
י ה ה	1110NZINKULM VOITEBON BOELOODEBUNOHENTULEITEETKNONEETVUL	Qy	1176 FDAF
326	AKSVGKDFNRITIDNSCGFERFLDEKLEKITAEBEEKLLIREAVEI 401	qq	1048F
0 0	ENTERTMENT TO THE CONTROL OF THE CON	Qγ	1230 NHDN
404	4 6	qa	1083 -IKN
136	IDTFINELSSIVE	Qy	1285N
196	E-ILNELQMEATEVERLEGRALPIT-TRILMALAPHSNFLANHEITIRIYY 493 ::::: : : :	qq	1 1119 IKIN
767	GCKI.DGHKPPGWGWPNYFGGTVVAKITGSRIPPYFPRKDPITGHTGI.NGHGHT.LGGHNA.	ΟY	1332 IIVK
255	SO	qq	1176K
550	GKHNLSPAHSINONVPKGNSGCKFPKDV	QY	
308	:: : TNVDNTKEEEAKQNYDKSNEHMTTIPTNEDEISKIISEVKTMKDEIL	qq	1233 KPTI
578	ALMVWEKWGOFAKTAIVAI	RES	RESULT 5
368	KETVNSBHSQFTEITDKIKAEVSDKELKK396	rho	o,o ptry pro
638		C; S	pecies: Date: Date: 15-0
397	CEOSENDINKSLINERKNSTEKEYONINITEKNDEY TRVCKSTRESTTRESSKOTTI	C; A	ccession
8	VGDFDVDDSVI VOKFDWKDFSCKWFTTRGI NDTFDAFDCOI HEFHTFF	Mol	Biocher
453	K DMI NONIK TUKETUSI DK. S. T.	A;R	A: Reference nu
, ,	ANT VANT GEBT DE DAG COMPANY DE VANDANDE ET VANDANDET TO VANDANET TO CO	A; S	tatus: p
(67		A; R	esidues:
508	IKYFSDLKANLGINEENMLYNQFTEKEKTFNDIKEKNIHINEEIS 552	A;C R;K	ross-refe een, J.;
791		MOI	Biocher 14
553	KIEIKIHASIYNISBETEREIGINIESLNTKVFEKVKENVTNLNKIKEKLKHYDFSDFGK 612	A; A	eference
815	GGSVLYTRSAVAV	A A	A; Status: prel
613	EGNIKYTDKIKKINDDIMAVSQQIDQHINGLDDIQKKSESYVSEMKEQINKLEKVSNTEI 672	A) R	A;Residues: 22 A:Cross-refere
850	KTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKL		
673	SNDNVEGIKKKQQIIVTKIDKKKNIYEEINKLLSEISKIEKDNTSLEKVKDINLSYGQNL 732	a	Query Match

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DKSNGYKTEADQNKKAIQKNKELFEQYKEEVTVLLNKYYAVELKNK------ 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCOLHEFHTEGDNKLVGNISWRIK-----TLDSGFFTRSAVOKFVQDPNQPGVLY 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLP---- 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------AITSIKVSVEPFKTKI 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SI------IPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGER 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVEEIBEBEVEKEVEKVGRTEMTLFOR-----LAEGFNELKQDEENFV---RELS 1381
                                                                                       SPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSA 1015
                                                                                                                                                                           FS-----TGIFDIVPLPSKNELKEL------TAP 1042
                                                                                                                                                                                                                                                              LVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIAN----PACAANVACLQT 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPT 1175
                                                                                                                  KKCHDKSK--NHKENISDIYDKSSKIIQDF-----SRESDINDIKNKLQKNVSE 842
                                                                                                                                                                                                  KELQRDEENFLRELSKEEM----DVLDGLKMEATEVEKLFGRALPIRKLMAV--AT 955
                         :||
| : : |: ||
|NEETNITNHFKNAEEYNKIVLSNFNNIEMADNKSQYILEIKKNNGTNDHDYNIKEL 997
                                                                                                                                                                                                                                                                                                                                                     PDETEC--QIKCGDLFENSVVDEFNEC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :
Qні 1239
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t-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000 128676; A45521 3. Keen, J.K.; Jogun, S.A.; Holder, A.A. Parasitol. 76, 329-332, 1996 Parasitol. 76, 329-332, 1996 arison of two members of a multigene family coding for high-molecular maumber: 220507; MUID:97077455
                                                                                                                                                                                                                                                                                                            iminary; translated from GB/EMBL/DDBJ
n - Plasmodium yoelii (fragment)
                                          smodium yoelii
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-2401 ASIN>
ences: EMBL:036927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
ences: EMBL:036927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
older, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Parasitol. 42, 241-246, 1990
rification of the gene for a Plasmodium yoelii rhoptry protein. Multiple
umber: A45521; MUID:91101660 pe: DNA _ 260-2401 <KEE> ences: GB:M34281 iminary

2.2%; Score 167.5; DB 2; Length 2401;

Be	st Loc tches	Best Local Similarity 16.7%; Pred. No. 0.21; Matches 260; Conservative 274; Mismatches 498; Indels 525; Gaps 71;
QY Dp	23	PCNERFHRSGQPPTNIIMMKIRSNNGYFNSFRLFTSYKTSSFSDSSHCKDKSQICSID 80 :: : : : : : : :
op ox	81 509	TSFEEIGRFDLKRGMTLILEKQWRQFIQLAIVLVCTFVIVPRVDAVDALKTCACLLKECR 14
Qy Dp	141 556	IELAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFENSVVD 185 ::
Oy Op	186	QFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWY 229 :
Sy Op	230	
op ov	290	YNHDNFFLHYQDDWYILSSQIENKPDDYIFVYYRGRN : : :
λ G	331	GYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEG 390 ::
Qy Dp	391	EKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEEN 436 : :: : :: ::
ζ Ω Ω	437	FVRELSKEEKEILNELQMEATEVEKLFGRALPIRK 471 ::::: : :::: :: GKSLGNLFLQQIDEEKKKAEHTIKAMEAYIDDLDNIKKKSQEIEKEMNINMDIKMDIHKE 907
ος. Op	472 908	LRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAK 518 ::
λα q	519	ICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGCKFPKDVA 578 ::
- AQ	579 999	LMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISN 631
y d	632	-PACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSD 685
- K - Q	686 1083	VGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRI 745
ž 8	746	RTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYK 805 :
y d	806 1143	GRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERL 865 :::
& Q.	866 1182	EKKVEBCERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMD 925 : : : : : : : : :
- 2 -	926	VLD-GLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITR 982

QQ	1227	ILDIQLSVEPFKIKFLKIKDLRTKSDDCLKETKDIETKISNLSIDTQETKL-IEN 1280
Qγ	983	LPP
ďΩ	1281	KNILNT-LEKLLESLKNQKNIEDQKKELDEVNSK 1314
ô	1043	LVGVLACAFL
g	1315	FKINE
QY	1086	112
g è	1122	ISPFRANDLEGIDTNKNLGRYNTEMNNIYEEFIKSYDLITHYLETVSKEFITYEGIKNKR 1422 VDERNECAVSRKKCVPRKSDLGEFDADDSVIJONENISDRMKWvTTGGINDTF 1176
ැ ති	1423	:
٥٧	1177	DSGFFTRSAVOK
qq	1481	DNISNSINNVKKSTDENLLLINILNQTKEMYANIVSKKYYSYK 1522
Qy	1237	HYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAK 1296
qq	1523	NIFINIPK
οy	1297	SIGRDFSTFIRTDNTGGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKE 1347
qa	1569	
οy	1348	E
qq	1612	INLIFENRELHDKVQATNELKDTLSDLKNKKEQILNKVKLLHKSNELNKL 1662
RES T38 hyp	SULT 6 3077 Sothetic	RESULT 6 T38077 hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
200	opecies: Date: 03	: Schizosaccharonyces pombe 7-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 nr. 138077
R;C Sub	Connor,	R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. to the EMBL Data Library. April 1996
A;R A;A	Referenc	se number: 221767
A; S	status:	preliminary; translated from GB/EMBL/DDBJ
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A C	Txperime	b.dwoodo, of Db. of Action of
) 4 4	Jene: SP Jene: SP Jap posi): 9:SPACIF3.06c †jon: 1
Ğ	4	
O m x	Nuery Ma Best Loc Matches	Ouery Match 2.1%; Score 158.5; DB 2; Length 1957; Best Local Similarity 17.6%; Pred. No. 0.54; Matches 265; Conservative 227; Mismatches 503; Indels 511; Gaps 68;
Qy	59	YKTSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQFIQLAIVLVCTFV 118
đ	305	
δ	119	IVPRVDAVDALK TCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIKC 175
qq	354	TIGSLKDSRTSNSQLEEEMVELKESNRTIHSQLT
Qγ	176	GDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFN 220
QQ	397	ONNESS
δ	221	MKDFSGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDG-GFFTRSAV 276

QY	1238 Y	YQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKS 1297
Qy		GRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVE 1345
qq	1349 8	SEKNFLRKEAEMTENIH-SLEEGKEETKKEIAELSSRLEDNQLATNKLKNQ 1398
Qγ	1346 :-	139
qq	1399 1	EDVLKEKESLIISLEESLSNQRQKESSLLDAKN
δλ		SEVEKL 1401 : :
QQ	1457 8	SLMEKI 1462
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T30822 lmp1 pr	322 1 protei pecies:	
C; DE	ste: 22	t-1999 #text_cha
R;Je Infe	ensen, l ect. Imm	Christiansen, G.
A; E	itie: Se eference	t defection marghes by cartivactors
A; A;	ccession tatus: I	n: T30822 prellminary; translated from GB/EMBL/DDBJ
A; W	olecule	140000 - Ata .
0 0 0 0 0 0 0 0	ross-re enetics ene: lmp	, FILLY SAMOLATING
ŌĂ	uery Ma¹ est Loca	B 2; Length 1365; 6;
ž	atches	vative 187; Mismatc
QY	272	TRSAVQTEVQDPDLPGALYNHDNEFLHYQDDWYLLSSQIENKPDDYIEVYRGRNDAWDG 331
qq	282	\sim
Qy	332	YGGSVIYTRSPTLPESII-PNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEK 385
qq	320	SNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVSNANTLSA 369
Qy	386	TAEEGEKLLIKEAVEIEEEVEKVEVEKVRDTEMTLFQRLLEGFKELQQDEENFVREL 441
QQ	370	KLTDKDNTIQQAKTELEKEVQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETF 425
Qy	442	SKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHK 501
qq	426	NKDKBAKFNELKQTRNQIQEF446
QY	505	RFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHS-I 560
qq	447	INTINKNNPNYSELISQLISKRDSKNSVTDSSNKSDIESANTEL 489
Qy	561	NQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKE 620
Op	490	KQALAKANDNLAKS 509
Qγ	621	CRIELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKV 680
qq	210	IKEQLNNSVSNTIQQAKTE 541
QY	681	PRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENK 736
ΩD	542	LEKEVQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETFNKDKEA 588

in the

C; Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

LVGNLSWRIRTPDGGFFTRS		737 LVGNLSWRIRTPDGGFFTRSAVQKFVQDFKYPGILYNHDNEYLLYQDDWYILSSKVENSP 796 	EDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIK 850 :	TDNTCGPEPPLVERLEKKVEEGERTIIKEVEELEEEVEKVRDKEVTLF 898 	899 SKLFEGFKELQRDEBNFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVAT 955 	956 HCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRS 1009 	SRPLSAFRSGFSKGIFDIVPLPSKNEL-KELTAPLLIKLVG 1049 	1050 VLACAFLIVPSADAVDALKTCACLIKGCRIELAKCIANPACAANVACLQTCN 1101 	1102 NRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQ 1155 : : :	1156 NFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTR- 1212	SAVQKFVQDPNQPGVLXNHDNEXLHYQDDWYILSSKIENKPEDYIFVYYRGRN 1265 	-DAWDGYGGAVVYTRSSVLPNSI 1300 : : : : : : : : : : : : : : : : : : :	DESTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEV 1348	KODRRNBVORISKERETERINE 1204
	737 589 797 627 851 677 956 766 1010 815 1050 863 1102 908 11156 968 11010 11010 11156 11010 11156 11010	' LVGNLSWRIRTPDGGFFTRSAVQKFV(EDYIFV		SKLFEGFKELQRDEENFLRELSKI 			VLACAFLIVPSADAVDALK : KADAIKNNPSSSKQALK	NRPDETECQIKCGDLFENSVVDEFNEC : : : : SNIGYRLFKLAQAEQENNSDVDKLKNR	NFNISDFNGKWYITSGLNPTFDAFI	SAVQKEVQDPNQPGVLYNHDNEYLE SI	-DAWDGYGGAVVYTRSSVLPNSI		EKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKME 1394

RESULT 8
H169378
conserved hypothetical protein AF1032 - Archaeoglobus fulgidus
conserved hypothetical protein AF1032 - Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C; Accession: H69378
R; Accession: H69378
R; Alek, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.F.; Mature 390, 344-370, 1997
Nature 390, 344-370, 1997

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-886 <KLE> A;Cross-references: GB:AE001032; GB:AE000782; NID:g2689355; PIDN:AAB90211.1; PID:g264956

27; 968 FFSSDDGIGRLGITRKRINGTFLLKILPPIQSA--DLRTTGGRSSRPLSAFRSGFSKGIF 1025 1026 DIVPLPSKNELKELTAPL-------LLKLVGVLACAFLIVPSADAVDALKTC 1070 1071 ACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130 1131 SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG 1190 -----DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYN-- 1230 1231 --HDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSII 1288 1289 PELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEV 1348 1349 EKVGRTEMTLFQRLAEGFN---ELKQDEENFVRELSKREMEFLDEIKMEASEVEKLFGKA 1405 ----SILEKLLSEINQALRDVEKREGDLTREAAGIQAQLKKAEE 329 797 EDYIFVYYKGRNDAWDGYGGSV--LYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTD-N 853 854 TCGPEPPLVERLEKKVEEGERTI---IKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQR 910 250 GLEEKLRELEKOLKEVVERIEDLEKKAKEVKEL---------KPKAERY- 289 330 D-----TLKPKMDRMQGIK-- 372 452 IMAEYTREMKRIAEELAKADEIEKKLKERLEKVEKALEKGETVLKYROMVDELKALENEL 511 512 SSHDAE------KLSAESEE-----YRKVKERLDGLRGOOKILLSSA---SRI 550 594 ------QSLRPFYNKWLELKDAESRLESELKRRE-KLEDEISEAIAKLEEANGKA 641 152 EDY-----ENAWKNLGAVIRMLEREKERLKEFLSQEEQIKRQKEEK-----KAEIE 197 911 DEENFLRELSKEEMDV---LDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIR 967 405 KLKKLIAKKSSLKTRGAQLKKAVEE------LKSAERTCPVCGRELDEEHRKN 451 Gaps 85; Mismatches 221; Indels 221; Length 886; Ouery Match 2.18; Score 155.5; DB 2; Best Local Similarity 20.68; Pred. No. 0.27; Matches 137; Conservative 1406 LPIR 1409 642 EEIR 645 290 ---a δ a ŏ g ò QQ δ a δ g ò g δy g q δ ŏ g ò ద

0 RESULT

reticulocyte-binding protein 1 - Plasmodium vivax

C; Species: Plasmodium vivax C; Date: 04 Mart-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995 C; Accession: A43771 R; Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W. Cell 69, 1213-1226, 1992 A; Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites. A; Reference number: A42771; MUID:92315338

A Accession: A42771
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2829 <GAL>
A; Experimental source: Belem strain, merozoites
A; Experimental source: Belem strain, merozoites
A; Note: sequence extracted from NCBI backbone (NCBIN:108114, NCBIP:108115)

Q M M	ery Ma est Locater	Ouery Match 2.1%; Score 155.5; DB 2; Length 2829; Best Local Similarity 17.4%; Pred. No. 1.4; Matches 283; Conservative 242; Mismatches 573; Indels 529; Gaps 76;	
ογ	57	TSYKTSSFSDSSHCKDKSQLCSIDTSFEEIQRFDLKRGMTLILEKQWRQFIQLA 110	
qq	1110	TSNKNEILKSVKEVEDKLNLVEQNEDYKKVKNPENEKQLEAIRGSMSKLKE 1160	
oy.		ELAKCIANPSCAANVACLQTCNNRPDETE 170 : : : : :	
ପୁପ	1161	VINKHVSEMTQLESTANTLKSNAKGKENEHDLEELNKTK 1199	
δ			
a	1200	GOMRDIYEKLKKIAEELKEGTVNELKDANEKANKVE-PEPERNIIGHVLERITVEKDK 1256	
Š ć	1257	SGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQD 282	
3 8		TABERNOENT REBREEKEL ODDOGREEKT TAGE ERRERGEN. OAT WIEDERSTAND. OAT WIEDERSTAND.	
5 6	n -		
- 8	342	NLOKAAKSVGRDFNNFITTDNSSVGRDFNN 372	
- · 8		ĪΛ	
δλ	373	CGPEPPLVERLEKTABEGEKLLIKEAVEIEEEVEKEVEKVRDT 415	
QΩ	1389	ANGEFTKAEGEEKNASARLAEAEKLKEQIVKDLDYSDIDDKVKKIEGIKREILKMKES 1446	
οy	416	EMTLFQRLLEGFKELQQDEENFVRELSKEEKEILNELQME455	
g	1447	ALTEWEE-SEKFKOMCSSHMENAKEGKKKIEYLKINGDGGKANITDSOMEEVGNYVSKAE 1505	
ò	456	- 22 ⋅	
qq	1506	HAFHTVEAQVDKTKAFCESIVAYVTKMDNLFNESL-MKEVKVKCEKKNDEAEKY- 1558	
0y	493	VGSKLPGHKRFSWGWEDJFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKH 552	
g	1559	SAKLKPYDGRI-KARVSENERKISELKEKAKVEKKESSQLNDVSTK 1603	
δλ	553	NLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALK 612	
g	1604	SLLQIDNCRQQLDSVLSNIGRVKQNALQYFDSADKSWKSVLPISELGAEKSLDKVK 1659	
οy	613	TCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQ-IKCGDLFENSVVDEF 669	
QQ	1660	AAKESYEKNLETVQNEMSRINVEEGSLTDIDKKITDIENDLLKMKKQYEEGLLQKI 1715	
δ	670	NECAVSRKKCVPR-KSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLH 728	
g	1716	KENADKRKSNFELVGSEINALLDPSTSIFI-KLKKKRYDMTGDLKNYGVKMN 1766	
δλ	729	EFHTEENKLVGNLSWRI	
g	1767	EIHGEFTKSYNLIETHLSNATDYSVTFEKAQSLRELAEKEEEHLRRREEEAIFLLNDIKK 1826	
δλ	761	FVQDPKYPGILYNHDNEYLLYQDDWYILS789	
q	1827	VESLKLLKEMMKKVSAEYEGMKRDHTSVSQLVQDMKTIVDELKTLNDISECSSVLNNVVS 1886	
οχ	790	SKVENSPE-DYIEVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN 846	
qq	1887	IVKKVKESKHADYGMEFN 1931	
ογ	847	TFIKTDTIIKEV 880	
q	1932	AEMKSNFKTDLELEIFSVISNSNELLKKIEQDSNDVIQKERESEQLAKDATDIYNVIKLK 1991	

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2167 -KCVDYIKDNSSSTDGYVETL------KGFYGSKLTFSSASEIVQNADTYSVNFAKH 2216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : || || : | |: | |: | 12313 SVNDHMHSMEAEMIKNGLKYIPESVQNINNIYSVIEAEVKTLEEIDRDYGDNYQIVEEHK 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2373 KQFSILIDRTN-----ALMDDIEIFKKENNYNLMEVNTETIHRVNDYIEKITNKLVQAK 2426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2427 TEYEQILENIKQNDDMLQNIFLKKVSIIEYFENVKKKKESILNDLYEQERLLKIGEHLDE 2486
                                                                                                                                                                                                                                                                             1051 LACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ 1110
                                                                                                                                                                                                                                                                                                                        2118 -----VIEMNSTIDELYK---LGKNCQAHWISLISYTANMKTSKKLIMINKEKENTE-- 2166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2253 LYDKLNEEKREMDELYRNISETKLKOMEHSTDVFKPMIELHKGMNETNNKSLLEKEKKLK 2312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1268 ------WDGYGGAVVYTRSSV--LPN--SIIPELEKAAKSIGRD------ 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1302 --FSTFIRTDNTCGPEPALVERIEKTVEEGE----RIIVKEVEEIEEEVEKEVEKV--GR 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1354 TE-----EFLDE 1390
                                                                                                                                                                                    995 PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNE----LKELTAPLLLKLVGV 1050
                                                                                                                                                                                                                                                                                                                                                                      1111 IKCGDLFE--NSVVDEFNECAVSRKKCVPRKSDLG-EFPAPDPSVLVQNFNISDFNGKWY 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1168 ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGV 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2217 EKESLNAIRD-IKKELYLFHONSDISIV-------EGGVONML-----A 2252
                                                                                                                                    2041 -ELENL-----KKMYTIY------RDKKSERESGLQEM---ENEMN-TYSNSI- 2077
                                                                                         935 TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL 994
881 EEIEEEVEKVRDKEVTLFSKLFEGFKELQRDE-----ENFLRELSKEEMDVLDGLKMEA 934
                                                                                                                                                                                                                                  ----DIEKLERSNEEMRNISEKISTIDSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1228 LYNHDNEYLHYQDDWYILSSKIENKPEDY-----IFVYYRGRNDA----
                               2078 -- TOLEGIVVSAGESKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1391 IKMEASE 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2487 IKRNVTE 2493
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"Mypothetical protein ORF64 - saimiriine herpesvirus 1 (strain 11)
C;Species: saimiriine herpesvirus 1
A;Note: host Saimiriine common squirrel monkey)
A;Note: host Saimirii sciureus (common squirrel monkey)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
C;Accession: H36812
R;Albrecht, J.
Submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A36806

A Accession: H36812
A Molecule type: DNA
Residues: 1-2469 (ALBA)
A; Residues: 1-2469 (ALBA)
A; Residues: 1-2469 (ALBA)
A; Cross references: GB:X64346; NID:g60320; PIDN:CAA45687.1; PID:g60385
A; Cross references: GB:X64346; NID:g60320; DIDN:CAA45687.1; PID:g60385
B; Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; J. Virol. 66, 5047-5084, 1920
J; Virol. 66, 5047-5084, 1920
A; Reference number: A37309; MUID:92333688
A; Contents: annotation; protein-coding frames
A; Note: neither protein nor nucleotide sequence is given
C; Genetics:
A; Genetics:

58; Gaps Query Match 2.1%; Score 155; DB 2; Length 2469; Best Local Similarity 17.3%; Pred. No. 1.2; Matches 230; Conservative 208; Mismatches 497; Indels 396;

 Qy 1:	1207 SGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYY 1261	
Db 1(
Oy 13	1262 RGRNDAWDGYGGAVVYTRSSVLPNSII	
Db 1	1125 KEVEEVLESVKNLKEAKLKSLLPNGPVFTPPKFDWIHYYESNVNFHLKTINLPKVSTVAH 1184	
Qy 13	1297 SIGRDFSTFIRTDNT-CGPEPALVERIEKTVEEGERIIVKEV 1337	
Db 1	1185 NIGHELSLESQALNSKTLPEAVVGTSLEQHAAKFSCMFKTLEATWHDHQVDTRTKIDEYI 1244	
Qy 1.	1338 EEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFL 1388	
Db 13	1245 EDLRNDTKKHIVAPQIQSPNRFLSPEDIQEINSLPKLFRDSLLENESRLASQKNEFQML 1304	
0y 13	1389 DEIKMEASEVE 1399	
DP TI	1305 -ENTVKAAELQ 1314	
RESULT	ULT 11	
repeat C; Spec	organellar protein - Plasmodium chabaudi es: Plasmodium chabaudi	
C; Date	ate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 ccession: T18372	
R; Werne	Ferner, E.B.; Taylor, W.R.; Holder, A.A. Blochem, Parasitol, 94, 185-196, 1998	
A; Title A; Refe	itle: A Plasmodium chabaudi protein contains a repetitive region with a preference number: 218922; MUID:98418765	edicted
A; Acce: A; Statu	.ccession: T18372 :tatus: preliminary; translated from GB/EMBL/DDBJ	
A; Molec	olecule type: DNA esiques: 1-1939 <wrr></wrr>	
A; Cross	ross-references: EMBL:U43145; NID:g1151157; PID:g1151158; PIDN:AAC63403.1	
Query	Query Match 2.0%; Score 151; DB 2; Length 1939;	
Matc	Mismatches 299; Indels 422; Gaps	50;
δy	380 VERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEEN 436	
qq	95 VKEYEVKIEELEKELKLEKEKQINKEYEKELNEKSEFIKROMELLKEKELNINLKEN 151	
Qy 4	437 FVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHE 487	
Db 1	152 KINNKEIITLKREEKLNDIESEYIEKNKEKEKLNYEVTNIKMSLD 196	
0y 4	МСW	
Db 1	197 KLTCEVQEKKDNLEKINKKVIEKENNLRELKEFMKEKNEIIESLDG 242	
Qy 5	548 SHGKHNLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADA 607	
Dp 5		
0у 6	608 VDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVD 667	
Dp 5	265 IEMLD	
9 YO	668 EFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQL 727	
Dp 5	288 KENEIIIEKLKDIESREKDFKSKEEKFASMENEL 321	
Qy 7	728 HEFHTEENKLVGNLS-WRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWY 786	
£ qq	322 NTLKSDLSKNACQMEVYKLEIKDLSQSLVEKEREIFEIKNEYDD 365	
Qy 7	787 ILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN 846	
Dp 3	366KINNMKEKLSSINDKGIDNIVLHSEEEKI-NKLKKEKETELNEIHKKYN 413	

	414 LEIETIKNELNEKEEELEKNKKAHTVEVTNLTKEIK 449	
o _y	LFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKLMA	
ga V	450 LLEKKTEDAKEGHKNELNELNELNNELSKLNKEKDNIKNENTEL	
a	: : :	
δλ	1013 LSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSADAVDALKTCAC 1072	
đ	513DLINNLKN 527	
S S	1073 LLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVD 1123 1	
Ωý	1124 EFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTF 1176	
qq	559 EIEKKYKNEIFMLEEKLKEKENYADLNDEISILRNSIYVKEKEFI 603	
δy	VGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLY	
qq	604EMKEFYENKINLFNKNFEEKKNIYENELNSLRLKYDNEQ 642	
à	EYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAMDGYGGAVYYTRSSVLPNSIIPELEK	
2	NMHMFKSICIKIDMFISEN	
λo λ	KTVEEGERIIVKEVEEIEEEVEKEVEK 13	
Q d	EMVAELEKRHAAIVAELEEKHKEEI	
Š		
qq	746 LGEGHKEVVLRLGEQHKEETIILEEKHKDVVTKLGEQHKENIIKLEEEHKDVVTKLG 802	
SAN TANKES CONTROL OF	RESULT 12 Myosin heavy chain beta chain, cardiac - pig Myosin heavy chain beta chain, cardiac - pig C.Species: Sus scrofa domestica (domestic pig) C.Species: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000 C.Accession: A59286 A.Accession: Accession: Accessi	

ΟŊ	256	VGNLTWRIKTLDGGFFTRSAVQTFVGNLTWRIKTLDGGFFTRSAVQTFVGNLTWRIKTLDGGFFTRSAVQTF
Dp	486	: : : 3.1 .: : : : : : : : : : : : : : : : : :
ΟŊ	281	DWYILSSQIENKPD-DYIFVYYRGRNDAWDGYGG
QQ	544	
Qy	335	SVIYTRSPTLPESIIPNLQRAA-KSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKL 393 :
ΟŸ	394	FKELQC
Ωp	645	: : : : CUVSALH-RENLINKLMINKLMINKSPGVID 685
ΟŊ	448	ILNELQMEAT-EVEKLFGRALPIRKLRMALAPHSNFLANHETIKYY 492
οp	989	NPLVMHQLRCNGVLEGIRICRKGFPNRILYGDFRQRYRILNPAAIPEGGFIDSRKGAEKL 745
ΟŊ	493	VGSKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKH 552
Dp.	746	LGSLDIDHNQYKFGHTKVFFKAGLLGLLEEMRDERLSRIITRIOAQSRGVLSRMEFKK 803
δy	553	NLSPAHSINQNVPKGNSGCKFPKDVALMVWEKMGQFAKTAIVAIFILSVASKADAVD 609
qq	804	LLERRDSLLIIQWNIRAFMSVKNW-PWMKLYFKIKPLLESAETEKEMA 850
Qy	610	
qq	851	TWKEEFGRLKEALEKSEARRKELEEKMVSLLQEKNDLQLQVQAEQDNLSDSEERCDQLIK 910
δλ	663	NSVVDEFNECAVSRKKCVPRKSDVGDFPVFDPSVLVQKFD 702
qq	911	NKIQLEAKVKEMTERLEDEEEMNAELTAKKRNVEDECSELKRDIDDLELTLAKVEKEK 968
Óγ	703	MKDFSGKWFITRGLNPTFDAFDCQLHEFHTEBNKLVGNLSWRIRTPDGGFFTRSAVQKFV 762
qq	696	HATENK-VKNLTEEMAGLDEIIAKLT 993
Qy	763	
Db	994	KEKKALQEAHQQALDDLQAEEDKVNTLTKAKVKLEQHVDDLAGSLEQEK 104;
Qy	823	SAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGP 857
Dp	1043	KVRMDLERAKRKLEGDLKLTQESIMDLENDKQQLDERLKKKDFELNALNARIEDEQALGS 110:
Qy	858	EPPLVERLEKKVEEGERT
QQ	1103	CLOKKLKELQARIEELEEEL-EAERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQI 116
Qy	890	VRDKEVTLFSKLFEGFKELQRDEENFLREL 919
Dp	1162	EMNKKREAEFQKMRRDLEEATLQHEATAAALRKKHADSVAELGEGIDNLQRVKQKLEKEK 122
Οy	920	SKEEMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLG 979
qq	1222	SEFKLELDDVTSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAE 126
Οy	980	FDIV
QQ	1265	FIGURE STATES TO THE STATE OF THE STATES OF
οy	1037	KELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC 109
Dp	1313	EDLKRQLEEEVKAKNALAHALQSARHAADLLREQYEEETETKAELQRVLSKANSEVAQ 137
Qy	1097	LQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQN 115:
рp	1371	WRTKYETDAIQRIEELEEAKKKLAQRLQDAEE 140

1157 FNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQ 1216

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R;Saez, L.J.; Gianola, K.M.; McNally, E.M.; Feghali, R.; Eddy, R.; Shows, T.B.; Leinw
Nucleic Acids Res. 15, 5443-5459, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I54254
                                                                                                                                                                   A; Accession: A27858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S12458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANGULE 13
C. Species: Homo saplens (EC 3.6.1.32)
C. Accession: A37102: 81273; A94224; E289308; A4497; A27858; I54254; S12458; S09331; S02
A.7T16: The complete sequence of the human beta-myosin heavy chain gene and a comparation of A. Reference number: A37102
A. Molecule type: DNA
A. Residues: 11935 C.ABS
A.CTOSS - Reference number: S12733, MUID:91065634
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 11935 C.ABS
A.CTOSS - Reference and organization of the human cardiac beta-myosin heavy chain A. Molecule type: DNA
A. Residues: 1203
A. Molecule type: DNA
A. Residues: 1203
A. Molecule type: DNA
A. Residues: 1203
A. Molecule type: DNA
A. Residues: 1206, W. J.; Liew, J.; Liew, C.C.
A. Title: Characterization of human cardiac myosin heavy chain genes.
A. Molecule type: DNA
A. Residues: 1206, W. J.; Liew, J.; Ling, D.; Liew, C.C.
A. Title: Characterization of human cardiac myosin heavy chain genes.
A. Accession: A3224
A. A. Molecule type: DNA
A. Residues: 1206, W. J.; Liew, J.; Ing, D.; Liew, C.C.
A. Title: Characterization of human cardiac myosin heavy chain genes.
A. Accession: A3224
A. Molecule type: DNA
A. Residues: 1803
A. Title: DNA
A. Resid
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A; Residues: 1412-1518, 'R',1520-1574,'NV',1577-1935 <KUR>
A; Cross-references: GB:N2166d the codon AGC for residue 108 as Arg
A; Note: the authors translated the codon AGC for residue 108 as Arg
R; Lichter, P.; Umeda, P.K.; Levin, J.E.; Vosberg, H.P.
Bur. J Biochem. 160, 419-426, 1986
A; Title: Partial characterization of the human beta-myosin heavy-chain gene which is
A; Reference number: A24997; MUID:87030293
                                                                                                                                                      1217 KFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVV 1276
                                                                                                                                                                                                                                        1439 AAALDKKQ----RNFDKILAEWKQKYEESQSELESSQKE------ARSL 1477
                                                                                                                                                                                                                                                                                                                      1277 YTRSSVLPNSIIPELE-----KAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE 1330
                                                                                                                                                                                                                                                                                                                                                                                                        1478 STELFKLKNAYEESLEHLETSKRENKNLQEEISDLTEQLGSSGKTIHELEKVRKQLEAEK 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1331 RIIVKEVEEIEEEVEKEVEKVGRTEMTLFQ-----RLAEGFNELKQDEENFVRELS-- 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1538 LELQSALEESEASLEHEEGKILRAQLEFNQIKAEMERKLAEKDEEMEQAKRNHLRVVDSL 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- KEEME-FLDEIKMEASEVEKLFGKA 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |::|| |:|::: | :: :| 1598 QTSLDAETRSRNEALRVKKKMEGDLNEMEIQLSHANRWAAEA 1639
                                                                         1403 ------AVEAVNAKCSSLEKTKHRLQNEIEDLMVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 682-721;975-1112;1854-1935 <LIC>
A; Cross-references: GB:X04627
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A; Molecule type: DNA
A; Residues: 1854-1865, A, 1867-1935 <SAE>
A; Cross-teferences: GB:X05631; GB:Y00362; NID:g34643; PIDN:CAA29119.1; PID:g34644
A; Cross-references: GB:X05631; GB:Y00362; NID:g34643; PIDN:CAA29119.1; PID:g34644
R; Diederich, K.W.; Eisele, I.; Ried, T.; Jaenicke, T.; Lichter, P.; Vosberg, H.P.
Hum. Genet. 81, 214-220, 1989
A; Tile: Isolation and characterization of the complete human beta-myosin heavy chain
A; Reference number: I54254; MUID:89154425
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Nucleic Acids Res. 14, 2951-2969, 1986
A;Title: Characterization of diverse forms of myosin heavy chain expressed in adult h
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A; Map position: 14q12-14q12
A; Introns: 67/3; 115/3; 164/1; 177/2; 213/3; 244/3; 266/1; 299/1; 313/3; 380/1; 419/3
A; Introns: 67/3; 115/3; 165/1; 1548/3; 1651/3; 1719/3; 1761/3; 1853/3; 1885/3; 1930/3
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Reywords: actin binding; AFP; cardiac muscle; coiled coil; heart; hydrolase; methyl
E; 188-766/Domain: myosin motor domain homology <AMO(T)
E; 170-185; Region: nucleotide-binding motif A; (P-loop)
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A,Residues: 'LLGVGELASG',1311-1312,'G',1314-1355,'R',1357-1358,'GD',1361-1438,'LQ',14
A,Note: the first ten codons of the sequence figure show the reverse complementary st
C,Genetics:
A,Gene: GDB:MXH7
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A;Residues: 785-1076, E',1078-1123, 'A',1125-1702, 'DE',1705-1935 <BOB>
A;Cross-references: EMBL:X51591; NID:929467; PIDN:CAA35940.1; PID:929468
A;Cross-references: EMBL:X51591; NID:929467; PIDN:CAA35940.1; PID:929468
Bur. J. Biochem, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
Bur. J. Biochem, 189, 55-65, 1990
A;Tille: Identification of three developmentally controlled isoforms of human myosin
A;Reference number: S09331; MUID:90235862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 786-830, Xx, 832-900, Xx, 902-970, Xx, 972-1040, Xx, 1042-1076, E, 1078-1110,
1,1602-1670, XX, 1672-1702, DE', 1705-1740, Xx, 1742-1810, Xx, 1812-1935 <BOW>
A;Cross-references: EMBL:X51591
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Hum. Genet. 76, 47-53, 1987
A;Title: Construction of a human ventricular cDNA library and characterization of a l
A;Reference number: S022229; WUID:87192738
A;Accession: S02229
A;Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
A;Reference number: A93669; MUID:87260010
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A;Residues: 1393-1702,'DR',1705-1935 <JAN>
A;Cross-references: EMBL:X06976; NID:934860; PIDN:CAA30039.1; PID:9825694
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A;Residues: 653-720 <RES>
A;Cross-references: GB:M27636; NID:g179511; PIDN:AAA79019.1; PID:g601916
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F;123/Modified site n6.N6.N6.trimethyllysine (Lys) #status predicted
F;184/Binding site: ATP (Lys) #status predicted
F;695,705/Active site: Cys #status predicted
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A; Reference number: $12458
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ò	203 1	DVGEFPVPDRNAVVONFNMKDFSGKWYITSGLNPTFDAFDCQLHEF 248
		LCINFTNEKLQQFF
Qy	249	HMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPGALYNHD 293
qq	521	- Ē
0у	294	GYGG
qq	558 (GKSANFOKPRNIKGKPEAHFSLIHYAGIVDYNIIGWLOKNKDPLNETV 605
		TDNSCGPEPPLVERLEKTAEEGEKL
		NGSSFQ1VSALR-KENLIN
ò_6	408 658	EVEKYKUTERILLEGKELEGEKELGQUEEBRYKELSKEEKETLUNELCMEATT 45/ L. 1 1 1 1 1 1 1 1 1 1
ŏ	28	LPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWG
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ò	507	WEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQN 563
- 8	160	: :
_ŏ.	564	VPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKEC 621
<u></u> 8	818	: IRAFMGVKNW-PWMKLYFKIKPLLKSABREKEMASMKEEFTRLKEALE 864
ò-	622	RLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNE 671
8 <u></u>	865	KSEARRKELEEKMVSLLQEKNDLQLQVQAEQDNLADAEERCDQLIKNKIQLEAKVKEMNE 924
_č.	672	CAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGL 716
_ 2_	925	RLEDEEEMNAELTAKKRKLEDECSELKRDIDDLELTLAKVEKEK968
-ŏ-	717	NPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDN 776
- 0 -	696	HATENK-VKNLTEEMAGLDEIIAKLTKEKKALQEAHQQAL 1007
-à	777	EYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSA 824
- 6	1008	DDLQAEEDKVNTLTKAKVKLEQQVDDLEGSLEQEKKVRMDLERAKRKLE 1056
. č.	825	VLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVE 863
- Q -	057	GDLKLTQESIMDLENDKQQLDERLKKKDFELNALNARIEDEQALGSQLQKKLKELQARIE 1116
-ò-	864	RLEKKVEEGERT 889
- 1 0-	1117	::: ELEBEL-ESERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQIEMNKKREAEFOKMR 1175
_ŏ.	890	VRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKME 933
-T	1176	:
-o-	934	ATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKI 993
- 0 -	232	TSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAEETQRSVNDL 1273
_ð-	994	LPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGV 1050
-g-	1274	TSQRAKLQTENGELSRQLDEKEALISQLTRGKLTYTQQLEDLKRQLEEEVKAK 1326
_ o _	1051	LACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLOTCNNRPDETECO 1110
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QQ	:	AVE 1405
Qγ	Qy 1171 GLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYN	LYN 1230
QQ	1406 AVNAKCSSLEKTKHRLQNEIEDLMVDVERSNAAAAALDKKQ	-RN 1448
QQ Dp	OY 1231 HDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVYYTRSSYLPNSIIPE	IPE 1290 EES 1491
Οŷ	1291	
QQ	1492 LEHLETFKRENKNLQEEISDLTEQLGSSGKTIHELEKVRKQLEA	
Qy	QY 1345 EKEVEKVGRTEMTLEQRLAEGFRELKOBENFYRELS	1381 :NEA 1611
ò	1382	
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RESU	RESULT 14	
nucl N;Al	0.7.7.0 nuclear migration protein NUM1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YD8358.06; protein YDR150w	
C; Sp C; Da	r-1996 #text_change 21	-Jul-2000
R; Mu	C. Murphy, L., Richards, C., Harris, D. submitted to the EMRI, Data Library, July 1995	
A; Re A; Ac		
A; MC	000000000000000000000000000000000000000	150cc
A; EX	; FID:gaysys; MIFS:	
R;KC Mol.	; Zimmermann, F.K.;	Xo,
A; Ti A; Re A; Ac	A;Title: Nuclear migration in Saccharomyces cerevisiae is controlled A;Reference number: S19052; MUID:92079907 A;Accession: S19052	ed by the highly re
A; Mc A; Re	A; Molecule type: DNA A; Residues: 1-1559, 'V', 1571-1821, 'K', 1823-1959, 'RHL', 1963-1970, 'RN', 1973-	,1973-2048,'N',205
A;Cr C;Ge	EMBL:X61236; NID:g4071; PIDN:CAA43554.1;	072
A; Ge A; Cr A; Ma	A;Gene: SGD:NUM1 A;Cross-references: SGD:S0002557; MIPS:YDR150w A;Map position: 4R	
Ma	Query Match 1.9%; Score 146; DB 2; Length 2/48; Best Local Similarity 17.9%; Pred. No. 4.7; Matches 283; Conservative 232; Mismatches 581; Indels 486;	Gaps 72;
QY	62 SSFSDSSHCKDKSQI	/LVC 115
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QY	QY 116 TFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDET	DET 169
Dp	Db 801 LAYLVEHAKATDHHLLSDSAYEELVKCKENPDMEFLKEKSÄKLGHTVVSNEAYSEL	SEL 856
δŏ	QY 170 ECQIKCGDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNAV	NAV 215
qq	Db 857 EKKLEQPSLAYLVEHAKATDHHLLSDSAYEDLVKCKENSDV-EF	668
Qλ	QY 216 VQNFNMKDFSGKWYITSGLNPTFDAFDCOLHEFHMENDKLVGNLTWRKTLDGGFFTRSA	RSA 275
qq	900EK	3DSA 948

δλ	276	VQTFVQ :	
QΩ	949		
žo ž	325	RNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDF	
à	364		
QQ	1063	::: ::	
Οy	409		
QQ	1123		
δy	464	GRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVAK 518	
QQ	1179	KLEQ	
οy	519		
QQ	1218	EFLKEKSAKLG	
δy	565		
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δy	618	LKECRLE-LAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFN 670	
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δy	671		
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οy	724	DCQLHEFHTEENKLYGNLSWRIRTPDGGFF	
g	1436	DVEL	
δy	774		
ДQ	1483		
οy	799	YIFVYYKGRNDAWDGYGGSVLY	
qq	1543		
οy	856	RTIIKEVEEIEEEVEKVRDKEVTLFSKLF	
qq	1577		
δý	912	-EENFLRELSKEEMDYLDGLKWEATEVEKLFGRALPIR 948	
QQ	1617	LEKPIVDNASKNDVLNLCSKFSLVPLSTEEYDNMRKEHTKILNILGDPSIDFLKEKCEKY 1676	
δÿ	949	KLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD 1001	
q	1677	QMLIISKHDYEEKQEAIENPGYEFILEKASALGYELVSEVELDRMKQMIDSPD 1729	
οy	1002	LRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELT	
q	1730	-II-	
δy	1062	DAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCG 1114	
g	1771	GMNKILVDQIEYDETIRKCNHPTRMELEESCH 1802	
λά	1115	13	
q	1803	HLNLVLLDQNEYSTLREPLENRNVEDLINTLSKLNYIAIPNTIYQDLIGKYEN 1855	
λα	1174	PTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLY 1229	

381	862	433	922	472	616	520	1038	559	1096	607	1152	999	1212	703	1271	738	1331	758	1390	802			
INISKDAPVPRLYDNWCGHNWGDIYHDNKVTWLAYYKDSINDQIKYTFLS	RNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLV		ERLEKKVEEGERTIIKEVEEIEEEVKVRDKEVTLFSKLFGFKELQRDEENFLRELSKE		EMDVLDGLKMEATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLG		ITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNE-LKE		LTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC	560 IMPTLSAKVFRTYNASITLDQQLKRIKEVYGKTTYSLYSG-ETELHKSK	1097 LQTCNNRPDETECQIKCGDLFENSVVDEFNECANSRKKCVPRKSDLGEFPAPDPSV	KRKSSHLTSDINILSDASDSTINDVNNEYDENGINKKLSYATTVGKENDVDDKNSP-IEV	LVQNENISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTR		SAVQKFVQDPNQPGVLYNHD-NEYLHYQDDMYILSSKIENKPEDYIFVYYRGRNDAWDGY				2 IIVKEVEEIBEEVEKEVEKVGRTEMTLFORLAEGFNELKODEENFVRELSKEEMEFLDE-		IKMEASEVEKLFGKALPIR 1409		
332	807	382	863	434	923	473	980	521	1039	260	1097	309	1153	667	1213	704	1272	739	1332	759	1391	803	
qq	٥y	QQ	οy	요	οy	g	δy	q	οy	q	δy	QQ	δλ	qq	οy	qq	Οy	qq	Οy	QQ	٥y	g	
_	•	_	_	_	_	_	•	_	_		-												

Search completed: November 6, 2001, 05:03:40 Job time: 6764 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

November 6, 2001, 05:15:07; Search time 67.97 Seconds (without alignments) 711.619 Million cell updates/sec Run on:

US-09-075-375A-6 7495 1 MALSLHTVFLCKEEALNLYA......MEASEVEKLFGKALPIRKVR 1412

Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 Total number of hits satisfying chosen parameters:

93435 seqs, 34255486 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_39:* Database :

	Description	0411 schi	Q00798 plasmodium	Q01056 herpesvirus		P12883 homo sapien		P02564 rattus norv	Q12176 saccharomyc						-	P15917 bacillus an			_	Q13439 homo sapien		Q39565 chlamydomon	lactococ	Q01550 xenopus lae		P29149 grapevine f	P57235 buchnera ap	067606 aquifex aeo	P11531 mus musculu	Q58445 methanococc	Q58357 methanococc	Q28178 bos taurus	03640 sacch	P53804 homo sapien
SUMMARIES	OI.	YD86_SCHPO	RBP1_PLAVB	TEGU_HSVSA	MYSB_PIG	MYSB_HUMAN	NUM1_YEAST	MYSB_RAT	MK21_YEAST	MLP1_YEAST	DMD_CHICK	MYSP_HUMAN	MSP1_PLAFK	MSP1_PLAFW	MYSB_MESAU	LEF_BACAN	YIO9_YEAST	HMW2_MYCGE	YM68_CAEEL	GOG4_HUMAN	USO1_YEAST	DYHB_CHLRE	NISB_LACLA	TANA_XENLA	HIS2_CANAL	POL1_GFLV	SYGB_BUCAI	METE_AQUAE	DMD_MOUSE	RPA1_METJA	SYI_METJA	TSP1_BOVIN	YMH2_YEAST	TTC3_HUMAN
	DB	1	ч	-	-	Н	Н	-	Н			Н	П	~	Н	Н	Н	Н	Н	Н	Н	-		Н	-	-	Н	-	Н	-	-	-	٦.	-
	Length	1957	2869	2469	1935	1935	2748	1935	1025	1875	3660	1937	1630	1639	93	809	1679	1805	1822	2230	1790	4568	993	1744	838	2284	069	761	3678	34	03	17	1545	2025
ď	Query Match	7							1.9				1.8			1.8					1.7			٠.	1.7								1.6	1.6
	Score		155.5	155	148.5	146	143	142.5	139.5	137.5	135	134.5	134	134	133.5	132	130	129.5	129	128	127.5	126.5	126	126	125.5	124	123.5	123.5	\sim	122.5	121.5		121.5	121
	Result No.		7	m	4	5	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33

34 120.5 1.6 2418 1 SPCA_HUMAN 35 120 1.6 610 1 CALG_HUMAN 37 120 1.6 1132 1 TRFT_CORYTR 39 120 1.6 4725 1 DYHC_DICDI 39 119 1.6 709 1 TOPI_WYCGE 40 119 1.6 967 1 SYL_PYRHO 42 119 1.6 1102 1 WYGAST 43 119 1.6 2411 1 WYSA_DROME 44 118 1.6 2663 1 CENE_HUMAN 45 117.5 1.6 887 1 PIFI_YEAST		076332 oxytricha t P41004 schizosacch				QU306U saccharomyc P05661 drosophila		P07271 saccharomyc
	SPCA_HUMAN	TERT_OXYTR CUT3_SCHPO	DYHC_DICDI	TOFI_MICGE ARP8_YEAST	SYL_PYRHO	YM66_YEAST MYSA_DROME	CENE_HUMAN	PIF1_YEAST
	п п	н н	Η,		Н,			1
	2418 610	1132	4725	881	967	2411	2663	857
34 120.5 35 120 37 120 37 120 39 119 40 119 42 119 44 118 45 117.5	1.6	1.6	1.6	9.1	1.6	1.6	1.6	1.6
00000004444444000000000000000000000000	120.5	120	120	119	119	119	118	117.5
	34	36	38	40	41	4 4 2 3 8	44	45

ALIGNMENTS

7 09:24:06 2001

Wed Nov

Οy	337	IYTRSPTLPESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIK 396	
qq	545	ISNSEHLSSQLSTLAAEKEAAVATNNELSESKNSLQT 581	
γο 42	397	BAVEIEBEVEKEVEKVRDTEMTLFORLLEGFKELQODEBNFVRELSKEEKEILN 450 : ::: :::	
67	451		
ф	641		
δy 6	496	VVAKICSSRRIPRYFRKSP	
3 8	0 1	EU LEANNERS LUNENGUE	
g S	553	NLSPAHSINONVPKGNSGCKFPKDVALMVWFKWGQFAKTAIVAIFILSVA 602	
کم ہو	603	SKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIK 656	
3		MASKINI PRESESALA	
Oy Dp	657	CGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDP 694 [: : :	
Qγ	695	SVLVQKEDM-KDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIR 746	
qq	882	QILTQLAELSKNYDSLEQESAQLNSGLKSLEAEKQLLHTENEELHIRLDKLTGKLK 937	
δλ	747	DGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKG	
g	938	IEESKSSDLGKKLTARQEEISNLKEENMSQSQAITSVKS 976	
OY Db	807	RNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLE 866 :	
ΟŸ	867	KKVE-EGERTIIKEVEELEEEVEKVRDKEVTLFSKLFEGFKELQRD 911	
Dp	1018		
δ δ	912	MAVATHC	
2	7/07	NINGENTIERNVQKELDEKDQRNVELEELTSKYGKLGEENAQIKDELEALRKK 1124	
Qy Db	958	FTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD 1001 :	
δλ	1002	LRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLACAFLIVPSA 1061	
οp	1184	MKKSLSDSDNVISVIRSDLVRVN 1206	
Qy	1062	DAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSV 1121 :	
qq	1207	DELDTLK 1240	
οy	1122	כז	
qq	1241	EESFNKYAVSLRELCTKSEIDVPVSEILDDNFVFNAGNFSELSRLTVLSLENYLD 1295	
Qy	1178	AFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLH 1237	
ò	1238	GGAVVYTRSSVLPNSIIPEL	
- q	1331		

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                                    1349 SEKNF-----LRKEAEMTENIH-SLEEGKEETKKEIAELSSRLEDNQLATNKLKNQ 1398
                                                                            1346 ----KEV---EKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFL--DEIKMEA 1395
                                                                                              Cell 69:1213-1226(1992).
-!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1150 TSNKNEILKSVKEVEDKLNLVEQNEDYKKVKNPENEKQLEAIRGSMSKLKE------ 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1201 -----VINKHVSEMTQLESTANTLK-----SNAKGKENEHDLEELN----KTK 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 IVLVCTFVIVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 TSYKTSSFSDSSHCKDKSQICSIDTSFEEI-----QRFDLKRGMTLILEKQWRQFIQLA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 155.5; DB 1; Length 2869;
Best Local Similarity 17.4%; Pred. No. 0.86;
Matches 283; Conservative 242; Mismatches 573; Indels 529; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 CQIKCGDLFE--NSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRNA---VVQNFNM-KDF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL ATTACHMENT SITE (POTENTIAL). CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
RETICULOCYTE BINDING PROTEIN 1.
1298 IGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.; "A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B9DBE442205EBCFF CRC64;
                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                           2869 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBUNIT: HOMODIMER (POTENTIAL).
-1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malaria; Receptor; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                            RETICULOCYTE BINDING PROTEIN 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-92315338; Pubmed-1617731;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium vivax (strain Belem).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252, 253 CELI
1030 1032 CELI
2599 2601 CELI
2869 AA; 330213 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M88097; AAA29743.1; -. HSSP; P36956; 1AM9.
                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2807
2826
2869
1032
2601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2869
                                                                                                                                                        1396 SEVEKL 1401
                                                                                                                                                                                             1457 SLMEKI 1462
                                                                                                                                                                                                                                                                                           RBP1_PLAVB
Q00798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                        RESULT 2
RBP1_PLAVB
                                                                            ă
                                                                                                                g
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λ	225	WYITSGLNPTFDAFDCOLHEF HMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQD	282
ą	1297		1340
λχ	283	DWYILSSQIENKPDDYIFVYYRGRN-DAWDGYGGSVIYTRS	341
ą	1341		1368
λζ	342		372
ą	1369	SAIQGNAGISKELNELKGVIELLISTNYSSILEYVKKNSSESVRFSQL	1428
λζ	373		415
ą	1429	ANGEFTKAEGEEKNASARLAEAEKLKEQIVKDLDYSDIDDKVKKIEGIKREILKMKES	1486
λζ	416	EMTLFQRLLEGFKELQQDEENFVRELSKEEKEILNELQME	455
q	1487	FWEE-SEKFKQMCSSHMENAKEGKKKIEYLKNNGDGGKANITDSQMEEVGNYVSKAE	1545
λά	456	SNFLANHETIKYY	492
q	1546		1598
ρλ	493	KLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKH	552
q	1599	SAKLKRESSQLNDVSTK SAKLEKKESSQLNDVSTK	1643
λά	553	NLSPAHSINQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALK	612
- q	1644	DSADKSMKSVLPISELGAEKSLDKVK	1699
δý	613	TCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQ-IKCGDLFENSVVDEF	699
q	1700	AAKESYEKNLETVQNEMSRINVEEGSLTDIDKKITDIENDLLKMKKQYEEGLLQKI	1755
λα	670	KWFITRGLNPTFDAFDCQLH	728
q	1756	KENADKRKSNFELVGSEINALLDPSTSIFI-KLKLKEYDMTGDLKNYGVKMN	1806
Σγ	729		760
ф	1807	EIHGEFTKSYNLIETHLSNATDYSVTFEKAQSLRELAEKEEEHLRRREEEAIFLLNDIKK	1866
οy	761	FVQDPKYPGILYNHDNEYLLYQDDWYILS	789
q	1867	VESLKLLKEMMKKVSAEYEGMKRDHTSVSQLVQDMKTIVDELKTLNDISECSSVLNNVVS	1926
δý	790	SKVENSPE-DYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFN	846
Dp	1927	IVKKVKESKHADYRRDANSMYESMVTLANYFLSDEAKISSGREFN	1971
οy	847	TFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEV	880
Dp	1972	A SEMKSNFYTDLELEIFSVISNSNELLKKIEQDSNDVIQKERESEQLAKDATDIYNVIKLK	2031
δλ	881	EEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEA	934
Db	2032	NEFNEKLEEBAKNKEEVVSEKVREALKRLSQVEGIRCHFENFHRLLDNTE	2080
οy	935	TEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKIL	994
qq	2081	- ELENLKKMVTIYRDKKSERESGLQEMENEMN-TYSNSI-	2117
δÿ	995	PPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGV	1050
QQ	2118	TQLEGIVVSAGESKEDIEKLERSNEEMRNISEKISTIDSK	2157
οy	1051	LACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQ	1110
QQ	2158	VIEMNSTIDELXKCKNCQAHWISLISYTANMKTSKKLIMINKEKENTE	2206

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                    2207 -KCVDYIKDNSSSTDGYVETL------KGFYGSKLIFSSASEIVQNADIYSVNFAKH 2256
                                                                                                                                                    2293 LYDKLNEEKREMDELYRNISETKLKQMEHSTDVFKPMIELHKGMNETNNKSLLEKEKKLK 2352
                                                                                                                                                                                                                                                                                                                   1354 TE------EFLDE 1390
                                                                                                                                                                                                                                                                                                                                       EKESLNAIRD-IKKELYLFHQNSDISIV-------EGGVQNML-----A 2292
                                                                                                                                                                                                                       2353 SVNDHMHSMEAEMIKNGLKYTPESVQNINNIYSVIEAEVKTLEEIDRDYGDNYQIVEEHK 2412
                                                                                                                                                                                                                                                       --FSTFIRTDNTCGPEPALVERIEKTVEEGE----RIIVKEVEEIEEEVEKEVEKV--GR 1353
                                                                                                                                                                                                                                                                                       2413 KQFSILIDRIN-----ALMDDIEIFKKENNYNLMEVNTETIHRVNDYIEKITNKLVQAK 2466
1111 IKCGDLFE--NSVVDEFNECAVSRKKCVPRKSDLG-EFPAPDPSVLVQNFNISDFNGKWY 1167
                                                             1168 ITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGV 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-9233688; PubMed-1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYNHDNEYLHYQDDWYILSSKIENKPEDY-----IFVYYRGRNDA----
                                                                                                                                                                                         -----WDGYGGAVVYTRSSV--LPN--SIIPELEKAAKSIGRD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure of the herpesvirus saimiri genome."; J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
PROBABLE LARGE TEGUMENT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 2469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X64346; CAA45687.1; -. EMBL; M86409; AAA46140.1; -. PIR; H36812; H36812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    2527 IKRNVTE 2533
                                                                                                                                                                                                                                                                                                                                                                                    1391 IKMEASE 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 OR EERF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEGU_HSVSA
Q01056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
TEGU_HSVSA
                                                                                               2257
                                                                                                                               1228
                                                                                                                                                                                                                                                          1302
                                                                                                                                                                                            1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                    δ
                               Db
                                                               Óγ
                                                                                           qq
                                                                                                                             Qγ
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                                                                                                                                                                                           Ω
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atch 230; Conservativ 230; Conservativ ETRSAVQTEVODPDLPGP : : : : : :	Db 984		Oy 1207 Db 1083	Qy 1262 Db 1125	Oy 1297 Db 1185	Oy 1338 Db 1245	Qy 1389 Db 1305	RESULT 4 MYSB_PIG ID MYSB_P		DE MYOSIN GN MYH7. OS SUS SC OC EUKARY		RC STRAIN RA KO Y.L RL Submit CC -!- FU		CY -1- DO CY CY CY CY CY CY CY CH	CC -1- MI CC -1- MI CC ME CC SP	CC -1 - MI CC -1 - MI CC -1 - SI	CC This Si CC This Si CC between	CC use by CC modification CC entition CC entition CC or sen	
SEQUENCE 2469 AA, 280165 WM, DZBABBDCO8644CDB CRC64; OURSTY MAACH BORL LOCAL SIMILATITY 17.3%; Pred. No. 0.75; DB 1; Length 2469; BORT LOCAL SIMILATITY 17.3%; Pred. No. 0.75; DB 1; Length 2469; BORT LOCAL SIMILATITY 17.3%; Pred. No. 0.75; DB 1; Length 2469; BORT LOCAL SIMILATITY 17.3%; Pred. No. 0.75; DB 1; Length 2469; 271 FTRSAVQTRYODDLOBALNHUNETHADDMYTISSOIEMENDDYIVATRY. 178 FSTSWINDALIENISPHONOTT-GSEVEYPRETISHSHENDORNENETHERSENISHS. 229 HOLD SOBSITERISHSHENDERFORMENTER PREMERSENISHSHENDORNENETHERSENISHS. 229 HOLD SOBSITERISHSHENDERFORMENTER PREMERSENISHSHENDORNENETHERSENISHSHENDORN			m &	L 8	o o m	0 0 0			2	4	0.0	0.10	10 01				ري د	9	
Match S 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. 2469 AA; 280165 MW;	2.1%; Score 155; DB 1; Length 2469; Similarity 17.3%; Pred. No. 0.75; 0; Conservative 208; Mismatches 497; Indels 396;	FTRSAVQTFVQDPDLPGALXNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYR	-GRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDFNNFI 			FGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDYFGSIVVA : : : : : : : : : : :	-KICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKG	NSGCKFPKDVALAVWEKWGGFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAK	CISNPACAANVACLQTCNNRPDETECQIKGGDLFENSVVDEFNECAVSRKKCVPRKSDVG ::	DFPVPDPSVLVQKFDM	DAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPG :	ILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVL	PESIIPELQTRAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTI-IKEVEE : :	IEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFG 	RALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQ	S-ADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLLL	KLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC ::: :: :: ::	
		Ouery Best 1 Matche								54	57	72	77	92	88	94	99	104	

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                                                                                                                                                                        PSRDVKTFIQNAPSMKAKQYAKKALKDQIQAMEIDVDPESVIEDNIKANGQKAWQ---- 1082
                                                                                    PSVLVQNF--NISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDN-KLVGNISWRIKTLD 1206
                                                                                                                                                                                                                                                                                                            --TAVDRPLKRELYNVIRKLQKQLKTLLEQQEFDNW-------KMEVDSF-VPT 1027
                                                                                                                                                                                                                                                   SGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIF-----VYY 1261
                                                                                                                                                                                                                                                                                                                                                                                                                           RGRNDAWDGYGGAVVYTRSSVLPNSII-----------PELEKAAK 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGRDFSTFIRTDNT-CGPEPALVERIE-----KTVE-----EGERIIVKEV 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEIEEEVEK----EVEKVGR----TEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFL 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   itted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
CINCTION: MUSCLE CONTRACTION.
SUBBUIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBBUITS (HLC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
OWARIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
SYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEFILDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFVEEVLESVKNLKEAKLKSLLPNGPVFTPPKFDWIHYYESNVNFHLKTINLPKVSTVAH 1184
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LIKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
LISCELLANDROUS: BACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
BROWYCSIN (LAM) AND I HEAVY BEROMYOSIN (HAM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND I ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
lia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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VICTURE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE IYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.

HOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.

HILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5C-1998 (Rel. 37, Created)
5C-1998 (Rel. 37, Last sequence update)
5C-1998 (Rel. 37, Last annotation update)
IN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1935 AA.
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                                                                                                                                                                                                                                                                                                                                                                                       217 ONFNMKDFSGKWYITSGLNPT-------FDAFDCQLHE---FHMENDKL 255
                                                                                                                                                                                                                                                                                                                                                                                                                429 KAVYEKMEN--WMVTR-INTTLETKQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 QDPDLPGALY-NHDNEFLHYQDDWYILSSQIENKPD-DYIFVYYRGRND----AWDGYGG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVIYTRSPTLPESIIPNLQKAA-KSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKL 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 NLSPAHS---INQNVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVD 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610 ALKTCTCLLKEC-----RLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFE 662
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                                                                                     Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Multigene family.

DOMAIN

GLOBULAR HFAD (S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                        -------VGNLTWRIKTLDGGFFTRSAVQTF------------V
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                                                                                                                             RODLIKE TAIL (S2 AND LMM DOMAINS)
                                                                                                                                                                                                                                                                                   Length 1935;
                                                                                                                                                                                          ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
MM: 149CDBFD910DBB08 CRC64;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                       166 PDETECQIKCGDLFENSWVDQFNECAVSRKKCVPRKSDVGEFPVPDRN-
                                                                                                                                          IQ.
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                   Query Match 2.0%; Score 148.5; DB 1; Best Local Similarity 16.7%; Pred. No. 1.3; Matches 248; Conservative 220; Mismatches 555;
                                                                                                                                                                  ATP (POTENTIAL).
ACTIN-BINDING.
                                    Pfam; PF01576; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
                                                            PRINTS; PR00193; MYOSINHEAVY.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                             223110
InterPro; IPR001609; -. InterPro; IPR002928; -.
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185
                         Pfam; PF00612; IQ; 1.
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1043 KVRMDLERAKRKLEGDLKLTQESIMDLENDKQQLDERLKKKDFELNALNARIEDEQALGS 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1265 ETQRSVNDL-----TSQRAKLQTENGELSRQLDEKEALISQLTRG-----KLTYTQQL 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1037 KELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC 1096
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                                                                         994 KEKKALQEAHQQALDDLQAEEDKVNTLTKAKVKLEQHV------DDLAGSLEQEK 1042
                                                                                                                                                                                                                                                                                                                                                             : :|:||| | :|:
1103 QLQKKLKELQARIEELEEEL-EAERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQI 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1222 SEFKLELDD----VTSNMEQIIKAKANLEKM-----CRT--LEDQMNEHRS----KAE 1264
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MEDLINE=91065634; PubMed=2249844;
Jaenicke T., Diederich K.W., Hass W., Schleich J., Lichter P.,
Jaenicke T., Vosberg H.P.;
"The complete sequence of the human beta-myosin heavy chain gene and
                                                                                                                                                                                                                                                                                                                858 E-----PPLVERLEKKVEEGERT-----IIKEVEEIEEEVEK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           890 ------REDESTEEPENFLER
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                          ---VLPESIIPELQTAAQKVG-----RDF----NTFIKTDNTCGP
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01-CCT-1989 (Rel. 12, Created)
01-UN-1994 (Rel. 29, Last sequence update)
01-GCT-2000 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.
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MYSB_HUMAN
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VARIANT CMH1 GLN-403.
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MEDLINE-92346810; PubMed=1638703;
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MEDLINE=90367131; PubMed=1975517;
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MEDLINE=94093568; Pubmed=8268932;
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IR-------AFMGVKNW-PWMKLYFKIKPLLKSAEREKEMASMKEEFTRLKEALE 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.9%; Score 146; DB 1; Length 1935; Best Local Similarity 16.9%; Pred. No. 1.8; Matches 238; Conservative 207; Mismatches 529; Indels 434;
                                                                                                           VARIANTS CMH1 CYS-513; ARG-716, AND TRP-719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [25]
VARIANTS CMH1 THR-349 AND TRP-719.
MEDLINE=95179132; PubMed=7874131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hum. Genet. 97:585-590(1996)
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----RLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSV-----VDEFNE 671
                                                                                                                                                                              --CAVSRK----KCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGL
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(Rel. 24, Last sequence update)
(Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: ADDITIONAL REGIONS OF LOWER HOMOLOGY TO THE REPEAT CONSENSUS (ALWAYS STARTING WITH PROLINE) ARE FOUND IN BOTH FLANKING DOMAINS OF THE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 SSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQF-----IQLAIVLVC 115
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                                                                                                                                                                                                     FUNCTION: CONTROLS NUCLEAR MIGRATION, NUMI SPECIFICALLY CONTROLS THE INTERACTION OF THE BUD NECK CYTOSKELETON WITH THE PRE-DIVISIONAL G2 NUCLEUS PERHAPS BY RECOGNIZING G2-SPECIFIC
                                                                                                                                                            "Nuclear migration in Saccharomyces cerevisiae is controlled by the highly repetitive 313 KDa NUML protein."; Mol. Gen. Genet. 230:277-287(1991).
-1- FUNCTION: CONTROLS NUCLEAR MIGRATION. NUML SPECIFICALLY CONTROLS
                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                               CYTOPLASMIC MICROTUBULI OR OTHER COMPONENTS OF THE NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9%; Score 143; DB 1; Length 2748; 17.9%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                             CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
                                                                                                    STRAIN-ATCC 28383 / FL100;
MEDLINE-92079907; PubMed-1745235;
Kormanec J., Schaäff-Gerstenschlaeger I., Zimmermann F.K.,
Perecko D., Kuentzel H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; B2FBD67C9F6211AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.5 X TANDEM REPEATS.
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PROSITE; PS50003; PH_DOMAIN; 1.
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NUCLEAR MIGRATION PROTEIN NUM1
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2748 AA;
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SGD; $0002557; NUM1
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Matches 283; Conserv
                                                                                            SEQUENCE FROM N.A.
             NUM1 OR YDR150W.
                                                                    NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 RND---AWDGYGGSV-----IYTRSPTLPESIIPN-----LQKAAKSVGRDF--- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NNFITTDNS-----CGPEPPLVERLEKTAEEGEKLLIKEAV-EIEEEVEKE--- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --VEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILNE--LQMEA-TEVEKLF 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    565 PKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKAD-----AVDALKTCTCL 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799 YIFV---YYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTC 855
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857 EKKLEOPSLAYLVEHAKATDHHLLSDSAYEDLVKC-----KENSDV-EF----- 899
                                                                                                          216 VONFNMKDFSGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSA 275
                                                                                                                                                                                                         ----LKEKSAKLGHTVVSNEAYSELEKKLEQ-----PSLAYLVEHAKATDHHLLSDSA 948
                                                                                                                                                                                                                                                                                                                         276 VQTFVQDPDLPGALYNHDNEFLHYQ------DDWYILSSQIENKPDDYIFVYYRG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ICSSRRIPRYFRKSPRICCGLDSRGL-QLFSHGKHNLSPAHSINQNV 564
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DLFENSVVDEFNECAVSRKKCVPRK-SDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLN 1173
                                                                                                                                                                                                         -----NHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDG 1270
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Mahdavi V., Periasamy M., Nadal-Ginard B.;
"Molecular characterization of two myosin heavy chain genes expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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MCNBALD E.W., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
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Comparisons suggest a molecular basis for functional differences.",
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-!- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROFIEIN THAT CONSISTS OF 2
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                                 Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
"Complete nucleotide sequence of full length cDNA for rat beta
                                                                                                                                          PTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLY
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15-DEC-1998 (Rel. 37, Last annotation update)
WYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM,
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MEDLINE-85179510; PubMed-6241892;
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01-OCT-1989 (Rel. 12, Last sequ
15-DEC-1998 (Rel. 37, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-:- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

-:- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEFTIDES,

-:- PIN: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-:- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO I LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 PDETECQIKCGDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRN-----AVV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 QNFNMKDFSGKWYITSGLNPT------FOAFDCQLHE---FHMENDKL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE RAT, TWO OF WHICH ARE SPECIFIC FOR ADULT CARDIAC MYOSIN HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 PDGTE-----EADKSAYLMGLNSADLLKGLCHPRVKVGNEYVTKGQNVQQVAYAIGALA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459; Gaps
                                                                                                                                                                                                                          MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE. MISCELLANEOUS: THERE ARE 10 OR MORE MYOSIN HEAVY CHAIN GENES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Multigene family.
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ACTIN-BINDING.
METHYLATION (FRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
IRK -> VRR (IN REF. 3).
D -> H (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
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Pfam; PF00063; myosin_head; 1.
PRIWTS; PR00193; MYOSINHEAVY.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X15939; CAA34065.1; -.
EMBL; J00752; AAA41654.1; -.
EMBL; M32698; AAA41659.1; -.
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PIR; A02989; A02989.
HSSP; P08799; IMND.
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ζ	256	VGNLTWRIKTLDGGFFTRSAVQ-TFVQ	
q	486	: : :: ::	
Δ	283	PDLPGALY-NHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAMDGYGGSVI	
ą	546	MTFKAKLYDNHLGKSNNFQKPRNIKGKQEAHFSLIHYAGTVDYNILGWL	
<u>λ</u>	338	YTRSPTLPESIIPNLQKAA-KSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIK	
ð	595	QKNKDPLNETVVGLYQKSSLKLLSNLFANY AGADAP - VDKGKGKAKKGSSFQTV	
ž q	397	EAVEIEEEVEKEVEKVRDTEMTLFQRLIEGFKELQQDEENFVRELSKEEKE 447	
	448	TINETOMEAR - PVEKT ECDALD TDKI DMALADHSHETANDI ANURTHAND CVVC	
ъ д	689	THE TRANSPORT OF THE STATE OF THE TRANSPORT OF T	
λ	496	KLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLS 555	
ą	749	LDIDHNOYKFGHTKVFFKAGLLGLLEEMRDERLSRITTRIQAQSRGVLSRMEFKKLLE 806	
λ	556	PAHSINQNVPKGNSGCKFPKDVALMVWEKNGQFAKTAIVAIFILSVASKADAV 608	
ð	807	RRDSLLIIQWNIRAFMGVKNWPWMKLYFKIKPLLKSAETEKEWANMKE 854	
λ	609	DALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLF	
ą	855	EFGRVKDALEKSEARRKELEEKMVSLLQEKNDLQLQVQAEQDNLADAEERCDQLIK 910	
Ϋ́	663	NSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFD	
ð	911	NKIQLEAKVKEMTERLEDEEEEMNAELTAKKRKLEDECSELKRDIDDLELTLAKVEKEK 968	
<u> </u>	703	MKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFV	
ā	969	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
Σ	763	QDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTR 822	
۵	823	SANTFIKTDNTCGP 857	
, <u>a</u>	1043		
Δį	858		
ą	1103	:	
λi	890	VRDKEVTLFS	
ą	1162	EMNKKREAEFQKWRRDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLEKEK 1221	
Δī	920	SKEEMDVLDGLK	
q	1222	SEFKLELDDVTSNMEQIIKAKANLEK	
Σ.	980	ITRKRINGTFLLKIL	
ð	1265	ETORSVNDLTRQRAKLQTENGELSRQLDEKEALISQLTRGKLTYTQQL 1312	
<u> </u>	1037	KELTAPLLLKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVAC ::	
ð	1313	EDLKRQLEEEVKAKNALAHALQSARHDCDLLREQYEEETEAKAELQRVLSKANSEVAQ 1370	
٠.	1097	LQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQN	
ð	1371	WRT	

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                                                                                   1217 KEVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVV 1276
                                                                                                                                                                   1277 YTRSSVLPNSIIPELE-----KAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGE 1330
1157 FNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQ 1216
                                           --VERSNAA 1438
                                                                                                                                                                                                         1478 STELFKLKNAYEESLEHLETFKRENKNLQEEISDLTEQLGSTGKSIHELEKIRKOLEAEK 1537
                                                                                                                                                                                                                                                                            1538 LELQSALEEAEASLEHEBGKILRAQLEFNQIKAEIERKLABKDEBMEQAKRNHLRVVDSL 1597
                                                                                                                          1439 AAALDKKQ----RNFDKILVEWKOKYEESQSELESSQKE-----ARSL 1477
                                                                                                                                                                                                                                                  1331 RIIVKEVEEIEEEVEKEVEKUGRTEMTLFQ------RLAEGFNELKQDEENFVRELS-- 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edskes H.K., Ohtake Y., Wickner R.B.;
"MakZip of Saccharonyess cerevisiae, a homolog of human CAATT-binding
protein, is essential for 60 S ribosomal subunit biogenesis.";
J. Biol. Chem. 273:28912-28920(1998).
-- FUNCTION: REQUIRED FOR 60S RIBOSOMAL SUBUNIT SYNTHESIS.
-- FUNCTION: MOCLEAR: NUCLEAR: NUCLEAR: NUCLEAR: LOCATION: NUCLEAR: NUCLEAR: NUCLEAR: SIMILARITY: BELONGS TO THE CBF / MAK21 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96381250; PubMed=8789263;
Brandt P., RamLow S., Otto B., Bloecker H.,;
"Nuclectide sequence analysis of a 32,500 bp region of the right arm of Saccharomyces cerevisiae chromosome IV.";
Yeast 12:85-90(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                             |:::| |:::: | :::| 1598 QISLDAETRSRNEALRVKKKKMEGDLNEMEIQLSHANRMAAEA 1639
                                                                                                                                                                                                                                                                                                                                   ----KEEME-FLDEIKMEASEVEKLFGKA 1405
                                         --AVEAVNAKCSSLEKTKHRLQNEIEDLMVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBOSOME BIOGENESIS PROTEIN MAK21.
MAK21 OR YDRO60W OR D4237 OR YD9609.14.
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POLY-ASP.
POLY-GLU.
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MEDLINE=99003241; Pubmed=9786894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X84162; CAA58976.1; -. EEMBL; Z74356; CAA98878.1; -. EEMBL; Z49209; CAA89089.1; -. SGD; S0002467; MAK21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S228C / AB972;
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DOMAIN 74 7
DOMAIN 117 12
DOMAIN 979 98
                                           1403 -----
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Q12176;
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                                                          41;
                                                                                PESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEI - - - 401
                                                                                              ----EEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEEN-- 436
                                                                                                                                                    460 PNADYHTTYYSVITLNQTILKRSEDSVANKLVK---TYFTLFEKFL----INTDKDNTN 511
                                                                                                                                                                            -FVRELSK -- EEKEILN------ELQMEATEVE-----KLF-----GRALPIR 470
                                                                                                                                                                                                  GVVKSNSKSYEEKRKKKNFKKGKHGGKSVKIEKTENEVLDEKNSKLFSALLTGINRAFPFA 571
                                                                                                                                                                                                                        471 KLRMA------LAPHSNF-----LANHETIKYYVGSKLPGHKRFSWGWEDYF 511
                                                                                                                                                                                                                                                                       512 GSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGC 571
                                                                                                                                                                                                                                                                                                                      572 KFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISN 631
                                                                                                                                                                                                                                                                                                                                     632 PACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPV 691
                                                                                                                                                                                                                                                                                                                                                                                                                   PDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFH----TEENKLVGNLSWRIRT 747
                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PKFANAEKSSLWEINNFIN------HFHPTVKTYANAYVTGETEOIAK 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDGGFFT------HDNEYLL 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDLGLFTLSHFLDRFVYRSAKQTNTARGTSIMQPLFSGSRVNDSVLVKASDIMHD-QGPV 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781 YQDDWYILSSKVEN-SPEDYIFVYY------KGR-------NDAWDGY 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERTIIKEVEEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKM 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QES--DQEEGLDEDIFYSFDGEQDNSDKK-RSFAESSEEDESSEEEKEEEENKEVSAKRA 995
                                                           Gaps
                                                                                                                                                                                                                                             QIPASVYEVHMETLFKITHSSNFNTSIQALVLINQVTVK----AKLNSDRYYRTLYESLF
                                                                                                                                                                                                                                                                                                                                                                                       ----PQIKNLLT--NTPVDYE-----YESDAEEEQGDKDIKRKEYDGRKRD-----
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Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                          283;
                                  Length 1025;
                                                           Indels
FB80378727ED71D8 CRC64;
                                                                                                                                                                                                                                                                                               D------PRLVNSS------KOGIYL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----FASADD 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EATEVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDD 973
                                Ouery Match 1.9%; Score 139.5; DB 1; Best Local Similarity 20.9%; Pred. No. 1.8; Matches 159; Conservative 94; Mismatches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-UNN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MYOSIN-LIKE PROTEIN MLP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1875 AA
 116676 MW;
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 1025 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 IRENDKIRKERNDTFVKFESVENEKMKLSSELEFVKRKLDDLTEEKKETQSNQQRTLKIL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCQLHEFHM---END-----KLVGNLTWRIKTLDGGFFT-----RSAVQTFVQDPDLPG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :| | : | |: | |: | |: DERLKEIELVRVENNSSUSECKKIRSTIMDLETKQQGYITNDLNSRTELERKTQELTL-- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 ALYNHDNEFLHYQDDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPES 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 IIPNLOKAAKSVGRDF----NNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 VILDIRNELNRLRNDFQMERTNNDVLKQKN-----NELSKSLQ--EKLL--EIKGLS 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSLNSEKQEF-SAEMSLKQRLVDLLESQLNAVKEELNSIRELNTAKVIADDSKKQTPENE 341
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                                                                                                                                                                                                                                                                                  MEDLINE=94205265; PubMed=8154186;
Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G.,
Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.;
"The complete sequence of a 15,820 bp segment of Saccharomyces
cerevisiae chromosome XI contains the UBIZ and MPL1 genes and three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: MYOSIN-LIKE PROTEIN THAT IS PROBABLY INVOLVED IN DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 421;
                                                                                                         Koelling R., Nguyen T., Chen E.Y., Botstein D.; "A new yeast gene with a myosin-like heptad repeat structure."; Mol. Gen. Genet. 237:359-369(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 1.8%; Score 137.5; DB 1; Length 1875; al Similarity 17.5%; Pred. No. 5.1; 252; Conservative 240; Mismatches 525; Indels 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 COLLED COIL (POTENTIAL).
78 COLLED COIL (POTENTIAL).
66 COLLED COIL (POTENTIAL).
01 R -> A (IN REF. 1).
218455 MW; 683A0D34C9066867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pattern; Coiled coil; DNA repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: SOME, TO THE TPR ONCOGENE.
-i- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1".
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EMBL, X73341; CAA51948.1; -.
EMBL, Z28320, CAA82174.1; -.
EMBL, S33173, S3173.
SGD, S0001803; MLP1.
Myosin; Heptad repeat pattern;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      new open reading frames.";
Yeast 9:1349-1354(1993).
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SEQUENCE FROM
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                                         STRAIN=S288C;
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SEQUENCE
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955 THCFTSPCHDRIRFFS-----SDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTG 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1242 WYILSSKIENKPE-----DYIFVYYRGRNDAWDGYGG-----AVVYTRSSVLPNSIIP 1289
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                                                                                                                                                                                                                                                                                                                          720 TILKQDSKTHETLNEYVSCKSKLSIVETELLNIKEE------QKLRVHLEKNLKQEL 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         771 NKLSPEKDSLRIMVTQLQTLQKEREDLLEETRKSCQKKIDELEDALSELK-KET---SQK 826
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  506 GWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVP 565
                                                402 HLONQIETFIVELEHKVPIINSFKERTDMLENELNNAALLLEHTSNEKNAKVKELN--A 458
                                                                                                 459 KNQKLVECENDLQTLTKQRLDLCRQIQYLLITNSVSNDSKGPLRKEEIQ--FIQNIMQED 516
                                                                                                                                                                                               DAV----DALKTCTCLLKECR--LELAKCISNPACAANVACLQTCNNRPDETECQIKCG- 658
                                                                                                                                                                                                                                             517 DSTITESDSOKVVTERLVEFKNIIOLOE------KNAELLKVVRNLADKLESKEKKSK 568
                                                                                                                                                                                                                                                                                              659 ---DLFENSVVDEFNECAVSRKKCVPRKSDVGD------FPVPDPSVLVQKFD 702
                                                                                                                                                                                                                                                                                                                                                                                            703 MKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFV 762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 NTCGPE------PPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKL 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               933 --TSQSLQQTNSKLDESFKDFT----NQIKNLT------------------------DEKTS 964
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                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                    Lemaire C., Heilig R., Mandel J.L.; "The chicken dystrophin cDNA: striking conservation of the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                     -I- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN,
                                                                                                                                                                                                                                                                                                                                                           : I - FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                untranslated regions between man and chicken."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3660 AA; 422874 MW; 85493DAF6D5B6D4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 SPECTRIN-LIKE REPEATS
                                                                                                                                                                                                Lemaire C., Heilig R., Mandel J.L.;
"Nucleotide sequence of chicken dystrophin cDNA.";
                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIN-BINDING
                                                                                                                                                                                                                             Nucleic Acids Res. 16:11815-11815(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                ABP-120, ABP-180, OR BETA-FODRIN).
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H %
                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=89098331; PubMed=3062582;
                                                                                                                                                                                                                                                                                     MEDLINE=89210800; PubMed=3072195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01159; WW_DOMAIN_1; 1.
PROSITE; PS50020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00569; ZZ; 1.
Pfam: PF00435; spectrin; 22.
PRINTS; PR00403; WMDOMAIN.
PROSITE: PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X13369; CAA31746.1; -.
                                                                                                                                                                                                                                                                                                                             coding and 3' untranslated EMBO J. 7:4157-4162(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, 001082; 1AA2.
InterPro; IPR0010433; .
InterPro; IPR001052; .
InterPro; IPR0011589; ..
InterPro; IPR001715; .
InterPro; IPR0020171; ..
InterPro; IPR002017; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
3000
3085
3357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1171
1869
1885
         01-OCT-1989 (Rel. 12,
01-OCT-1989 (Rel. 12,
01-OCT-2000 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S02041; S02041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00307; CH; 2
Pfam; PF00397; WW; 1
                                                                                                                                                                                                                                                                                                                                                                            PLASMA MEMBRANE
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50021;
                                                                                                                                         NCBI_TaxID=9031;
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3052
3086
1171
1869
                                                                                                                                                                                                                                                                            TISSUE=Muscle;
                                                      DYSTROPHIN
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DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
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Score 135; DB 1; Length 3660; Pred. No. 17;

1.8%; 17.6%;

Query Match Best Local Similarity

STANDARD;

DMD_CHICK

RESULT 10 DMD_CHICK

17 KDKSGICSIDFSEEDGRFULKRAN-TIL-LEXCHARGE 1932 KREDIANNAROARRISCOAMAKAPETTU/LIKKNARGE-T

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GITRKRINGTFLLK------ILPPIQ-----SADLRTTGGRSSRPLSAF 1016
                                                                                RSGFS----KGIFDIVPLP---SKNELKELTAPLLLKLVGVLACAF--LIVPSAD----A 1063
                                                                                                                                                                                                                                                                                                                                                      RLFLADQPVEGLEKVYPEPRDLSPEERAQNVTKVLRRQADDVRTEWDKLNLRSADWQKKI 2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //DALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIK------1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDLFENSVVDEFNECAVSRKKCVPRK-----SDLGEFPAPDPSVLVQNFNIS---DFN 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKWYITSGLNPTFDAFDCQLHEFHTE-GDNKLVGNISWRIKTLDSGFFTRSAVQ---KFV 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|: | | | | | |||| |: |
| FRWKV---LQVAIDERIRQLHEAHRDEGPT------SQHFLTTSVQGPWERA 3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ification of three developmentally controlled isoforms of human
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NE-95324556; PubMed-7601129;
an E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S., an H.H., Rubinstein N.A.; and H.H., Rubinstein N.A.; acterization of a human perinatal myosin heavy-chain cript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 R., Leinwand L.A.;
cultar genetic characterization of a developmentally regulated
perinatal myosin heavy chain.";
11 Biol. 108:1791-1797(1989).
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Yota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
lia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The state of the s
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E=Skeletal muscle;
E=Skeletal muscle;
M=S90323631; PubMed=2373371;
N-Mizrachi I., Feghali R., Shows T.B. Jr., Leinwand L.A.;
rration of a full-length human perinatal myosin
--chain-encoding cDNA.";
89:289-294(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Q14910;
N-1990 (Rel. 13, Created)
L-1998 (Rel. 36, Last sequence update)
T-2000 (Rel. 40, Last annotation update)
N HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1937 AA
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IE-89234168; PubMed=2715179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy chains.";
Biochem. 189:55-65(1990),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICE OF 502-1937 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||: ||:
|SPNKVPYYINHETQ 3076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDPNQPGVLYNHDNE 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          =Skeletal muscle;
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          Esser K., Tidhar A., Myszkowski M.;
"Isolation and characterization of the human perinatal MHC promoter.";
submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: MUSCLE CONTRACTION.
                                                         SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES, WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE, ARE
                                                                                                                                                                                           MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                               MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50096; IQ; I. Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RODLIKE TAIL (S2 AND LAM DOMAINS) COLLED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
A -> R (IN REF. 2).
A -> R (IN REF. 1 AND 4).
M -> N (IN REF. 1 AND 4).
N -> H (IN REF. 1 AND 4).
N -> H (IN REF. 1 AND 4).
E -> G (IN REF. 1 AND 4).
E -> G (IN REF. 1 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Methylation; Alkylation; Heptad repeat pattern;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KY -> NT (IN REF. 3).
EN -> AH (IN REF. 1 AND 4).
E -> D (IN REF. 1 AND 4).
D -> H (IN REF. 2).
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14 D ->
222762 MW;
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EMBL; 238133; CAA86293.1; -.
EMBL; X51592; CAA35941.1; -.
EMBL; M35250; AAA36346.1; -.
EMBL; AF067143; AAC21557.1; -.
PIR; A30220; A30220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00612; 10; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
SEQUENCE OF 1-46 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000048; -. Interpro; IPR001609; -. Interpro; IPR002928; -.
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1072
1247
1252
1261
                                                                                                                                                                                                                     SUBFRAGMENT (S2).
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1847
1914
1937
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261
297
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 ADLLKALCYPRVK-VGNEYVTKGQTVQQVYNAVGALAKAVYEKMFLWMVTR-INQQLDTK 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------FDAFDCQLHE---FHMENDKLVGNLTWRIKTLDGGFFTRSAVQ-TF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 OPROYFIGVLDIAGFEIFDFNSLEQLCINFTNEKLOOFFNHHMFVLEQEEYKKEGIEWTF 513
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                                                                                                                                                                                                                                                                                                                                                     99 LEKQWRQFIQLA-----AVDALKTC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                282 AERSYHIEYQITSNKKPDLIEMLLITTNPYDYAFVSOGEITVPSIDDQEELMATDSAIDI 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 ACLLKECRIELAKCIANPSCAANVACLQTCNN---RPDETECQIKCGDLFENSVVDQFNE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 LGFTPEEKVSIYKLTGAVMHYGNMKFKQKQREEQAEPDGTEVADKA-----AYLQSLNS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .90 CAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGK-----WYITSGLNPT---- 237
                                                                                                                                                                                                                                                239 VRNDNSSRFGKFIRIHFGTTGKLASADIETYLLEKSRV------TFQLK----- 281
                                                597; Indels 529; Gaps
                                                                                                                                                43 IRSNN----GYFNSFRLFTSYKTSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLI 98
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Best Local Similarity 17.0%; Pred. No. 7.8; Matches 280; Conservative 243; Mismatches
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1113 ELQARIEELGEEIEAERASRAKAEKORSDLSRELEEISERLEEAGGATSAQVELNKKREA 1172	890	928 DGLÉMEATEVEKLEGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRING 987 	988 TFLLKILPPIQSADLRTTGGRSSRPLSAFRSGFSKGIFDIVPLPSKNELKELTAPLL 1044 1	1045 LKLVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRP 1104 	SDFNG 116 EAVNA 141	1165 KWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQ 1224	1225 PGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGÄVVYTRSSVLP 1284	1285 NSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEBIEEEV 1344 :	1345 EKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELS	1382KEEME-FLDEIKMEASEVEKLFGKAL 1406 :: : ::: : : :: 1615 LRVKKKMEGDLNEMEIQLNHANRLAAESL 1643	LIT 12 PLAFK WSP1_PLAFK WSP1_PLAFK WSP1_PLAFK WSP1_PLAFK WSP1_PLAFK WSP1_PLAFK WSP1_PLAFK WSP1_PLAFK WSP1_PLAFK WSP1_DLAFK WSP1_DSG (Rel. 34, Last sequence update) 01-FEB-1996 (Rel. 34, Last annotation update) WERCZOTTE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS) Plasmodium falciparum (isolate K1 / Thailand). WSP-1
1113	890 1173	928		ω «		ω n	1225	رد م <u>ا</u>	345	382	LT 1 PLARE PLARE P
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Best Local Similarity 18.0%; Pred. No. 6.7;
Matches 246; Conservative 207; Mismatches 473; Indels 444; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 VDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWYITSGLNPTFDAFDC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 QLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTF--VQDP-----DLPGALYNHDNE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499 NFEKMMGKRYSYKVEKL----THHNTFASYENSKHNL-EKLTKALKY---MEDYSLRNI 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 KITKDENKPDEKILEV----SDIVKVQVQKVLLM-----NKIDELKKTQLILKNVELKH 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 IENINELIEESKKTIDK-----INKNATKEEEKKKLYQAQYDLS-----IYNK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 IEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNID--ISAKVETKESTEPNE-Y 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNLOKAAKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLI-----KEAVEIEEE 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVEKLFGR---ALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDY-FGSI 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             550 VVEKEL-----KYYK------NLISKIENEI---ETLVENIKKDEEQLFEK 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLE- 624
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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MEROZOITE SURPACE PI
MEMBRANE ANCHOR.
N'LINKED (GLCNAC.
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1436 1436
1517 1517
1630 AA; 187289 N
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TRANSMEM
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1280 SSVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGERIIVKEVEE 1339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   992 KILPPIQSADLRTTGGRSSRP---LSAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLV 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1254 EAVTPSVI---------DN------DN-----ILSKIE---NEYEVLYLKPLAG 1282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1158 ---TGNSPS-----ENNTDVNNALE---SYK-KFLPEGTDVATVVSESGSDTLEQS 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     928 NIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRK-----K 980
637 NIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPST 696
                                                  ECQI-----KCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQ-- 699
                                                                                                       697 EGEITGQATTKPGQQAGSALEG---DSVQAQAQEQKQAQP-----PVPVPVPEAKAQVP 747
                                                                                                                                                          700 ------KFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRI 745
                                                                                                                                                                                                    748 IPPAPVNNKTENVSKLDYLE-------KLYEFL------NTSYIC 779
                                                                                                                                                                                                                                                               746 RIPDGGFFTRSAVQKFVQDPKYPGILYNHD--NEYLLYQDDWYILSSKVEN----SPED 798
                                                                                                                                                                                                                                                                                                                 780 H-----YKITKEEESKLSSCDPLD 815
                                                                                                                                                                                                                                                                                                                                                                       799 YIF-----VYYKGRNDAWDGYGGSV-----LYIRSAVL-----PESIIPELQIAAQ 839
                                                                                                                                                                                                                                                                                                                                                                                                                         816 LLFNIQNNIPVMY----SMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAK 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               840 KVGRDFNTFIKTDNTCGPEP-PLVERLEKKVEEGERT------IIKEVEEI----- 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 872 KV----STSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNK 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      884 -----EEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLK 931
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MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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1283 VYRSLKKQLE---NNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKD 1329
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-FEB-1996 (Rel. 33, Last seq
01-FEB-1996 (Rel. 33, Last anno
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70;
                                Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 1.8%; Score 134; DB 1; Length 1639;
Best Local Similarity 18.0%; Pred. No. 6.7;
Matches 246; Conservative 207; Mismatches 473; Indels 444; Gaps
                                                                                                                                                                                                                                                -!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 VDQFNECAVSRKKCVPRKSDVGEFPVPDRNAVVQNFNMKDFSGKWYITSGLNPTFDAFDC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 IENINELIEESKKTIDK-----INKNATKEEEKKKLYOAQYDLS-----IYNK 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 QLEEAH----NLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKK 346
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                                                                                                                                                                                                                                                                   KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                            Holder A.A.;
Dubitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLUIAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                   "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfan, PF00008; BGF: 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
MEROZOITE SURFACE PROTEIN 1.
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2C255B6616C87F6E CRC64;
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MEDLINE=86014355; PubMed=2995820;
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                                                                                                                         Nature 317:270-273(1985).
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                                                                       Freeman R.R.;
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                                         508 NFEKMMGKRYSYKVEKL----THHNTFASYENSKHNL-EKLTKALKY---MEDYSLRNI 558
                                                                                                                                                                                                                                                                                                                                         646 NIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPST 705
                                                                                          515 VVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHSINQNVPKGNSGC--- 571
                                                                                                                                                                                                                                              596 KITKDENKPDEKILEV----SDIVKVQVQKVLLM-----NKIDELKKTQLILKNVELKH 645
                                                                                                                                                                                                                                                                                                                                                                                                ECQI-------KCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQ-- 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEENKLVGNLSWRI 745
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458 EVEKLFGR---ALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHKRFSWGWEDY-FGSI
                                                                                                                                              559 VVEKEL-----KYYK------NLISKIENEI---ETLVENIKKDEEQLFEK
                                                                                                                                                                                             572 -----KFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=F1B; TISSUE-Liver;
MEDLINE-95115033; PubMed=7815459;
Wang R., Sole M.J., Cukerman B., Liew C.-C.;
"Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain gene from Syrian hamster.";
J. Mol. Cell. Cardiol. 26:1155-1165(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: THEK FILAMENTS OF THE MYOFIBRILS.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4, HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

MISCELLANEONS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT WHYTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Jandreski M.A., Sole M.J., Liew C.-C.; "Sequence of cDNA encoding the Syrian hamster cardiac beta-myosin heavy chain.";
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RODLIKE TAIL (S2 AND LMM DOMAINS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Methylation; Alkylation; Multigene family.
DOMAIN 1 838 GLOBULAR HEAD (S1).
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                                MYSB_MESAU STANDARD; PRT; 1934 AA. P13540; Q60540; Q60540. 13, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM
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                                                                                                                                                              Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 16:4737-4737(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 962-1935 FROM N.A. MEDLINE=88247788; Pubmed=3380703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01576; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
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PROSITE; PS50096; IQ; 1.
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HSSP; P08799; 1MND.
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                                                                                                                                                                                                                                                                                                                                                                                                                               447 ETKQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKLQQFFNHHMFVLEQEEYKKEGIE 506
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507 WTFIDFGMDLQACIDLIEKPMRIMSILEEECMFPKATDMTFKAKLYDNHLGKSNNFQKPR 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              825 NWPWMKLYFKIKPLLKSAETEKEMATMK-EEFGR---------VKDALEK 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 MTERLEDEEEMNAELTAKKRKLEDECSELKRDIDDLELTLAKVEKDK------- 967
                                                                                                                                                                                                                                                                                                                                                                                 390 NSADLLKGMCHPRVKVGNEYVTKGQNVQQVSYAIGALAKSVYEKMFN--WMVTR-INATL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DPDLPGALY-NHDNEFLHYQDDW 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                616 LSNLFANY-----AGADAP-VDKGKGKAKKGSSF---QTVSVLHRENLNKLMTNLRST- 664
                                                                                                                                                                                                                                                                                                                                                    188 NECAVSRKKCVPRKSDVGEFPVPDRN-----AVVQNFNMKDFSGKWYITSGLNPT- 237
                                                                                                                                                                                                                                                                                                                                                                                                           238 ------FDAFDCQLHE---FHMENDKLVGNLTWRIKTLDGGFFTRSAVQ 277
                                                                                                                                                                                                                                                                                                         Local Similarity 17.0%; Pred. No. 8.9;
nes 251; Conservative 211; Mismatches 525; Indels 493; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 CTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSV----VDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 MTLFQRLLEGFKELQQDEENFVRELSKEEKE-----ILNELQMEAT-EVEKLFGRA
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                                                                                                                                                                                                                                                                                           1.8%; Score 133.5; DB 1; Length 1934;
17.0%; Pred. No. 8.9;
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                      ALEARKT (IN REF. 2)
                                                                                                                                                                                                                                                    FDBAC58310B0B57D CRC64;
                                          D -> E (IN REF. 2).
T -> TE (IN REF. 2).
E -> Q (IN REF. 2).
DLQAEED -> ALEARKT (IN
                                                                                                   222928 MW;
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1934 AA;
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1273 ISQRAKLQTENGELSRQLDEKEALISQLTRG-----KLTYTQQLEDLKRQL----- 1318
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                                                                                                  1064 SIM-----DLENDKQQLDEKLKKKDFELNALNARIEDEQALGSQLQKKLKELQARIEEL 1117
                                                                                                                                                                                1118 EEEL-EAERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQIEMNKKREAEFQKMRRD 1176
                                                                                                                                                                                                                                               996 PIQSADLRTTGGRSSRPL---SAFRSGFSKGIFDIVPLPSKNELKELTAPLLLKLVGVLA 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EEEVKAKNTLAHALQSARHD-------CDLLREQYEEETEAKAE 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1159 ISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKF 1218
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                                                          824 AVLPESIIPELQTAAQKVG-----RDF----NTFIKTDNTCGPE-----PPLVERL 865
                                                                                                                                                                                                                       ------VRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEAT 935
                                                                                                                                                                                                                                                                                                     EVEKLFGRALPIRKLMAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILP 995
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MEDLINE=90034185; PubMed=2509294;
Bragg T.S., Robertson D.L.;
"Nucleotide sequence and analysis of the lethal factor gene (lef)
                                                                                                                                                                                                                                                                                                                                           1233 NMEQIIKAKANLEKM-----CRT--LEDQMNEHRS-----KAEETQRSVNDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1356 LQCVLSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEE------
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1599 SLDAETRSRNEALRVKKKMEGDLNEMEIQLSHANRMAAEA 1638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
LETHAL FACTOR PRECURSOR (EC 3.4.24.-) (LF).
                                                                                                                                              EKKVEEGERT------IIKEVEEIEEEVEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from Bacillus anthracis.";
Gene 81:45-54(1989).
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P15917;
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KOCHI S.K., SCHIAVO G., MOCK M., Montecucco C.;

Tainc content of the Bacillus anthracis lethal factor.";

Tainc content of the Bacillus anthracis lethal factor.";

FEMS Microbiol. Lett., 124:343-348(1994).

GENTION: ONE OF THE THREE PROTEINS COMPOSING THE ANTHRAX TOXIN,

C. I- FUNCTION: ONE OF THE THREE PROTEINS COMPOSING THAT WHEN ASSOCIATED DEATH. LF IS THOUGHT TO BE A LETHAL FACTOR THAT, WHEN ASSOCIATED WITH PA, CAUSES DEATH. LE IS NOT TOXIC BY ITSELF. PA IS THOUGHT TO BE NOT DEATH. LE SON THE SELF. THEREBY FACILITATING THE INTERNALIZATION OF LF OR FF.

C. I- SUBUNIT: SECRETED ANTHRAX TOXIN IS COMPOSED OF THREE DISTINCT EDEMA FACTOR (EF). NONE OF THESE IS TOXIC BY ITSELF.

C. I- SUBCELULAR LOCATION: SECRETED.

C. I- SUBCELULAR LOCATION: SECRETED.

C. I- SUBCELULAR LOCATION: SECRETED.
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Best Local Similarity 17.2%; Pred. No. 3.4;
Matches 139; Conservative 117; Mismatches 254; Indels 300; Gaps
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Hydrolase; Metalloprotease; Zinc; Toxin; Signal; Repeat; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA-BINDING REGION (POTENTIAL)
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8C16B4D7277310AE CRC64;
                                                                                                   Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO PEPTIDASE FAMILY M34 (ZINC
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Search completed: November 6, 2001, 05:15:32 Job time: 671 sec

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1338 ------EEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRE----- 1379
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MAVATHCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD----LRTTG 1006
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                                                          --NRIQVDSSNP----LSEK--EKEFLKKLKLDIQPYDINQRLQDTG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                      492 ------DNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDNERLKWRIQLSPDTR 543
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                                                                                                                                                                                     430 GLIDSPSINLDVRKQYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATL----
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model November 6, 2001, 05:13:20 ; Search time 119.14 Seconds (without alignments) 1568.027 Million cell updates/sec Run on:

US-09-075-375A-6 7495 1 MALSLHTVFLCKEEALNLYA......MEASEVEKLFGKALPIRKVR 1412 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

425026 Total number of hits satisfying chosen parameters: 425026 seqs, 132305027 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:* 1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:* sp_organelle:*
sp_phage:*
sp_plant:* SPTREMBL_16:* 44... 55... 77... 110... 14... 14... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	040593 nicotiana t	040251 lactuca sat						Ω	O26216 plasmodium	049525 mycoplasma	090337 cvprinus ca	029230 archaeoglob	09s722 arabidopsis	025662 plasmodium	Oghaw4 homo sapien	O9dz84 mus musculu	Oguço Dasmodium	O9qz76 plasmodium	Q9h1d5 homo sapien
ı	ID	040593	040251	039249	Q9SM43	09SJD9	Q9FUS5	095J13	026223	026216	049525	090337	029230	098722	025662	Q9HAW4	090Z84	0900PQ	92Z56	Q9H1D5
	DB	10	10	10	10	10	10	10	S	Ŋ	7	13	П	10	S	4	11	S	2	4
	Query Match Length DB	478	473	462	472	244	289	522	2269	2771	1365	1933	988	1055	1939	1332	2473	1786	1387	1935
æ	Query Match	34.1	33.5	32.4	21.4	17.3	16.3	2.8	2.6	2.2	2.1	2.1	2.1	2.0	2.0	2.0	2.0	2.0	2.0	1.9
	Score	2557	. 2508	2430	1604.5	1300	1219.5	210	194.5	161.5	156	156	155.5	151	151	150.5	148.5	147.5	146.5	146
	Result No.	1	7	٣	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Q03767 saccharomyc Q9vnh4 drosophila Q26024 plasmodium O51465 borrelia bu Q9y6y2 homo sapien		0921vO helicobacte 061201 caenorhabdi 099krl sus scrofa 066583 aquifex aeo	Q49547 mycoplasma Q9dgd5 pennahia ar Q59066 methanococc Q9uqh3 homo sapien Q9sb74 arabidopsis	Q99996 homo sapien Q99212 homo sapien Q9fii7 arabidopsis Q9n2m3 plasmodium	Q9uqq4 homo sapien O60772 homo sapien Q00772 homo sapien Q00756 oryctolagus O23332 arabidopsis
9 2748 3 003767 9 1116 5 09VNH4 9 839 5 026024 2 166 5 051465 9 3899 4 09Y6Y2	2000	9 1819 2 Q9ZLVO 9 5105 5 O61201 9 1935 6 Q9GKRI 9 1002 2 O66583	9 1302 2 Q49547 9 1930 13 Q90GD5 8 800 1 Q59066 9 3595 4 Q9UQH3 9 2712 10 Q9SB74	4 4 C C C C C C C C C C C C C C C C C C	8 3908 4 090004 8 1088 4 060772 8 1109 6 000756 8 1676 10 023332
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241 FDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPGALYNHDNEFLHYQ 300
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                                                                                             RGLNPTFDAFDCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYN 773
                                                                                                                                                HDNEYLLYQDDWYILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPE 833
                                                                                                                                                                                                   LQTAAQKVGRDFNTFIKTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDK 893
                                                                                                                                                                                                               VAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETEC 180
                                          OIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVOKFDMKDFSGKWFIT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bugos R.C., Yamamoto H.Y.;
"Molecular cloning of violaxanthin de-epoxidase from romaine lettuce and expression in Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 93:6320-6325(1996).
EMBL; U31462; AAC49373.1;
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca.
                                                                                                                                                                                                                                                                   421 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 477
                                                                                                                                                                                                                                                       894 EVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLFGRALPIRKL 950
                                                                   181 QIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFIT
    Length 473;
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1B22522DC2C62699 CRC64;
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01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
VIOLAXANTHIN DE-EPOXIDASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.5%; Score 2508; DB 10; Best Local Similarity 100.0%; Pred. No. 4.2e-135; Matches 473; Conservative 0; Mismatches 0;
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InterPro; IPR000566; -.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Led J., Led Z., Li, J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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                                                           DDWYILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVG 360
                                                                                                                                                                                                                       361 RDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLF 420
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORLLEGFKELQQDEENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLR 473
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Pred. No. 1.1e-130;
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Interpro: Toponofic
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462 AA;
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                                                                                               DNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIE 1250
                                                                                                                                                      NKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDN 1310
                                                                                                                                                                                                           1311 TCGPEPALVERIEKTVEEGERIIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELK 1370
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
                                          SRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQLHEFHTEG
                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emanuelsson A.K., Eskling M., Akerlund H.E.; "Cloning and sequencing of Spinacia olercea violaxanthin de-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases EMBL; AJ250433; CAB59211.1; -.
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53658 MW; 12B4C8C69AB61E12 CRC64;
                                                                                                                                                                                                                                                                 1371 QDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 1412
                                                                                                                                                                                                                                                                                 421 QDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 462
                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
VIOLAXANTHIN DE-EPOXIDASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.4%; Score 1604.5; DB 66.4%; Pred. No. 1.1e-83;
                                                                                                                                                                                                                                                                                                                                                                    472 AA
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                                                                                                         1323 EKTVEEGERIIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSK 1382
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                                                                                                                           263 KTPDGGFFTRTAVQKFAQDPSQPGMLYNHDNAYLHYQDDWYILSSKIENQPDDYVFVYYR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence for Arabidopsis thaliana BAC T27G7 from chromosome
                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
12767.23 (FRAGMENT).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantee; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Exassicaceae; Arabidopsis.
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NON_TER 244 244
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InterPro; IPR000566; -.
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MEDLINE=20083487; Pubmed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Moffat K.S.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
                                                                                                                                                                                                                              STRAIN=CV. ZHENHUI-249;
Lin R.-C., Xu C.-C., Li L.-B., Kuang T.-Y.;
"Molecular cloning and expression of rice violaxanthin de-epoxidase.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288196; AAF97601.2;
                                                                                                                                                                                                                                                                                                                                                                                                                               1123 DEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPTFDAFDCQ 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1243 YILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDF 1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1183 LHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDW 1242
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                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
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Welsrycha; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                       Oryza sativa subsp. indica.
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.3%; Score 1219.5; DB 10; Length 289; Best Local Similarity 74.8%; Pred. No. 4.7e-62; Matches 217; Conservative 43; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1363 AEGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR 1412
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                                                                                                                                                                                                                                                                                                                         SEQUENCE 289 AA; 33496 MW; B91C7BBD4CE1770D CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VIOLAXANTHIN DE-EPOXIDASE (FRAGMENT).
                                289 AA
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                                PRELIMINARY;
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                                                                                                                                                                                    NCBI_TaxID=39946;
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"A gene coding for a high-molecular mass rhoptry protein of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      741 LSWRIRTPDGGFFTRSAVQKFVQDPKYP----GILYNH--DNEYLLYQDDWYILSSKVE 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 --WRRR------WTIVD--VS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 DDLSWGLFHYHGAARVAGQSYTGAVLVTPDGSYPAEKDKERLQSALEKCGIKEWELF-AV 487
                                                                                                                                                                                                                                                                                                                                                                      68 PEPPV--KLIALVGKGEVSPLK-STSWEEVMLHTARRLKWVD------EGYEMLVFDD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 E----IVSSNDQRAMN-LTQELNQTDILVVVA--------VNNSESV---- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495 SKLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNL 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 -----NMIQINSKNVKNMIC-----FESSPNLMNRLGG------ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 TDVGSVNKD------KEVTEVVKTVGDAWERRNSDDIRFCLLVIINAYIRPVPVL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 ONLRSK-----GFSTLSCMVKNCGPQILNCLLDPNCRKALQCLNQCS--PVDQVCSYRCI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 659 DLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPSVLVQKFDMKDFSGK------ 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     794 NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLP-ESIIPELQTAAQKVG-RDFNTFIKT 851
                                                                                                                                                                                                                                                                                                                           375 PEPPLVERLEKTABEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                          435 ENFVRELSKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVG 494
                                                                                                                                                                                                  2.8%; Score 210; DB 10; Length 522;
21.1%; Pred. No. 0.0003;
tive 77; Mismatches 186; Indels 194; Gaps
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
Nature 402.761-768(1999).
EMBL; AC007019; AAD20404.1; -
SEQUENCE 522 AA, 59287 MW; 63EF3102F3E96C21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555 SPAHSINQNVPKGNSGCKFPKDVALMV-----WEKWG----QFAKTAIVAIFILSV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 ---ASKADAVDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCG
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 DNCSCENPPL-----GIPQGSRLHSRISIIEEPDSEEK 520
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                                                                                                                                                                                                                                                                   Matches 122; Conservative
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                                                                                                                                                                                                                                           Local Similarity
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A B C	Query Mö Best Loc Matches	Amatch Local Similarity 18.4%; Score 194.5; DB 5; Length 2269; Local Similarity 18.4%; Pred. No. 0.017; nes 255; Conservative 213; Mismatches 436; Indels 483; Gaps	65;	
οy	304	35	2	
QQ	34	YIISNQIKNKINVSTYPEGREGFTSSLELAKSWEKTKLETITELTKSNEETVRL 87		
۶۵ و	356	AKSVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEI 401	-	
3 6	0 0	LDEEAERNI LEGLALELNAKIANI IAKIET VKNIVEL	v	
A 점	136	EBEYVER	വ വ	
Qy	447	E-ILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYV 493	e	
Dp	196		4	
οy	494	54	on.	
QQ	255	YDEISKELNKMLEDFKNKEKELSNKISDYDKKREQL-SEYKSKMLEIRNHYNSQ 307	7	
Οý	550	KGNSGCKFPKDV 577	7	
qq	308	TNVDNTKEEEBAKQNYDKSNEHMTTIPTNEDEISKIISEVKTMKDEILSKVNTYIDFNKKY 367	7	
οy	578	ALMVWEKWGOFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAKCISNPACAAN 637	4	
οg	368	: : : :	S	
ζ	638	68	22	
qq	397	KNSI	2	
οy	989	VGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDAFDCQLHEFHTEE- 734		
QQ	453	KDMLNQNIKTVKETNSIDKS-YIEKFE-QILIGKQIKLENKFTEFSLNNHEANNNEL 507	,	
οy	735	NKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNFYLLYQDDWYILSS 790	0	
QD	508	IKYFSDLKANLGINEENMLYNQFTEKEKTFNDIKEKNIHINEELS 552	~	
οy	791	KVENSPEDYIFGY 814		
QQ	553	: 	0	
٥y	815	84	6	
QQ	613	: :	2	•
δý	850	KTDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEKVRDKEVTLFSKL 901		
QQ	673	SUDNVEGIKKKQQIIVTKIDKKKKNIYEEINKLLSEISKIEKDNTSLEKVKDINLSYGQNL 732	~	
οy	902	MEATEVEKLEGRALPIRKLMAVAT 95	2	
дq	733	GNLFLE-QIDEEKKKAENTIKSMEAYIDDLDNIKKKSQEIETEMDIKMDINKEMEALKIS 791	_	
οy	926	HCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSADLRTTGGRSSRPLSA 101	51	
οp	792	HDDDKKCHDKSKNHKENISDIYDKSSKIIQDFSRESDINDIKNKLQKNVSE 842	01	
οy	1016	FRSGESTAP 1042	12	
qq	843	SQNHNSDINQCLNEVANIYNILKLNKIKKIIDKVKEYTSEIEKNKKNINDELNNSEK 899	Φ.	
ογ		AFLIVPSADAVDALKTCA	66	
QQ Op	900	VIKKIEGDLS	m	

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68;
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                                                                                                                                                                                                                        1083 -IKNEKIHIEDE--VANNDKSNK------AITSIKVSVEPFKTKI 1118
                                                                                                                                                                                                                                                                                           -AVSRKKCVPRKSDLGEFPAPDPSVLVQNFNISDFNGKWYITSGLNPT 1175
                                                                                                                                   1176 FDAFDCQLHEFHTEGDNKLVGNISWRIK-----TLDSGFFTRSAVQKFVQDPNQPGVLY 1229
                                                                                                                                                                                                    1230 NHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLP---- 1284
                                                                                                                                                                                                                                                                    1285 ---NSI-----IPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERIEKTVEEGER 1331
                                                                                                                                                                                                                                                                                                                                        1332 IIVKEVEEIEEEVEKEVEKVGRTEMTLFQR-----LAEGFNELKQDEENFV---RELS 1381
                       939 -NILNEETNITNHFKNAEEYNKIVLSNFNNIEMADNKSQYILEIKKNNGTNDHDYNIKEL 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.2%; Score 161.5; DB 5; Length 2771; Best Local Similarity 16.5%; Pred. No. 1.7; Matches 250; Conservative 269; Mismatches 481; Indels 519; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 YKTSSFSDSSHCKDKSQICSIDTSFEEIQRFDLKRGMTLILEKQWRQFIQLAIVLVCTFV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sinha K.A., Keen J.K., Ogun S.A., Holder A.A.;
"Comparison of two members of a multigene family coding for high-molecular mass rhoptry proteins of Plasmodium yoelil.";
Mol. Biochem. Parasitol. 76:329-332(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green J.L., Holder A.A.; "Structure of the E8 gene encoding a high molecular mass rhoptry protein of Plasmodium yoelii."; Mol. Biochem. Parasitol. 0:0-0(2000).
                                                                                                   998 KSHKDKSNGYKTEADQNKKAIQKNKELFEQYKEEVTVLLNKYYAVELKNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holder A.A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U36927; AAB41263.3; -.
SEQUENCE 2771 AA; 325640 WW; COCCB9AB6E7ACF36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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1100 CNNRPDETEC -- QIKCGDLFENSVVDEFNEC --
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STRAIN-YM;
MEDLINE-97077455; PubMed-8920022;
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SEQUENCE FROM N.A.
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>-	119	IVPRVDAVDALKTCACLLKECRIELAKCIANPSCAANVACLQTCNNRPDETECQIK : :	
Ω >	175	- LKKVDDY IKVC	
r a	952	TINGENSIDKIYIDKFENILIDKKTELETKFTGLSLNNHESNNKELLTYFYDLKANLGK-	
λ	208	PVPDRNAVVQNPNMKDFSGKWYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLD 267	
Q	1011	NKENMLYKQFNEKEKAVEDIKKKNVDINKIVSNIEITIYT 1050	
¥	268	GGFFTRSAVQTFVQDPDLPGALYNHDNEFLHYQDDWYILSS 308	
Q	1051	SIYNINEDTENBIGKSIELLNTKVLEKVKANVTNLN 1086	
<u>ک</u> بخ	309	QIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDFNNFIT 368	
a	1001	ETABRIANDI DEQUE	
չ. գ	369	TONSCGPEPPLYERIAEGEKLLIKEAVELEEFEKKEVEKEVEKRITENTIEV 425 ::	
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Δi	505	-WGWEDYFGSIVVAKICSSRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSP 556	
ą	1315	DESEESYINDIKKELEKNVLESQNNNTDINQYLSKIENIYNILK 1358	
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Δį	844	DFNTF	
ą	1539		
Ϋ́	904	GFKEL	
ą	1584	EDEVAKNNKSNKAILDIQLSVEPFKIKFLKIKDLRTKSDDCLKETK 1629	
λi	961		
ą	1630	DIETKISNLSIDTQETKL-IENKNILNT-LEKLLESLKNQ1667	
λ	1021	SKGIFDI	
q	1668	KKNIEDQKKELDEVNSKIKNIESNVNQHKKNYEIGIVEKINEIAKANKDQ 1717	
ζį	1064	1064 VDALKTCACLLKGCRIELAKCIANPACAANVACLQTCNNRPD-ETECQIKCGDL 1116	

qa	::::
δλ	1117FENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPSVLVQNF 1157
q	- F
δλ	58 NISDFNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSA 121 :: : : : : : : : :
qq	1831 KLNDVNDKFTNEYSKVNKGFDNISNSINNVKKSTDENLLLNILNQTKEMYANIV 1884
Qy	5 VQKEVQDPNQPGVLYNHDNEYLHYQDDWYILSSKIENKPEDYIFVYYRGRNDAWDGYGGA 127 1:
qq	GI 191
δλ	75 VVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDNTGGPEPALVE
Q D	920 DEFKNINIAILPYLDSQKKDILTFIPSPEKIISEITIKISD 193
δο i	333IVKEVEFIEEEVEKEVEKVG
Q	60 SYNTLLDILKRSQELQKKEQQALNLIFENKLLHUNVQAINELADILSDLANNAR ZUI
oy G	1386 EFLDEIKMEASEVEKL 1401
RESULT Q49525 ID 04	11T 10 525 049525 PRELIMINARY, PRT: 1365 AA.
A C	049525;
888	01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
E	LMP1.
SOS	to the second
88	Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
R OX	NCBI_TaxID=2098; [1]
RP P	SEQUENCE FROM N.A.
KX KX	
R R	Jensen L.T., Laderoged S., Birkelund S., Christiansen 5.; "Selection of Mycoplasma hominis PG21 deletion mutants by cultivation
RT	in the presence of monoclonal antibody 552.";
2 Z Z	EMBL; U21962; AAA81013.1; SEDIENCE 1365 AA. 1365 AA. 13692 WW. 847A04992410867F CRC64;
ý o	
ŌĂĬ	Query Match 2.1%; Score 156; DB 2; Length 1365; Best Local Similarity 16.8%; Pred. No. 1.3; Matches 209; Conservative 187; Mismatches 420; Indels 430; Gaps 52;
δλ	272 TRSAVQTEVQDPDLPGALYNHDNEFLHYQDDWYILSSQIENKPDDYIEVYYRGRNDAWDG 331
qq	282 TRNOIQEFINTSKNSYTDS 319
Qy	332 YGGSVIYTRSPILPESII-PNLQKAAKSVGRDFNNFIITDNSCGPEPPLVERLEK 385
qq	320 SNKSDIESANTELKQALAKANADKVQADNLAKSIKEQLNNSVSNANTLSA 369
Óγ	386 TAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVREL 441
qq	370 KLTDKDNTIQQAKTELEKEVQKADQAIKSNNTASMQSAKSSLDAKVAËITKKLETF 425
δy	442 SKEEKEILNELQMEATEVEKLFGRALPIRKLRMALAPHSNFLANHETIKYYVGSKLPGHK 501
qq	

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1125 DLSNFTLNHOKNOFTAKDITPKISLLENKLNEINQYLLPIIKEKAVSKISEIEKN-KKEL 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           956 HCFTSPCHDRIRFFSSDDGIGRLGITRKRINGTFLLKILPPIQSAD-----LRTTGGRS 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-----RPLSAFRSGFSKGIFDIVPL------PSKNEL-KELTAPLLLKLVG 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1102 NRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPD-----PSVLVQ 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1156 NFNISD--FNGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTR- 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1213 --SAVQKFVQDPNQPGVLYNHDNEYLHYQDDW-----YILSSKIENKPEDYIFVYYRGRN 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1010 GIESLOKW-QDLMDDSVLSVDDS----LKDDFNKALRVLVGDYTKNPPVSSWFINKRNRS 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1266 -DAWDGYGGAVVYTRSSVLPNSI-------IPELEKAAKSIGR----- 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1065 IENYQNLRNLILVRENEILLDKAKDLDKRAEKTIKFVDENINSLDQRAKRLKQEILNAKN 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFSTFIR-----TDNTCGPEPALVERIEKTVEEGERIIVKE-----VEEIEEEVEKEV 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1050 VLACAFLIVPSADAV-----DALKTCACLLKGCRIELAKCIANPACAANVACLQTCN 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------KADAIKNNPSSSKQALKDSSQQVQKLGNELLKTITE----EFGKVETKN 907
502 RFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGLQLFSHGKHNLSPAHS-I 560
                          ---ANTLSAKLTDKDN--TIQQAKTE 541
                                                                                                                                                                                                                                                                                         542 LEKE------VQKADQAIKSNNTASMQSAKSSLDAKVAEITKKLETFNKDKEA 588
                                                                                                                                                                                                                                                                                                                                   737 LVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSP 796
                                                                                                                                                                                                                                                                                                                                                                                                                       797 EDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIP-----ELQTAAQKVGRDFNTFIK 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 727 AKVAEITKKLETFNKDKEAKFNELKQTRNQI-----QEFINTNK-------- 765
                                                                                                                                                                                                                                                                                                                                                                                                                                               561 NONVPKGNSGCKFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKE
                                                                                                                         ------ADKVQA----DNLAKS
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                                                                                                                                                                                                                                                    681 PRKSDVGDFPVPDPSVLVQKFDMKDFSGKWFITRGLNPTFDA----FDCQLHEFHTEENK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 TDNTCGPEPPLVERLEKKVEEGERTIIKEVEEIEEEVEK-----
                                                                                                                                                                                                        510 IKEQLNNSVSN-----
                                                                                                                      490 KQALAKAN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-97176447; PubMed-9023993; Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.; "CDNA cloning of myosin heavy chain isoforms from carp fast skeletal muscle and their gene expression associated with temperature
                                                                                                    Cyprinus carpio (Common carp).

Cyprinus carpio (Common carp).

Cypring Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.

NCBI_TaxID=7962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirayama Y., Watabe S.; "Structural differences in the crossbridge head of temperature-associated myosin subfragment-1 isoforms from carp fast skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1933;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN HEAVY CHAIN.
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17.0%; Pred. No. 2.1;
tive 181; Mismatches 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 246:380-387(1997).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=FAST SKELETAL MUSCLE;
MEDLINE=97352533; Pubmed-9208928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 181;
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J. Exp. Biol. 200:27-34(1997).
EMBL; D89990; BAA22067.1; -.
EMBL; D504/4; BAA69067.1; -.
HSSP; P08799; 1LVK.
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J. Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gooayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1071 ACLLKGCRIELAKCIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAV 1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SILEKILSEINQALRDVEKREGDLTREAAGIQAQLKKAEE 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Mismatches 221; Indels 221; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
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886 AA; 103633 MW; D35641D499AA8B58 CRC64;
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Interpro; IPR002017; ...
Interpro; IPR003439; ...
Pfam: PF00470; RecF; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                  Nature 390:364-370(1997
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                                                                                                                                                                                                                                                Venter J.C.;
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FPVPDPSVLVQKFDMKDFSGKWFITRGLNPTF-----DAFDCQLHEFHTEENKLV--- 738
                                                                                                                                                                                                                ------NPTFLNVLVDQSGVERQVLAENYEEGKAVAFG 593
                                                                                                                                                                                                                                                                  ---GNLSWRIRTPDG-GFFTRSAVQKFVQD-PKYPGILYNHDNEYLLYQDDWYILSSKVE 793
                                                                                                                                                                                                                                                                                                                                                               NSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDN 853
                                                                                                                                                                                                                                                                                                                                                                                                          NE----INQCMRRKREAEENLEELELKVRQLKKHRSQAEKVLTTKELEMHDLK-----N 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                            854 TCGPEPPLVERL-EKKVEEGERTIIKEVEEIEEE---VEKVRD--KEVTL----FSKLFE 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 VERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQD---EEN 436
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                                                                      630 SNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVS-RKKCVPRKSDVGD
                                                                                                                   -----TLRGCANEANYRNLKI-----IIYDFSRPRLNIPRHMVPQTEHPTI
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Best Local Similarity 17.5%; Pred. No. 4.1;
Matches 189; Conservative 167; Mismatches 299; Indels 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium chabaudi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Werner E.B., Taylor W.R., Holder A.A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U43145; AAC63403.1; -
SEQUENCE 1939 AA: 229001 MW; B35E462001C6F22F CRC64;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 07, Last annotation update)
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265 IEMLD------SKLIEKEENFAN------
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                  555 FSVIDSD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AILTALCIAFGCRARGTQRAATLKDFIKTGCSYAVVQVEMKNSGEDAFKSEIYGGVIIIE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 SVVDQFNECAVSR----KKCVPRKSDVGEFPVPDRNAVVQNFNM-------KDFSGK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WYITSGLNPTFDAFDCQLHEFHMENDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYI-----LECK----GN-----SSSFLRNLLQ---QVNDLLQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALYNHONEFLHYQDDWYILSSQIEN--KPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIYEHLTKATAIVD------ELENTIKPIEKEISELRGK-------IKNMEQV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESIIPNLQKAAK-----SVGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEIAQRLQQLKKKLAWSWVYDVGRQ------LQEQTEKIVKLKERIPTCQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVEIEEEVEKEVEKVRDT-----LQQD 433
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                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brasslcaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 FNHKCNYVQKIKDRVRRLERQVGDINEQTMKNTQAEQSEIEEKLKYLEREVEK-----
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MEDLINE=99380167; PubMed=10449416;
Mengiste T., Revenkova E., Bechtold N., Paszkowski J.;
"An SMC-like protein is required for efficient homologous recombination in arabidopsis.";
EMBO J. 18:4505-4512(1999).
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SEQUENCE 1055 AA; 121349 MW; E9F0C0427FB602E4 CRC64;
                                                                                                                                                                                       (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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Matches 182; Conservative 119; Mismatches 306;
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                                                                                                                                            PRT; 1055 AA
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EMBL; AF120932; AAD54769.1;
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01-MAY-2000 (
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Q9S722;
                                                                                          RESULT 13
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: : : : : KENEIIIEKLKDIESRE	HEFHTEENKLVGNL : :: : ::	NTLKSDLSKNACQMEVYKLEIKD ILSSKVENSDEDVIEVVYKGBND	LESKVENSPEDILFY : : KINNMKEKLSSI	TFIKTDNTCGPEPF : LEIE	LFSKLFEGFKELQR 	VATHCFTSPCHDRI : : NDKI	LSAFRSGFSKGIFD	LLKGCRIELAKCIA	EFNECAVSR : EIEKKYKNEIFMLE	DAFDCQLHEFHTEG :: : EMKEFY	EYLHYQDDWYILSS : : GLIKQIDELNIQKI	AAKSIGRDFST-FI : IKGSDLVDFVTAYI	VGRTEMTLFQRLAEGFNE :	15 15 691AW4 PRELIMINAR O9HAW4 PRELIMINAR O9HAW4; O9HAW4; O1-MAR-2001 (TrEMBLrel O1-MAR-2001 (TrEMBLrel O1-MAR-2001 (TrEMBLrel HU-CLASPIN, Homo sapiens (Human). Bukaryota; Metazoa; Ch Mammalia; Eutheria; Pr NCBL_TAXID-9606; SEGUENCE_FROM N.A. MEDLINE=21000493; Pubm MEDLINE=21000493; Pubm Kumaqai A., Dunphy W.G ONA replication checkp Mol. Cell 6:839-849(20 EMBL; AF297866; AAG245 EMBL; AF297866; AAG245 EMBL; AF297866; AAG245 EMBL; AF297866; AAG245 EMBL; ARSQ245 EMBL; ARSQ245 AA; AA; AA; AA; AA; AA; AA; AA; AA; AA
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                                                                                                                                                                                                                                                                                                   186 LKKKETKNQEDDVEQPFNDSGCLLVDKDLFETGLEDENNSPLEDEESLESIRAAVKNKVK 245
                                                                                                                                                                                                                                                                                                                                        440 ELSKEEKEILNELOM--EATEVEKLFGRALPIRKLRMA--LAPHSNFLANHETIKYYVGS 495
                                                                                                                                                                                                                                                                                                                                                                       246 KHKKKEPSLESGVHSFEEGSELSK--GTT---RKERKAARLSKEALKQLHSETQRLIRES 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               609 DALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDE 668
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                                                                                      307 SSQIENKPDDYIFVYYRGRN------DAWDGYGGSVIYTRSPTLPESIIPNLQKA 355
                                                                                                                             83 SAEEENKEN----LYAGKNTKIKRIYKTVADSDESYMEKSLYQEN--LEAQVKPCLELS 135
                                                                                                                                                                     356 AKS-VGRDFNNFITTDNSCGPEPPLVERLEKTAEEGEKLLIKEAVEIEEEVEKEVEKVRD 414
                                                                                                                                                                                                    -----TEMTLFQRLLEGFKELO-QDEE-----NFVR 439
                                                                                                                                                                                                                                                                                                                                                                                                                            496 --KLPGHKRFSWGWEDYFGSIVVAKICSSRRIPRYFRKSPRICCGLDSRGL----QLFS 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 ALNLPYH---------MPENKTIHDFFKRKPRPTCHGNAMALLKSSKYQSS 342
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Query Match 2.0%; Score 150.5; DB 4; Length 1332; Best Local Similarity 19.3%; Pred. No. 2.6; Matches 255; Conservative 182; Mismatches 405; Indels 477; Gaps
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